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### Remarks:

The applicant has subsequently filed a sequence  
listing and declared, that it includes no new matter.

## (54) Genomic DNA sequences of *Ashbya gossypii* and uses thereof

(57) The present invention relates to the terminal sequencing of random genomic fragments performed with the filamentous fungus *A. gossypii*, to the sequences obtained therewith and the use of the sequences for forensic identification, to characterize genes and gene organization of this ascomycete by inter-genomic comparison, to identify biosynthetic genes that can be used as selection markers, to isolate promoters and terminators

for application in a homologous as well as heterologous context, to find putative centromere containing clones, chromosome mapping, chromosome identifying, general information about chromosome organization and in addition to identify ORF containing SRS sequences with no homology to *S. cerevisiae* or any other organism which allows the identification of *A. gossypii* specific genes.

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## Description

The present invention relates to genomic DNA sequences obtained from terminal sequencing of random genomic fragments of the filamentous fungus *Ashbya gossypii* and uses thereof.

The phytopathogenic fungus *Ashbya gossypii* is a filamentously growing ascomycete that was first isolated as a plant pathogen in tropical and sub-tropical regions. It infects the seed capsule of cotton plants (Ashby S.F. and Nowell W. (1926) Ann. Botany 40: 69-84) and has also been isolated from tomatoes and citrus fruits (Phaff H.J. and Starmer W.T. (1987) In "The Yeasts", Vol. I Rose A.H., Harrison, J.S. (eds), Academic Press, London, 123 ff; Dammer K.H. and Ravelo H.G. (1990). Arch. Phytopathol. Pflanzenschutz, Berlin 26: 71-78 Dammer and Ravelo, 1990). The infection of the seed capsule is caused by transmission of *A. gossypii* mycelium pieces or spores by stinging-sucking insects and causes a disease called stigmatomycosis.

Studies characterising the karyotype of *A. gossypii* have been performed (Wright, 1990; Wendland, 1993; Gaudenz, 1994, "The small genome of the filamentous fungus *Ashbya gossypii*. Assessment of the karyotype", Diploma Thesis, Department of Applied Microbiology, Biocenter, University Basel). It has been found using yeast chromosomes of precisely known length as size markers that the genome of *A. gossypii* has a total nuclear genome size of 8.85 Mb.

*A. gossypii* is systematically grouped to the endomycetales belonging to the family of sperophthoraceae (Lodder J (1970) General classification of the yeasts. In: "The Yeasts", Lodder J. (ed.), North Holland Publishing Company, Amsterdam-London, 1ff Lodder, 1970). This classification is based on the observation that the spores that develop in hyphal compartments called sporangia look like ascospores, which are defined as endproducts of meiosis (Muller E. und Löffler W. (1971) Mykologie. Grundriß der Pilzkunde. DTV-Thieme, Stuttgart, 37 ff). However, in several respects, *A. gossypii* more closely resembles the budding yeast *Saccharomyces cerevisiae* than other filamentous fungi. For example, homologous recombination has been found to be the main mode of integration of transforming DNA (Steiner S. (1991). Diplomarbeit, Institut für Mikro- und Molekularbiologie der Justus Liebig Universität Gießen Steiner *et al.*, 1995), which is in contrast to findings made in many other filamentous fungi (reviewed by Fincham J.R.S (1989) Transformation in fungi. Microbiol. Rev. 53 (1): 148-170).

Additionally, sequence analysis of the *A. gossypii* *TEF*, *LEU2* and *THR4* genes (Altmann-Jöhl and Philippsen, 1996; Mohr, May 1997; Steiner and Philippsen, 1994) has identified high sequence homology to their functional homologues in *S. cerevisiae*. In addition, for the latter genes, syntenic (positionally conserved) arrangement of adjacent homologous ORF's has been found. The growing number of completely sequenced reference genomes, such as for example *S. cerevisiae*, offers new prospects for rapid comparative gene and genome analysis of so far less characterized organisms, such as *A. gossypii*, in parallel or even before the application of genetic techniques.

In view of the above, the present invention provides genomic DNA sequences obtained from terminal sequencing of random genomic fragments of *Ashbya gossypii*. The present invention particularly relates to genomic *A. gossypii* DNA sequences that are obtainable from the series of clones listed in Table 1 and presented in the attached Sequence Listing. Some of these *A. gossypii* sequences are homologous to *S. cerevisiae* sequences and to sequences from other filamentous fungi, e.g. ORF's specifically required for growth in filamentous fungi. Others of these *A. gossypii* sequences, such as those set forth in Table 2, have no homology to *S. cerevisiae* sequences, including sequences which have no homology to known sequences from any other fungus. The sequences of the invention find particular use in forensic identification, chromosome mapping, chromosome identification, and tagging of genes of known and useful function. Procedures such as these can easily be carried out by those of ordinary skill in the art.

The present invention also concerns chimeric genes comprising the sequences of the invention, recombinant vectors comprising such chimeric genes, wherein the vectors are capable of being stably transformed into hosts, as well as hosts stably transformed with such vectors. Preferred hosts are fungi such as *A. gossypii* as well as bacteria.

Furthermore, the present invention relates to the identification and characterization of *A. gossypii* ORF's based on the high homology of primary structures in *A. gossypii* and *S. cerevisiae* and the sequences obtained therewith. The present invention also relates to the use of the *A. gossypii* sequences provided in the Sequence Listing to characterize genes and gene organization of this ascomycete by inter-genomic comparison, to identify biosynthetic genes that can be used as selection markers, to isolate promoters and terminators for application in a homologous as well as heterologous context, to find putative centromere containing clones, general information about genome organization and in addition to identify ORF's containing single read sequences (SRS) with no homology to *S. cerevisiae* or any other organism, which allows the identification of *A. gossypii*-specific genes.

Encompassed by the present invention is a method of sequencing the termini of randomly picked *A. gossypii* shotgun clones to obtain linked pairs of genomic sequences. Said linked pairs of genomic sequences can be used for identification of open reading frames (ORFs) showing or lacking homology to functionally characterized or uncharacterized genes from *S. cerevisiae*, other fungi or other organisms. The sequence information provided herein in the attached Sequence Listing is sufficient to generate gene deletions in *Ashbya* by using, for example, by PCR-based gene targeting methods as described herein.

One of the main prerequisites for success in such an analysis is a relatively compact, organized genome. This is

required to obtain a maximum of information from the limited length of single read sequence (SRS) analysis. *A. gossypii* represents such a compact genome. The presence within the *Ashbya* genome of short intergenic regions and rare occurrence of introns increases the probability of finding matches to open reading frames (ORF's) in the majority of SRS's.

Thus one embodiment of the present invention is a method to identify and characterize *A. gossypii* ORF's by sequence comparison of their *S. cerevisiae* homologues without the requirement of complete sequence information for the *A. gossypii* ORF's.

Further encompassed by the invention is a method for characterization of an *Ashbya* gene, the knockout of which leads to a non-growth phenotype.

In a specific embodiment of the invention a method for characterization and validation of an *Ashbya* gene is provided comprising

- (a) inserting into *Ashbya* sequences of genomic pAG clones as provided herein in the attached Sequence Listing a chimeric gene construct comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector;
- (b) selecting clones carrying *Ashbya* sequences disrupted by the selection marker gene in a suitable host system;
- (c) transforming *Ashbya* with a disruption cassette according to (a);
- (d) revealing the disrupted open reading frame by DNA sequence analysis around the site of integration of the selection marker module and determining the orientation of the selection marker module;
- (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.

A further embodiment of the invention relates to a method for characterization and validation of an *Ashbya* gene comprising

- (a) designing cassette for gene targeting comprising terminal Short Flanking Homology regions encompassing a selectable marker module;
- (b) transfecting the gene targeting cassette of (a) into *A. gossypii* and selecting transformants;
- (c) verifying correct gene targeting by applying suitable testing procedures;
- (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.

Further comprised by the present invention is a method for characterization and validation of an *Ashbya* gene involving a triple selection marker module which method comprises

- (a) inserting of a reporter, a selectable marker and a strong promoter, which is preferably a regulatable promoter, in front of the start codon of a coding sequence of interest (promoter exchange mutant) within the *Ashbya* genome
- (b) applying potential antifungal agents for growth to the promoter exchange mutant of (a) and to a wild-type strain, respectively;
- (c) identifying a growth or non-growth phenotype of the strong promoter exchange mutant.

Within this novel process any DNA encoding a selectable marker can be used that, upon transformation, is capable of conferring a resistance phenotype to *A. gossypii* or any other advantage based on which the transformant can be separated from non-transformed clones such as, for example, ScLEU2, kanMX, kanSC or GEN3.

Promoters that can be suitably used as part of the triple selection marker module are those that are capable of functioning in *Ashbya* and in heterologous systems such as, for example, *S. cerevisiae* or *K. lactis*. Preferred within this invention is a heterologous promoter from *S. cerevisiae* or *K. lactis*, which is not only to be qualified as a strong promoter also within the *Ashbya* system but is also well regulatable in *Ashbya*.

A reporter that can be suitably used within the triple selection marker module is one that is easily detectable such as, for example, the green fluorescent protein.

If the activity or expression of the gene product is inhibited by one or more agents, the inhibitory effect for growth will be overcome in the strain overexpressing the gene product. If the reporter expression, controlled by the wild-type promoter, is not changed one can conclude that the agent inactivates the gene product and not a transcription factor or signaling factor for expression of the gene product. If the reporter expression is much lower, the agent most likely affects the expression of the gene product and not the gene product itself.

The present invention further relates to a DNA molecule comprising a DNA sequence selected from the attached Sequence Listing which molecule is validated as a potential target in a pesticide screen based on the use of said molecule in a gene disruption method as described herein.

Further encompassed by the present invention is the use of sequences selected from the attached Sequence Listing to identify substances having antifungal activity; the use of sequences selected from the attached Sequence

Listing to identify substances having pesticidal activity; the use of sequences selected from the attached Sequence Listing to identify biosynthetic genes that can be used as selection markers; the use of sequences selected from the attached Sequence Listing to identify promoter and terminator regions including downstream non-translated regions and up-stream nontranslated regions, respectively; the use of sequences selected from the attached Sequence Listing to identify putative centromere-containing clones; the use of sequences selected from the attached Sequence Listing to identify ORFs containing SRS sequences with no homology to *S. cerevisiae*; the use of sequences selected from the attached Sequence Listing to identify ORF's containing SRS sequences with no homology to any other organism, which allows the identification of *A. gossypii*-specific genes; the use of sequences selected from the attached Sequence Listing to characterize genes and gene organization of this ascomycete by inter-genomic comparison; and the use of sequences selected from the attached Sequence Listing to identify and characterize the genome organization of *Ashbya gossypii*.

In particular, the present invention encompasses the use of a DNA sequence selected from the Sequence Listing to identify *Ashbya gossypii* promoter and terminator regions including downstream non-translated regions and up-stream nontranslated regions, respectively.

The invention further relates to the use of a DNA sequence selected from the Sequence Listing wherein a putative promoter region is identified by sequence alignments and the ORF of a genetic selection marker plus start codon and terminator is placed downstream of said putative promoter region.

Further comprised is the use of an a DNA sequence selected from the Sequence Listing and variants thereof in a screening method for identifying compounds capable of inducing broad spectrum disease resistance in plants.

The suitability of the DNA sequence to be used in such a screening assay is determined in gene disruptions in the *Ashbya* genome. For that purpose a disruption cassette may be used comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector.

In a further embodiment of the invention a DNA sequence selected from the Sequence Listing or parts thereof is used within a gene targeting procedure involving short target sequence homologies added to both ends of a DNA molecule encoding a selectable marker.

In a further embodiment according to the invention a DNA sequence selected from the Sequence Listing may also be used for distinguishing among different species of plant pathogenic fungi and for distinguishing fungal pathogens from other pathogens such as bacteria.

It is one embodiment of the present invention to use sequences selected from the attached Sequence Listing to identify promoter and terminator regions including downstream non-translated regions and up-stream nontranslated regions, respectively. In many cases, the attached sequences allow to locate the precise boundaries between open reading frames and promoter or terminator regions either from the first single read or after additional sequencing. The promoter and terminator regions so obtained are also part of the present invention.

In particular, sequence alignments can reveal 5' ends of open reading frames plus adjacent sequences of their putative promoter regions. By placing the ORF of a genetic selection marker plus start codon and terminator downstream of this putative promoter sequence, one can identify and use novel *Ashbya gossypii* promoters.

The promoter and terminator regions so obtained are also part of the present invention.

The DNA sequences provided in this application are especially suitable to be used in gene disruptions in the *Ashbya* genome. This can be performed, for example, using classical procedures involving gene disruption cassettes.

Said gene disruption cassettes essentially consists of a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector. This transformation selection module upon expression of the selection marker gene preferably leads to resistance in yeast and filamentous fungi and also in bacteria such as, for example, *E. coli*. This module is inserted into *Ashbya* sequences of genomic pAG clones as provided herein in the attached Sequence Listing. To this purpose the selectable marker is released from the cloning vector by cleavage with a suitable restriction enzyme such as, for example, BamHI, Sall or XhoI. It is ligated into cloned *Ashbya* DNA cleaved with a corresponding restriction enzyme that is, for example either BglII, XhoI (partial) or Sall (partial), respectively. Clones carrying *Ashbya* sequences disrupted by the selection marker gene are selected in a suitable host system such as, for example, *E. coli*. DNA sequence analysis around the site of integration of the selection marker module (i1 and i2sequences in the attached *Ashbya* data base) reveal the disrupted open reading frame and determine the orientation of the selection marker module.

A selection marker that is especially suited to be used within the scope of the present invention is kanMX0 expressing G418 resistance in yeast and filamentous fungi and kanamycin resistance in *E. coli* (International Patent Application No PCT/EP 91/01116; Steiner *et al*, 1995).

Especially preferred within the scope of the present invention is a new PCR-based *Ashbya* gene targeting procedure provided herein. Gene targeting in *Ashbya* relies on homologous recombination in this fungus (Steiner *et. al.*, (1995) Genetics (in press 1995)). Short target sequence homologies added to both ends of a DNA molecule encoding a selectable marker are sufficient to mediate sequence specific gene targeting in *Ashbya*. The length of the target sequence homologies is preferably in the range of between about 20 to 80 nt, more preferably between 35 and 60 nt,

and most preferably is about 45 nt. Within this novel process any DNA encoding a selectable marker can be used that, upon transformation, is capable of conferring a resistance phenotype to *A. gossypii* or any other advantage based on which the transformant can be separated from non-transformed clones.

The fragment designed for gene targeting thus carries terminal Short Flanking Homology regions encompassing the selectable marker module. These fragments are transfected into *A. gossypii* by a suitable method such as, for example, electroporation and transformants are selected. Verification of correct gene targeting is achieved by suitable testing procedures such as, for example, PCR testing the presence of the new junctions between target DNA and integrated marker using specific verification primers. Verification of the gene targeting can also be performed by DNA-hybridization experiments.

In using verification primers it proved advantageous to use specific primer pair combinations. One pair of verification primers, for example, may be derived from the open reading frame of the selectable marker gene. Whereas a second pair of primer sequences can be derived from the single read sequence and correspond to regions upstream and downstream, respectively, of the homology regions used for the targeting process. Using this PCR-based targeting approach sequences can be manipulated that are app. 150 nt in length. A criterium matched by all single read sequences of the attached *Ashbya* database. This is of major advantage considering classical methods of gene disruption that are laborious and require cloning steps to incorporate a selectable marker within rather large flanks of surrounding target sequence homology.

After clonal purification (spore isolation) it can be easily determined whether deletion/insertion at the targeted locus results in any phenotypic alterations such as, for example, a reduction or abolition of fungal growth, decrease or loss of viability, etc. Once such a phenotypic alteration can be established for one of the *Ashbya* disruption or knockout mutants it is further examined whether said mutant qualifies as a target to be used in a pesticide screen, preferably a fungicide screen.

Owing to the provision within the scope of this invention of a novel and powerful gene disruption process, there is no longer a need to know the exact biological function of the protein product encoded by a gene comprising or, in the alternative, being flanked by one of the *A. gossypii* DNA sequences provided herein.

Those sequences that have no homology neither to *S. cerevisiae* nor to any other organism and are thus *A. gossypii* specific are especially useful, as they are promising candidates to be used in a pesticide screen for identifying substances which have pesticidal and, preferably, fungicidal activity, but are non-toxic to other organisms especially mammals. Though nothing is known about the exact biological function of the genes comprising said DNA sequences or being flanked by said DNA sequences, they are nevertheless especially valuable owing to their being unique to the fungal pathogen. Thus, any pesticidally active substance being identified in a pesticide screen involving one or more of those sequences have a high potential of exhibiting a biological activity that only affects *A. gossypii* and possibly other pathogenic fungi having (yet unidentified) homologous sequences, but do not interfere with any vital functions in other organisms such as, for example, mammals.

It is thus a further embodiment of the present invention to identify genes within the *A. gossypii* genome which are potential targets for the action of pesticidally active compounds, but especially fungicidally active compounds, by using those *Ashbya* sequences identified in the Sequence Listing corresponding to ORF's with 100 and more codons showing less than 20% homology to a yeast gene classified as 3 or as "none".

#### ABBREVIATIONS

LIPS    Linked Pairs of Sequences  
MCS    Multi Cloning Site  
ORF    Open Reading Frame  
SRS    Single Read Sequence  
RP    Reversed Primer  
UP    Universal Primer

#### DESCRIPTION OF TABLE 1 AND THE SEQUENCE LISTING

The sequences in the Sequence Listing correspond to the PAG names in Table 1. Thus, Table 1 describes each sequence in the Sequence Listing in six columns: "PAG name", "Yeast", "Gene Name", "Brief Description", "Homology Class", and "Additional Comments", the details of which are as follows:

PAG Name: Number of *Ashbya gossypii* plasmid clone (e.g. PAG1001) followed by RP (sequence obtained using the reverse primer) or by UP (sequence obtained using the universal primer) or 11 or 12 (internal sequences obtained after insertion of kanMX0 in the *Ashbya* DNA at a BglII, XhoI or BamHI site and sequencing in both directions from these sites using sequencing primers binding to the 5' and 3' region of kanMX0). CRP and CUP mark sequences from rare chimeric genomic clones, the ends of which map to different genomic regions. For a few clones, only RP or UP

sequences are listed. 5% of the plasmid clones carry ribosomal DNA sequences, as concluded from high sequence homologies of their RP and UP sequences to ribosomal DNA of *S. cerevisiae*. These overlapping clones representing tandem copies of the 8.2 Kb *Ashbya* ribosomal DNA repeat are not listed in the *Ashbya* genome data base. The PAG name is set out above each individual sequence in the Sequence Listing.

Yeast name: Systematic name of *S. cerevisiae* gene with highest homology to the *Ashbya* sequence, as determined by the search algorithm. For some *Ashbya* sequences, two systematic names are listed because they carry information from two *Ashbya* ORF's with homology to *S. cerevisiae* genes. Sequences of high (significant) homology are distinguished from those with low (insignificant) homology by the classification in column 5 (Homology Class). If no systematic gene name is listed, the *Ashbya* sequence shows either no homology to *S. cerevisiae* genomic DNA or it is mitochondrial DNA (around 80% AT base pairs and homology to genes coded by the mitochondrial genome).

Gene name: *S. cerevisiae* gene name used in the literature.

Brief Description: Brief description of the *S. cerevisiae* gene showing highest homology to the *Ashbya* sequence.

Homology Class (HC): Significant homologies to *S. cerevisiae* genes are classified as 1. Intermediate homologies (about one quarter to one third identity on the amino acid level) are classified as 2. ORFs with 100 and more codons showing less than 20% homology to a yeast gene are classified as 3. *Ashbya* sequences lacking ORF's of 100 and more codons and showing less than 20% sequence homology to *S. cerevisiae* are classified as 4.

Additional Comments: Useful comments concerning (a) presence of promoter or terminator sequences as judged by the presence of 5' ends (N-terminus) and/or 3' ends (C-terminus) of ORF's and adjacent DNA, (b) identification of novel *Ashbya* ORFs (minimum size in nucleotides (nt) as only ORF in frames +1 to +3 or -1 to -3 and lacking significant homology to yeast and fungi, (c) syntenic, (d) reason for changes of ORF classification, (e) matches to tRNA genes, (f) presence of intron, judged from interruption of regions of high level of protein homology and confirmed, in addition, by applying the *S. cerevisiae* intron-recognition rules, (g) high CAI (codon adaptation index) marking a well expressed gene and with that a strong promoter. Further abbreviations are explained in the MIPS yeast data base.

## EXAMPLES

### Example 1: Construction of a Genomic Library

#### A.) Preparation of Partially Digested DNA

Genomic DNA of *A. gossypii* (strain ATCC10895) was partially digested with *Sau3A* and separated on a low melting agarose gel. Two regions were cut out off the gel: A first the gel piece containing DNA fragments in the range of 3.5-6 kb in length and the second gel piece from containing DNA fragments in the range of 5-8 kb in length.

#### B.) Ligation and Cloning (standard procedures and media as described in Sambrook et al Cold Spring Harbor Press, 1989)

*Sau3A* fragments of different sizes, derived from the partial digestion of the genomic DNA, were cloned into the yeast shuttle vector pRS416 (Sikorski and Hieter, 1989, Genetics 122: 19-27). For this purpose pRS416 was cut with *Bam*HI. The 5'-phosphate group of the linearized vector (4.8 kb) was removed with Calf Intestinal Phosphatase to minimize the recircularization of the vector during ligation. DNA of the two size fractions, one with fragments in the range of 3.5-6 kb and the other with fragments in the range of 5-8 kb were cloned separately into the vector. The ligation samples were separately transformed into the *E. coli* strain XL1-blue yielding together approximately 21,500 colonies on 55 plates. 80 % of the colonies (17,000) were white indicating insertion of a *A. gossypii* DNA. The 21,500 colonies derived from the two size fractions were combined by washing each plate with 2 ml full medium (2\*YT). Approximately 120 ml cell suspension were obtained. 100 ml of the cell suspension were used to inoculate once a 1 litre culture for the isolation of plasmid DNA. The remaining 20 ml cell suspension were mixed with 5 ml glycerol and stored divided into two aliquots at -70 °C. The ratio of white to blue colonies stayed stable after growth in selective full medium ON. The isolated plasmid DNA was purified over a caesium chloride density gradient and separated on agarose gel. The total yield of plasmid DNA isolated from the 1 litre culture was approximately 5 mg.

All plasmids of the genomic library had a common structure based on plasmid pRS416. The average insert length was approximately 4 kb. The genomic library with 17,000 recombinant clones carrying an insert therefore covers 8 times the 9.7 Mb *A. gossypii* genome (Gaudenz, 1994).

## Example 2: Sequence determination

## A.) Sequencing the partial Sau3A fragments at both ends

Approximately 350 to 450 ng of plasmid DNA was taken for cycle sequencing (T3 and KS primer or similarly binding primers) with the Peikin Elmer AmpliTaq FS PRISM™ Ready Reaction Dye Terminator Cycle Sequencing kit using the protocol of the manufacturer (addition of 1% DMSO to the sequencing reaction, 95 °C denaturing temperature) and the 373A automated sequencing system (Perkin Elmer) for electrophoresis and fragment detection. SRS's were named with the plasmid name and the suffix UP or RP was added to mark the side of the insert from which the sequence was derived regardless, of which primer present at this side of the multiple cloning site was actually used.

## B.) Sequence processing

Concerning the pAG1001 to pAG1000 and 1201 to 1700 series of clones, the vector part of the sequences was removed, obvious base-calling errors were edited and, depending on the quality of the sequence, an individual end point was determined. SRS of the pAG1001 to pAG1100 and 1201 to 1700 series were not further edited and were taken as provided. All sequences were transferred on a VAX system and put into GCG format. Query sequences were translated in all six reading frames and run in a BLAST search (Altschul *et al.*, 1990) against MIPS data base at <http://www.mips.biochem.mpg.de/mips/yeast/>

Alignment of sequences from mitochondrial or rDNA clones was performed with the SeqMan module of the Lasergene software package (DNASTAR, Ltd., London, UK) on a Macintosh Power PC.

## Example 3: Classification of the BLAST search results

In the evaluation of the BLAST results, four different categories of homology class (HC) were used. HC 1 and 2 represent SRS's showing a significant hit to an *S. cerevisiae* ORF. The border between category 1 and 2 was made at approximately 40 % identity in the aligned protein sequences. SRS's showing no convincing homology (around 20 % identity and lower) but with an possible open reading frame (with or without ATG) of at least 300 nt length were assigned to HC 3. All SRS's with no significant homology and no possible open reading frame of at least 300 nt were put into HC 4. However, the described values for classification were not applied as strict rules. Factors such as length of homologous block, in cases of several blocks the overall homology, relation of scoring hit to possible open reading frames, position of homologous block within the *S. cerevisiae* protein sequence (for example very N- or C-terminus), a biased sequence, etc. were taken into account for classification.

Almost 30% of the clones listed in the attached Sequence Listing show synteny with *S. cerevisiae*. Thus, *Ashbya* genes of interest for antifungal screening assays (e.g. homologues of essential fungal or yeast genes) can be found due to positional conservations (synteny) when RP and/or UP sequences match adjacent *S. cerevisiae* homologues. Applying the rules of ancient synteny, the frequency of such predictions increases by a factor of 2 or even more.

Over 5% of RP and UP sequences identified open reading frames of 100 and more codons with no apparent homology to sequences in data bases. In Table 1, they are marked as class 3 or 4. These sequences are therefore candidates for novel lead target genes. Fungal pathogens (e.g. *Candida albicans* or phytopathogenic fungi) carrying homologues of these genes can be treated by compounds which were developed based on assays using the *Ashbya* I ad target.

Example 4: Use of the *Ashbya gossypii* sequences for isolation of *Ashbya gossypii* promoters

Sequence alignments can reveal 5' ends of open reading frames plus adjacent sequences of their promoter regions. By placing the ORF of a genetic selection marker plus start codon and terminator downstream of this promoter sequence, one can identify and use novel *Ashbya gossypii* promoters. For example, an ORF of 67 amino acids was identified on the SRS of pAG1245rp. This ORF shows 98 % homology to the *S. cerevisiae* Ribosomal Protein S28.e. 12 in a BLAST search (Altschul *et al.* (1990) J. Mol. Biol. 215: 403-410). The ORF (AgRPS33B) for the putative *A. gossypii* Ribosomal Protein is located from 195 to 395 on the SRS with 700bp, leaving 300bp for the promoter. Based on these findings plasmid pAG1245 may be used for isolation of a novel promoter using the AgLEU2 marker in PCR-targeted gene exchange in *S. cerevisiae*.

## A.) PCR synthesis of a DNA fragment carrying the AgLEU2 marker

Two primers, RP5 and RP3, are selected for the amplification of the AgLEU2 gene. Both primers are 60 mers showing beside 20 bp homology to AgLEU2 in addition to 40 bp homology to pAG1245.

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Primer RP5: 5'TTT TAC TAG ATA TTT TAT ATC CAA GAA GCA ATA GAT CAA AAT GGC TGC GGT AAA GAG AAT 3'. The 40 bp at the 5'end of RP5 are homologous to 40 nucleotides in front of the ATG start codon of AgRPS33B. The 20 bp at the 3' end of RP5 are homologous to the first 20 nucleotides of the AgLEU2 ORF, including the ATG start codon.

5 Primer RP3: 5' CTG GAG CTC CAC CGC GGT GGC GGC CGC TCT AGA ACT AGT GCG CCA ACG TTG CGA GAT ATA 3', The 40 bp at the 5' end of RP3 are homologous to 40 nucleotides in the pBlISK+ multiple cloning site (Alting-Mess M. A. and Short J.M. (1989) Nuc. acids Res. 17(22): 9494) of pAG1245 covering the SacI, SacII, NotI, EagI, XbaI and SpeI restriction sites. The 20 bp at the 3'end of RP3 are homologous to 20 nucleotides in the AgLEU2 terminator region (1261-1281).

10 Sequence carrying the AgLEU2 coding region and the AgLEU2 terminator sequence (the ATG start codon of AgLEU2 is written in bold letters and the stop codon (1117-1119) is underlined):

15

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(1) ATGGCT GCGGTAAGA GAATTGTGGT GCTTCGGGGC  
 GACCACATCG GCCGCGAGGT CGTGGAGGAG GCGGTGAAGG TGCTTGGCGC CGTGGAGCAG AGCCTGTCCG ACGTGCACCTT  
 TGACTTCCAG TACCACCTGG TCGGCGGGGC GGCCATCGAC GCCACGGGGT CCGCGCTGCC GGACGAGGCG CTGGGGCGCGG  
 CGAAGGAGGC GGACGCGGTA CTGCTGGGG CAGTTGGCGG ACCGAAGTGG CAGGGCGGCG CCGTCAGGCC GGAGCAGGGC  
 CTGCTGAAC TGAGACAGGA GTTGGGCGTG TACGCGAACC TGCGTCCCCTG CAACTTTGCG GCGGACTCGC TGCTCGAGCT  
 GTCGCCGCTG CGCCCCGAGA TTGCCCGGGA TACCGATATT ATGGTGTGTC GGGAGCTGCT GGGCGGGAGC TACTTCCGGCG  
 AGCGCCACGA GGACGAGGGC GACGGAGTCG CGTGGGACAC CGACAAGTAC ACCGTGAAGG AGGTGCAGCG CATCGCGCGC  
 ATGGCGGGGT TCCTGGCTCT GCAGCACGAC CCGCCGCTAC CTGTGTGGTC GCTGGACAAG GCGAACGTCC TGGCCAGCTC  
 CCGCCTGTGG CGCAAGACCG TGGAGGAAAC CTTCCAGAGT GAGTTCCCA ACGTGCAATT GCAACACCAG TTGATAGATT  
 CAGCTGCAAT GATTTGGTC AAGAACCCGC GGGCGTTCAA CCGGGTCTGT GTGACGAGCA ACATGTTCCG GGACATTATC  
 TCTGACGAAG CGTCGGTGAT CCCAGGGTCC CTAGGGTTGC TGCCATCCGC CTCGCTCGCG TCCTTGGCCG ATAGCAAGAG  
 CGCCTTTGGC CTCACGAGC CCTGCCACGG CTCTGCCGCC GATCTGCCCG CCGGGAAGGC GAACCCGATC GGATGCATCC  
 TCTCTGCTGC CATGATGCTG AAGTTGTCGT TGAACATGGT TGCTGCCGGC GAGGCGGTCTG AGCAGGCAGT GCAGGAGGTG  
 TTGGACTCGG GAGTCAGAAC GGGCGACCTG CTCGGCTCGA GCTCCACTTC GGAGGTTGGC GACGCCATTG CGCTTGCACT  
 TAAGGAAGCC TTGCGCAGGC AATCCGCAGC TGGTCTGAGC TAGCCTCGAG GACCCTTCTC TTTAGACTAT TCTACTCTTA  
 TGCACGTAAA AAATCTAGG AAATAATGAT TAACTAGGAG TAAATAACC GGCTAGTGGC ATTCATATAG CCGTCTGTCT  
 ACATCTACAT CACACATTTT GAGTGTATAT CTCGCAACGT TGGCG (1281)

The PCR reaction is performed in a Thermocycler from ams Biotechnology. As a template, the isolated 3.1 kb BamHI/Sall fragment from plasmid pAG150 (Mohr Ch. (1997) Ph.D. Thesis, Institute of Applied Microbiology, University

of Basel) carrying the AgLEU2 gene is used. 100 ng template are added for a 50µl reaction volume supplemented with 0.2mM of dATP, dCTP, dGTP and dTTP. 5µl of 10\*Thermo Pol Buffer (Biolabs). The concentration of primer RP5 and primer RP3 in the reaction is 1µM. After the hot start, 1µl enzyme mixture (Taq Polymerase (Pharmacia) and Vent Polymerase (Biolabs) 5:1) is added. PCR is executed under the following conditions: hot start 2 min at 94 °C, 30 cycles of 30 sec at 94°C, 30 sec at 55°C and 2 min at 72°C and finally 4 min at 72°C.

Analysis of the PCR reaction on a 1% agarose gel shows a concentration of 100ng/µl for the 1.36 kb PCR product, which can be used to transform *S. cerevisiae*.

#### Example 4.2: Transformation of *S. cerevisiae*

For the direct exchange of the ORF of AgRPS33B on plasmid pAG1245 in *S. cerevisiae* with the AgLEU2 marker via homologous recombination a cotransformation is carried out. As a recipient strain, YP98 with the phenotype a, ura3-52, lys2-801<sup>amber</sup>, ade2-101<sup>ochre</sup>, trp1-Δ1, leu2-Δ1 (Sikorski R.S. and Hieter P. (1989) Genetics 122: 19-27) is used. Transformation is performed according to Gietz et al. (1992) Nuc. Acid Res. 20 (6): 1425.

2µg plasmid DNA of pAG1245 and 2µg PCR product are cotransformed into strain YP98. Plasmid pAG1245 carries the CEN6/ARSH4 cassette and the URA3 gene providing replication and selection in strain YP98. Recombination between the 40 bp at the ends of the PCR product, which are homologous to parts of the pAG1245rp SRS, leads to excision of the AgRPS33B open reading frame and integration of the AgLEU2 marker gene. Transformants are double selected for URA<sup>+</sup> and LEU<sup>+</sup> on SD-minimal medium supplemented with lysine, adenine, tryptophan and lacking uracil and leucine (Sikorski R.S. and Hieter P. (1989) Genetics 122: 19-27). As a positive control, 2µg plasmid DNA of pRS415 and pRS416 (Sikorski R.S. and Hieter P. (1989) Genetics 122: 19-27) were cotransformed. Plasmid pRS416 carries the CEN6/ARSH4 cassette and the URA3 gene, and pRS415 carries the CEN6/ARSH4 cassette and the LEU2 gene for replication and selection. Transformants are also selected on SD-minimal medium supplemented with lysine, adenine, tryptophan and lacking uracil and leucine. As a negative control, 2µg PCR product are transformed to exclude the possibility of genomic integration of the AgLEU2 marker gene. Selection for the negative control is carried out on SD-minimal medium plates supplemented with lysine, adenine, tryptophan, uracil and lacking leucine. After 2-3 days of incubation, the first transformants appear, and after 5 days the transformation efficiency is calculated. The negative control, only transformed PCR product; has no transformants. The positive control, pRS415 and pRS416, has a transformation efficiency of 300 transformants/µg DNA. The cotransformation of pAG1245 and the PCR product shows a transformation efficiency of 10 transformants/µg DNA. For verification of the integration of the AgLEU2 marker gene into pAG1245, the new plasmid, which is named pAG1245-1, is isolated from the transformants and further investigated.

#### C.) Verification of the integration of the AgLEU2 marker into pAG1245

Genomic DNA from several independent *S. cerevisiae* transformants harboring the newly generated plasmid pAG1245 is isolated according to Philippsen P. et al., (1991) Methods in Enzymology 194: 169-182, Guide to Yeast Genetics and Molecular Biology, Academic Press.

The genomic DNA is transformed into the *E. coli* strain XL1-blue (Bullock W.O. et al., (1987) Bio Techniques 5 (4): 376-378) using the protocol described by Dower J.W., (1988) Nuc. Acids Res. 16: 6127-6145). Plasmid DNA of pAG1245-1 is isolated and integration of the AgLEU2 marker gene is verified via analytical PCR. A primer pair with one primer located in the multiple cloning site and one primer in the promoter region of AgRPS33B indicates excision of the ORF of AgRPS33B and integration of the AgLEU2 marker gene. For this purpose, two primers RP1 and RP2 are selected. RP1 (5'CAT GAT TAC GCC AAG CGC GC 3') is homologous to 20 nucleotides in the pBlISk+ multiple cloning site (Alting-Mess M. A. and Short J.M. (1989) Nuc. acids Res. 17(22): 9494) in pAG1245 adjacent to the Reverse Primer binding site. RP2 (5'CCA AGC ACA TTT CAC CTG CG 3') is homologous to 20 nucleotides to the pAG1245 SRS from 521-540. With this primer combination, the expected PCR product is 0.6kb for pAG1245 and 1.5kb for pAG1245-1. PCR reactions were performed using plasmid DNA from pAG1245 and from pAG1245-1, originated from two independent *S. cerevisiae* transformants, as templates. 100 ng template are added for a 50µl reaction volume supplemented with 0.2mM of dATP, dCTP, dGTP and dTTP. 5µl of 10\*Thermo Pol Buffer (Biolabs). The concentrations of primer RP1 and primer RP2 in the reaction is 1µM. After the hot start, 1 µl enzyme mixture (Taq Polymerase (Pharmacia) and Vent Polymerase (Biolabs) 5:1) is added. PCR is executed under the following conditions: hot start 2 min at 94 °C, 30 cycles of 30 sec at 94°C, 30 sec at 55°C and 2 min at 72°C and finally 4 min at 72°C.

Analysis of the PCR reaction on a 1% agarose gel shows a band at 0.6 kb for pAG1245 and a band at 1.5 kb for pAG1245-1. This result demonstrates the right integration of the AgLEU2 marker gene in pAG1245.

#### Example 5: Isolation of new fungal DNA elements based on synteny of linked sequence pairs

With the initial bi-terminal SRS's of the DNA insert of plasmid PAG1489 (PAG1489RP and PAG1489UP), synteny

is discovered to the centromeric region of *S. cerevisiae* CEN2. This synteny reveals homology to the yeast genes YBL003c and YBR001c. The complete double stranded insert sequence shows synteny to the yeast genes YBL003c (97% identity), YBL002w (94% identity), YBL001c (69% identity), and YBR001c (73% identity) as determined by BLAST searches to the Yeast Genome Database (Altschul, Stephen F., Gish, Warren, Miller, Webb, Myers, Eugene W., and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-410). In yeast, the centromere of chromosome II is placed between YBL001 c and YBR001c. Homologous sequences to the yeast centromere II are found in the *A. gossypii*. DNA sequence of PAG1489 between positions 2900 to 3200. This homology comprises the essential Centromere DNA Elements CDEI, CDEII, and CDEIII. Making use of the synteny of RP and UP sequences of a single pAG-plasmid to a reference genome, the detection of potential antifungal drug targets can be inferred in the same way as the centromere on PAG1489. In addition, using *Ashbya gossypii* as a reference genome, potential antifungal drug targets of other pathogenic fungi can be isolated.

#### Sequence of pAG1489 insert DNA :

GATCGTAACATTGCCCAATAGCTTGTTTAGCTCGTCATCGTTTCTGATGGCTAGCTGTAGATGTCTT  
 GGGATGATTCTGGTCTTCTTGTGTCTCTGGCGGCGTTACCGGCCAACTCTAGGATTTTCGGCGGCCA  
 AGTATTCTAGCACAGCGGTTAGGTACACAGGCGCGCCCGACCCGATTCTCTGTGCGTAGTTGCCCTT  
 TCTGAGCAATCTGTGGACTCTACCGACAGGGAAAGTCAAACCGGCCTTAGCCGATCTCGACTGCGAA  
 GCCTTGGCGGCAGAACCAGCTTTACCTCCTTTACCAGACATTATTTGTGTTGTGTGTGTGTGTGTGT  
 GTTTAGTGTGAACTGCGTGTGCTATGAGAAAACACTACGCTGAAACTGCTAAATAATCCAGACAGGT  
 CCCCCACCGCAAAGGATCCACGCTATACTTCTCTCTACATATTTATACTTGTCCTTTTGCCTTCTA

ATCCTCGATCGTACGCGTCTGACGCTTCAACAGACGCTTCACCTAGACGCTCGACCTGTGCGGCCTG  
 GTTTTTTCGCATGACATGTCCGTGCTGGTTTTTTTCGCGCTGAAAAGGAAAGCGCGTGGCTCCCAGCA  
 5 CCAGAGCCGTACTAGCTCTTTTCGCGTGCTGTCCTATGTGCACGCGAAATTTTCATACTGTAGAGTGT  
 GCCATCAGCTTCACAGAGTACAAACGGTAGGCGAGTGGATACGCGTCTTGTAGCCGGACGTGAATGG  
 CAGAACTTTTTTGGCAGTCGCGTAATCTTAGATTGAAAGTATTTAAGTGGAAACGTATAAAACAAAAGT  
 TCGGGCTGAAGAGGACCTCTTTTGGCGSTCTGCTACTTCCCAGTTATCTGTTGGATACTAAGCATAT  
 10 CGAACTCTAATTGCAATTCTAAAGATGGCACCAAAGGCTGAGAAGAAACCTGCTTCCAAGGCCCCAG  
 CGGCAAAGAAGACCACTGCTTCTACCGACGCTTCTAAGAAGCGGACGAAGACTAGAAAGGAGACCTA  
 CTCCTCTTACATTTACAAGGTTCTTAAGCAGACTCACCCAGATACTGGTATCTCGCAGAAGTCTATG  
 TCCATTTTGAAGTCGTTTGTGAACGATATCTTTGAGAGAATCGCGTCTGAGGCATCCAAGCTTGCGG  
 15 CCTACAACAAGAAGTCTACGATCTCTGCTAGAGAAATCCAGACTGCTGTCAGATTGATCTTGCCCCG  
 TGAGCTAGCCAAGCACGCCGTGCTGAGGGTACCAGAGCTGTTACCAAGTACTCGTCTTCTACCCAA  
 GCCTGAATGGAACCTCATTCTTAGAATGAAAGAACTTCCTTCAAGAAGGTTCTCGTCAGCTAGTGCTT  
 GTGGGACCCGCCCTCTTATTCAGAGCAGCTGCGGCAGAGCGGTATGTGGTACGTTCCGTTTCATCAT  
 20 TTTGTATTATTAGTACATGTAGAAATAGGGTTTTCTGGTTTTCATAATTCGGTATAAATTCCAACGTA  
 ATGTATATTAGATAAGTTTTAACTAGTAATCGGAGAGCTTCTTTTCAACCACGTCTACCTTGCTTT  
 GCGCAGTCTGCTGTTTGTCTGTTCTAGTTCGGAGCCTCATTTCGGTGTGGATTCTAACGTATCCCAA  
 25 TTCGTGGCTGTATTTCGTGCAACTGGCCGATGAGGCTCATGACCTCGTCCCAAGGGCCCTCAATCGTC  
 GTTCCAAAGCTGTGCATAGTGCTTTTCAAGTGACTCTCCCTAATTCGTTTCTCAATCTTGGTGACAT  
 AGTCTGAGACACTTGGTGAGCTAGTACCTAGCTATGATTCAAAGTTTAGTATATTGTTTTATATAT  
 GCAGCTGGAGATGTGAACATACCGGCACCATGCAAATGTCCACTAATGTGTGCAGCTTCGACATTTT  
 30 GATTTCTACCTTCAGAGTATTGGAATATGTTCTTGATGTAACGTCTACTAATTTTCTGGTTTTATAT  
 CGCTGATCTTAAGGGAGATAATTTTCGTTTACCCATCACACAGAAGTTTTAAGTACAAAACCTTGTCCTC  
 CAGATATAGCAAGTCATCAATTCAGGTATAATTTGGTGTGCATGCTAATTTGAAGGGCTGTTATATAG  
 35 TTGAAGTTGTTCTTTTGGCATTGAGCCAAATTTGGATTCTATTTCAGTAGTATTGAACATCAAGTCTC  
 CAAAGCTGAAGTCTGAAGCAAAACATCTCAATAGCTATAGAACTCTAGCAAACAACAGACCAGAGCT  
 TATATCATGACACATTATAAGCTCAGCTATTACTCTGAGTGATAGAGTGACCCTCAATTAGTTGGTT  
 CATTTTATATATAAAAAATATAAACTATAGCTATTTCAAATGACTACTAATAATACGAGAGAAGAA  
 40 AACAAATTAAACACGATGGTCTACAGATAGCTTGAAAGAGACACTAAGAGAAATTTTCAGGAAACAGT  
 TCAGAAAATAGCCATTCAGCTCTACAGCTCTCTTTATTATCAAGAGTACAGTTTCTTTCACTAATAT  
 CGCTTAATTAATTATATTTCTTGCCATTAAATGCGACGGTGACGGGATAACAATTTTGGCAATTCT  
 TCATATTTTGATTTAAAAAACAATTTACCAGAATTAGACGAAATAGTCGCTTACTACAAACAG  
 45 GTTCAGCCACTGGATAAATCTCATAGTTTAAAATATTGAGTTACAGAAATTGGCTTACAGAAAGCAC  
 TAGCGATTAGGCCATTTGCCATTGATTTAAACATGAACCTAACGAACCTCCATGAATTACAATAACCA  
 CAAATTTAACCGGACAATTAATTTTATGTAGCAGGCTCTGCCATGGGAATAGCTTTACGTGAACAGG  
 50 ATATTTAACGTATATCCTTGTTATGATAAAGACTTTGATAGGTGCTTATACTTGCAAGTTCATATTT  
 TACAGTTAAATATCTAAATTTAATATATTACGCAGTTCACGCAATGTAGCACGTGACATAAATATGA  
 AATTTACTATGTGCTTGCTTTATTTAAATAAGTTTATAAAGTTAGTAAAAATATCAGAGTATATAT  
 ATTTAATTAATAATATCCTAAATATATACTAATAACAATTTATCAATTAAGCTTTATACACTTTATAA  
 55 ATAGTTATAATTATAGATGTGTATACGATTTCCGAAACATAAAAAATTTTCACTGCTTTTCGTGAAAA

ATAATTTTTTTATTATAAAACAATCCCTAATATAGTATTACCTCCAATTATGAGTCTATCGTAATAT  
 ATGAAGTACTACCAAATTTACCACTGATTTTTCAAAAAAAAAACACCATTTTTCAAAAATATTTTA  
 5 TTAAGTGAATTTTTTATAATTAATTTTTTATATCTATATAGAATATCTATTATACGCAAGAAAAAC  
 CAAAAGTACCCTATAAGTAGGTACCGCTTGTCACATTATAATAAAAAAGTGAAGTACTCATCAA  
 TACTTTTTATTTAGGATACCTGCAGTCTAATATCCCTTCACGTAAGTTACTTAGTGCACAATATTCAC  
 10 AGTGAGTTAGTAACCCGGTTCAGATCAAGGCATACCGAGCTTCTCTTCTGGCTTCATATGCTTAAA  
 GAAATATCAGGGACGGTGCAGTTAGCTAAAGCTCTCTTAGCATAAGTATTCATAAATTTCAAACCT  
 AAGATATAACTGGAATTGACCCAGCCAAATCCCTCAGTAGCAACACCTTTAAAGTCTGCACCTTGGT  
 TACCATATTCGGCATCAACTCTATGAGGATCTGTGCCTCTGGTAACGTCGTATTTCTCTACTACGAT  
 15 ACCATTGTAGTCGACAAATGCCCTGGTCATTAAAAATAACCACCTATAGGCCAACCTTCTTGCAACT  
 CCTGTAAATCCGTAATTATCTAACCCTGTCAGCAAGCATTTGATGAGGGGCCCAACCATAAGGGT  
 AATCCCATTTGCCCTGCTTGGTCTATTCAATTGTTATCTCACCCGAGACTCCTCAGTACAGGCAACCAG  
 GCCTCCTAGCATTTCAAGCCTTGGCAATGCCCTTCTCGACCATAGCGTTGGCTTGTTCTCTGGGTTGCC  
 20 AAGCCTGCCCACATGGCCCAAAATGTTGTTGCAGAATCGTAAGATGTTCTCTTTCCAATATGGACAT  
 TGTAAGTCATAGAAAAGCCTGTTTCCCTCGTCCCACAAATATTTTCGTGATTCTTTTGCTTACGAATGTC  
 TGCAAGTGCCCTCCCAATGAGAAGAAGTGGTGGTTTCACCAGCATAATCAGTAATACTATCATCGAAG  
 25 TACTTGGAACACATATGCAATATCTTTTCGTACTTGTATAGTAACGAATTCAAATCAATCGTCG  
 CTAAGTAAGCACAGACGTTCTCTAGACGGTAAGAGGTGTCATGTCCACTCTCACGTACAGCACGATC  
 ATGCAAAAAGAACTCATCTAGTTTCGGGCTCGTGTAATTCGCCGGCATCGTACATGCACCTGAACTCC  
 GGAATCGTTACATTGTGCTTTTCCGCAAAATTTCCGGCAAAATGCGTCAAAGTGGTCAGGCTCGGTTT  
 30 CTGGTGGGAAACCGATACCATCTGGATGATAACATGAAAGACCCGTGGTTTTGTCTGACCGCGGTTT  
 TGCCATCCATACACTCTTGATTTCTTAATGGCTGCGATGAATGCTCTTTTCAAGAAATCCACAGCG  
 GTAGGATTTTGGTCAACACCGAACTTTTTCAAGACCTTCAAAGCCATGTCGGTTAGGAACGGGGTT  
 GTGACCGACAGAGGTAGTAGCTCCTATTGGCGTTCAATATTTTACCGTAATGCTCTATCTCAAAGAT  
 35 GAAATGCTCAACCATCCCACGTGCTATGTCCACTTTGTTACAGTCTAGAAGACCCAAAGCCATTAGG  
 TATGAGTCCCAGCCGTAAAGTTCATTAAAAACGACCGCCCGGAACAACGTAGGGAAAACCAACCAATG  
 TACTCTACCGGTAATTGGGTCCCTGTGACTCTCCATCGCCAAAGCAAGCAACCCCGGGCTTTTCGTT  
 40 CAATGATTGCACGTGCTCCGGCGTGATC

Example 6: Identification of antifungal drug targets represented in the attached *Ashbya gossypii* database

A.) Principle of gene disruption using Short Flanking Homology (SFH)-PCR mediated transformation of *Ashbya gossypii*

Gene disruptions in the *Ashbya* genome represented by sequences provided in the Sequence Listing are performed using a new PCR-based *Ashbya* gene targeting procedure. Gene targeting in *Ashbya* relies on homologous recombination in this fungus (Steiner et al., 1995). It has been found that short (approximately 45 bp) target sequence homologies added by PCR to both ends of a selectable marker (e.g. GEN3) are sufficient to mediate sequence-specific gene targeting in *Ashbya*. The PCR fragment for gene targeting thus carries terminal Short Flanking Homology regions encompassing the selectable marker module. These PCR fragments are transfected into *A. gossypii* (e.g. by electroporation) and transformants are selected for G418 resistance. Verification of correct gene targeting is achieved by PCR-testing the presence of the new junctions between target DNA and integrated marker using verification primer pairs G1-G2 and G3-G4 as described by Wach et al. (1997) P. Yeast 13: 1065-1075. Also, verification of the gene targeting can be performed by DNA-hybridization experiments. The verification primers (G2: 5' GTTTAGTCTGAC-CATCTCATCTG 3' and G3: 5' TCGCAGACCGATACCAGGATC 3') are derived from the open reading frame of the selectable marker gene GEN3. G1 and G4 primer sequences are derived from the single read sequence and correspond to regions upstream and downstream, respectively, of the homology regions used for PCR-based targeting. Using this

PCR-based targeting approach, sequences can be manipulated that are approximately 150 nt in length, a criterium matched by all single read sequences of the attached *Ashbya* database. This is of major advantage considering classical methods of gene disruption that are laborious and require cloning steps to incorporate a selectable marker within rather large flanks of surrounding target sequence homology.

After clonal purification (spore isolation) it is determined whether deletion/insertion at the targeted locus results in any phenotypic alterations (e.g. decrease or loss of viability) identifying a potential target for antifungal drugs.

#### B.) Protocol for Short Flanking Homology (SFH)-PCR mediated transformation of *Ashbya gossypii*

1.) Selection of S1 and S2 primers is done in order to link app. 45 nt specific of the target locus sequence to 20 nt homologous to pGEN3 in order to allow amplification of the selection marker *GEN3*. The standard sequence on the 5' side of *GEN3* corresponds to 5' GCTAGGGATAACAGGGTAAT 3', which includes the recognition site of the rare cutting endonuclease I-SCE1 to the PCR fragment. This restriction site is not found in the nuclear genome of *A. gossypii* and can be used to physically map the position of the *A. gossypii* insert DNA to a chromosomal location. The sequence on the 3' side of *GEN3* corresponds to 5' AGGCATGCAAGCTTAGATCT 3'. Put together, the S1 and S2 primers comprise a total of app 65 nt. Selection of verification primers G1 and G4 which are neither part nor overlap with S1 and S2 primer sequences is dependent on the target locus sequence.

2.) Generation of SFH-PCR fragment is achieved by using the S1 and S2 primers to amplify *GEN3* to an amount of approximately 10mg from linearized pGEN3 cleaved by the restriction endonucleases *EcoRI* and *BamHI* (Biolabs). To increase the fidelity of the PCR-product a mixture of Taq DNA Polymerase (Pharmacia) and Vent DNA Polymerase (Biolabs) is used in a ratio of 10: 1-2 units.

Standard PCR conditions are:

Step 1: Initial denaturation	at 96°C for 2min.
Step2: Denaturation	at 96°C for 30s.
Step3: Primer annealing	at 50°C for 30s.
Step4: Elongation period	at 72°C for 2.5min.

Steps 2-4 are repeated for 25-35 times.

Step5: Terminal elongation period:	at 72°C for 5min.
Step6: Storage at 4°C (optional).	

3.) Transfection of the SFH-PCR product into *A. gossypii* is done by electroporation (Steiner et al., 1995 with modifications):

- 1.) Inoculate 100-200ml YPD or AFM (YPD: 2% casein peptone, 2% glucose, 1% yeast extract; AFM: 1% casein peptone, 2% glucose, 1% yeast extract, 0.1% myo-inositol) with a spore suspension of app.  $10^7$  spores.
- 2.) Incubate at 30°C for a max. of 18h under rotation of 200rpm.
- 3.) Collect the mycelium by filtration and wash once with sterile H<sub>2</sub>O.
- 4.) Resuspend 1g of wet weight mycelium in 40ml of 50mM potassium phosphate buffer, pH 7.5 containing 25mM DTT and incubate at 30°C for 30min with gentle shaking.
- 5.) Collect the mycelium by filtration and wash once with 50ml cold STM buffer (STM: 275mM sucrose, 10 mM Tris-HCl, pH 7.5, 2mM MgCl<sub>2</sub>.)
- 6.) Resuspend to a densely packed mixture of mycelium in STM buffer.
- 7.) Mix app. 150ml of mycelium with max. 50 ml of SFH-PCR product in an Eppendorf tube and transfer the mixture into an electroporation cuvette (BioRad 4mm).
- 8.) Apply an electric field pulse of 1.5kV, 100%, 25 mF which will result in a pulse length of app 2.3ms. Add 1 ml of YPD or AFM and spread equal amounts onto 3 pre-dried AFM plates.
- 9.) Incubate at 30°C for a min. of 4h.
- 10.) Overlay with 8ml 0.5% agarose top layer containing Geneticin/G418 at a final concentration of 200 mg/ml.
- 11.) Incubate at 30°C for a max. of 4 days.

C.) Examples of gene disruptions revealing potential antifungal drug targets using Short Flanking Homology (SFH)-PCR.

#### 1.) Disruption of PAG1025RP

The amino-terminal part of the *RHO 3* gene is located on PAG1025RP. The location of the homology region to the target locus of the four primers (S1, S2, G1, and G4) necessary to construct and verify the SFH-PCR transformants are indicated in section E.) below. Using the S1 and S2 primers (including the 20 nt homologous to pGEN3 at the 3' end of the homology region to the target locus as indicated in A) together with pGEN3, the plasmid carrying the selectable marker gene *GEN3*, (linearized by cutting with *EcoRI* and *BamHI* restriction nucleases [Biolabs]), a PCR fragment is generated that carries terminal Short Flanking Homology regions encompassing the selectable marker module. Primary transformants, which are heterokaryotic with respect to transformed and untransformed nuclei, are clonally purified by spore isolation using a micromanipulator. Germination of spores deleted for *RHO 3* on selective medium is only obtained by adding osmotic stabilizers such as 1 M sorbitol. Verification of the set deletion is performed by PCR using the verification primers G1 and G4 that are unique to the target locus and are not used in the initial transformation event, as well as the primers G2 and G3 that are specific to the selectable marker. PCR products indicative of a homologous gene targeting event can be obtained by using the verification primers in the combination G1-G4 (which amplifies the entire locus in which integration of *GEN3* is targeted), G1-G2 (which amplifies the 5' novel joint that is created by insertion of *GEN3*) and G3-G4 (which amplifies the 3' novel joint that is created by insertion of *GEN3*).

#### 2.) Disruption of PAG1634RP

The amino-terminal part of the *BAL 1* gene is located on PAG1634RP. The location of the homology region to the target locus of the four primers (S1, S2, G1, and G4) necessary to construct and verify the SFH-PCR transformants are indicated in section E.) below. Using the S1 and S2 primers (including the 20 nt homologous to pGEN3 at the 3' end of the homology region to the target locus as indicated in A) together with pGEN3, the plasmid carrying the selectable marker gene *GEN3*, (linearized by cutting with *EcoRI* and *BamHI* restriction nucleases [Biolabs]), a PCR fragment is generated that carries terminal Short Flanking Homology regions encompassing the selectable marker module. Primary transformants, which are heterokaryotic with respect to transformed and untransformed nuclei, are clonally purified by spore isolation using a micromanipulator. Germination of spores deleted for *BAL1* on selective medium is only obtained by adding osmotic stabilizers such as 1 M sorbitol. Verification of the gene targeting event is done as described in C.1)

#### 3.) Disruption of PAG1486RP

The aminoterminal part of the *BUB1* open reading frame is located on PAG1486RP. The location of the homology region to the target locus of the four primers (S1, S2, G1, and G4) necessary to construct and verify the SFH-PCR transformants are indicated in section E.) below. Using the S1 and S2 primers (including the 20 nt homologous to pGEN3 at the 3' end of the homology region to the target locus as indicated in A) together with pGEN3, the plasmid carrying the selectable marker gene *GEN3*, (linearized by cutting with *EcoRI* and *BamHI* restriction nucleases [Biolabs]), a PCR fragment is generated that carries terminal Short Flanking Homology regions encompassing the selectable marker module. Primary transformants, which are heterokaryotic with respect to transformed and untransformed nuclei, are clonally purified by spore isolation using a micromanipulator. Germination of spores, deleted for *BUB 1* cannot be obtained indicating that this gene is essential in *A. gossypii*. Verification of the gene targeting event is done as described in C.1)

SFH-PCR mediated marker integration into the *A. gossypii* DNA can be applied to all RP and/or UP sequences of the attached data base. Further applications of SFH-PCR mediated gene targeting in *A. gossypii* are:

- 1.) Generation of antisense transcripts.
- 2.) Overproduction of mRNA and presumably overexpression of a protein.
- 3.) Addition of reporter genes to a target sequence (e.g. GFP, lacZ).
- 4.) Introduction of longer deletions using RP and UP sequences.

## D.) Examples of gene disruptions revealing potential antifungal drug targets by classical procedures

## 1.) Construction of disruption cassettes

As a selectable marker, kanMX0 is used. This is a transformation selection module expressing G418 resistance in yeast and filamentous fungi and kanamycin resistance in *E. coli* (International Patent Application No PCT/EP 91/01116). This module is inserted into *Ashbya* sequences of genomic pAG clones. The module is a chimeric kanamycin gene plus adjacent multiple cloning regions from the cloning vector pAG-231 (Steiner, Wendland, Wright, and Philippsen, Genetics 1995: 140, 973-987). To this purpose the selectable marker is released from the cloning vector pAG-231 (by cleavage with either BamHI, Sall or XhoI. It is ligated into cloned *Ashbya* DNA cleaved with either BglII, XhoI (partial) or Sall (partial), respectively. Clones carrying *Ashbya* sequences disrupted by kanMX0 are selected in *E. coli* by kanamycin resistance. DNA sequence analysis around the site of integration of the kanMX0 module (i1 and i2 sequences in the attached *Ashbya* data base) reveal the disrupted open reading frame and determine the orientation of the kanMX0 module.

## 2.) Disruption of PAG1010i1/i2, PAG1017i1/i2, PAG1021i1/i2, and PAG1044i1/i2

Disruption cassettes are released from the plasmids leaving several hundred base pairs of *Ashbya* DNA flanking kanMX0 (e.g. by cleavage with NotI and KpnI in the multicloning region). Transformation of *Ashbya* with the disruption cassettes induces homologous recombination into the target locus (Steiner et al., 1995). Primary transformants are selected on G418 containing plates and analyzed by DNA hybridization experiments or by PCR, followed by clonal purification (spore isolation). Chromosomal mapping of the target loci is achieved by I-SceI endonuclease mapping of chromosomal DNA separated by pulsed-field gel electrophoresis.

Primary transformants are heterokaryotic, carrying nuclei with a wild type allele and nuclei with a disrupted allele. Spores with single haploid nuclei develop in the older mycelium and allow clonal purification of transformants (e.g. by single spore isolation with a micromanipulator, Steiner et al., 1995). Spore isolation is followed by a growth assay. The disruption of *Ashbya* ORF's identified for example in sequences PAG1010i1/i2, PAG1017i1/i2, PAG1021i1/i2, and PAG1044i1/i2 do not grow on reveals no growth of spores on G418 medium thereby classifying the products of these ORF's as essential for growth (novel antifungal targets).

One advantage of using *Ashbya*, a fungus with a small genome and apparently very few gene duplications, for novel drug target identification is demonstrated by the fact that the ORF represented by PAG1017i1/i2 is essential in *Ashbya* but the highly homologous ORF Yer082c of *S. cerevisiae* is not (Smith, Chou, Lashkari, Botstein, and Brown Science 1996: 274, 2069-2074).

Clonally purified disruptions of several other ORF's do grow on G418 medium, sometimes identifying mutants that display slow growth phenotypes (e.g. disruption of AgDHC1).

## E.) Construction of pGEN3

The GEN3 selection module is designed specifically to allow homologous recombination in *Ashbya gossypii* using short flanks of DNA sequence homology to the desired target locus. GEN3 consists of the open reading frame of the kan<sup>R</sup>-gene which is under the transcriptional control of the *S. cerevisiae* TEF2 promoter and terminator. GEN3, which confers resistance to the antibiotic drug geneticin, bears no sequence homology to the *A. gossypii* genome.

To construct pGEN3, the ORF of the kan-gene is amplified from pFA-kanMX4 (Wach, A., Brachat, A., Poehlmann, R., and Philippsen, P. (1994). New heterologous modules for classical or PCR-based gene disruptions in *Saccharomyces cerevisiae*. Yeast 10:1793-1808) using primers PTEF2-kan and TTEF2-kan (table 1) that contain an additional 40 bp of short flanks of homology to the *S. cerevisiae* TEF2 gene. The diploid yeast strain FY1679 is transformed with this SFH-PCR product (Wach et al., 1994). Genomic DNA of transformants resistant to G418 is checked for integration of the PCR product at the TEF2 locus by analytical PCR using primers TEF2-150RPG and TEF2-BglII. Because of the diploid background a wild-type band 2.26 kb and a replacement band of 1.7 kb is generated. This 1.7 kb fragment contains the kan-ORF flanked by 609 bp of the TEF2-promoter region and 274 bp including the TEF2-terminator. This gene is termed GEN3. The fragment is extracted out of an agarose gel and ligated as an BglII-fragment into the BglII site of pAF100 (Thierry A., Fairhead, C., and Dujon, B. (1990). The complete sequence of the 8.2 kb segment left of MAT on chromosome III reveals five ORF's, including a gene for a yeast ribokinase. Yeast 6:521-534) yielding pGEN3. The usefulness of GEN3 as a marker gene in *A. gossypii* is corroborated by recloning of the gene in an ARS containing vector (Sikorski, R.S. and Hieter, P. (1989). A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in *Saccharomyces cerevisiae*. Genetics 122:19-27.) that allows free replication upon transformation in *A. gossypii*.



Oligonucleotide primers <sup>1)</sup>

PTEF2-kan GTTTTTAGAAATATACGGTCAACGAACTATAATTAACATAAACAatccgctaagcaaaaagacica  
 TTEF2-kan GGTATATAAAAATATTATATGGAAGCAATAATTATTACTCttagaaaaaactcatcaaca  
 TEF2-150RPG gcgagatctGGTGTATTACCAATAAT  
 TEF2-BglII gcgagatctGATGAGGCCGTCTTTTGTG

<sup>1)</sup> Upper case letters correspond to *S. cerevisiae* DNA used as homology regions. Lower case letters correspond to homologies to pGEN3, pFA-kanMX4 (double underlined), or represent additional nucleotides containing the restriction site BglII (bold) used in the cloning of pGEN3.

## Example 7: Forensic identification using PCR-based diagnostic techniques

The DNA sequences of the present invention are also useful for distinguishing among different species of plant pathogenic fungi and for distinguishing fungal pathogens from other pathogens such as bacteria. Particularly, the DNA sequences of the invention can be used as primers in PCR-based analysis for fungal identification, as well as primers derived from these DNA sequences. DNA sequences that vary among different pathogens can be used to identify and distinguish among those specific specific pathogens. For example, the presence of *Gaumannomyces graminis* in infected wheat has been detected using PCR of sequences specific to the pathogen mitochondrial genome (Schlesser *et al.*, 1991; *Applied and Environ. Microbiol.* 57: 553-556), and random amplified polymorphic DNA (*i.e.* RAPD) markers have been able to distinguish numerous races of *Gremmeniella abietina*, the causal agent of scleroderris canker in conifers. U.S. Patent No. 5,585,238 describes primers derived from the ITS sequences of the ribosomal RNA gene region of strains of *Septoria*, *Pseudocercospora*, and *Mycosphaerella* and their use in the identification of these fungal isolates using PCR-based techniques.

Methods for the use of DNA sequences in PCR analysis are well known in the art. See, for example, see U.S. Patent Nos. 4,683,195 and 4,683,202, as well as Schlesser *et al.* (1991) *Applied and Environ. Microbiol.* 57:553-556. See also, Nazar *et al.* (1991; *Physiol. and Molec. Plant Pathol.* 39: 1-11), which used PCR amplification to exploit differences in the ITS regions of *Verticillium albo-atrum* and *Verticillium dahliae* and therefore distinguish between the two species; and Johanson and Jeger (1993; *Mycol. Res.* 97: 670-674), who used similar techniques to distinguish the banana pathogens *Mycosphaerella tijiensis* and *Mycosphaerella musicola*. Similarly, the sequences of the present invention set forth in the Sequence Listing can be adapted for use in such PCR analysis.

Table 1: Description of *Ashbya gossypii* genomic fragments in the Sequence Listing

<u>pAG name</u>	<u>Yeast Name</u>	<u>Gene Name</u>	<u>Brief Description</u>	<u>HC</u>	<u>Additional Comments</u>
PAG1001RP	YNR030w		weak similarity to SMP3 protein	1	
PAG1001UP	YCR069w	SCC3	peptidyl-prolyl cis-trans isomerase precursor	1	
PAG10021I	YIL014w		similarity to Mnn1p (alpha-1,3-mannosyltransferase)	2	homology due to PAG100212-hit
PAG100212	YIL014w		similarity to Mnn1p (alpha-1,3-mannosyltransferase)	2	
PAG1002RP	YIL105c		similarity to hypothetical protein YNL047c	3	open frame > 450 nt in -2
PAG1002UP	YBL009w		homology to DNA damage responsive ALK1 protein	4	
PAG1003RP	YCR053w	THR4	threonine synthase (o-p-homoserine p-lyase)	1	Terminator, Syntenie, see PAG1003UP
PAG1003UP	YCR057c	PWP2	periodic tryptophan protein	1	Syntenie, see PAG1003RP
PAG1004RP	YLR102c		hypothetical protein	2	Syntenie, see PAG1004UP
PAG1004UP	YLR100w		hypothetical protein	1	Syntenie, see PAG1004RP
PAG1005RP	YBR216c		homology to hypothetical protein (chromosome VII)	3	open frame > 350 nt in -1
PAG1005UP	YNL068c	FKH2	homolog of <i>Drosophila</i> forkhead protein	3	open frame 300 nt in -3
PAG1006RP	YDR432w	NPL3	nucleolar protein	3	open frame > 450 nt in -3
PAG1006UP	YOR290c	SNF2	component of SWI/SNF global transcription activator complex	3	open frame > 350 nt in -1
PAG1007RP	YER091c	MET6	5-methyltetrahydropteroyl triglutamate-homocysteine methyltransferase	1	Syntenie, see PAG1007UP

PAG1007UP	YER093c		weak similarity to <i>Staphylococcus epidermidis</i> PepB protein	1	Syntenie, see PAG1007RP
PAG1008I1	YHR196w		hypothetical protein	1	does not fit in Syntenie of PAG1008RP, UP and I2
PAG1008I2	YJR133w		similarity to hypothetical D9509.18p	1	Promotor + Terminator (the latter according to PAG1008I1), 279 nt.Syntenie, see PAG1008RP and UP
PAG1008RP	YJR132w	NMD5	putative Upt1p-interacting protein	2	Terminator, Syntenie, see PAG1008I2 and UP
PAG1008UP	YJR134c		unclear similarity to paramyosin, myosin	1	Terminator, Syntenie, see PAG1008I2 and RP
PAG1009RP	YNL218w		homology to <i>C.burnetii</i> trxB, spolIIE and serS genes	1	Syntenie, see PAG1109UP
PAG1009UP	YNL219c		probably membrane protein	2	Syntenie, see PAG1109RP
PAG1010I1	YLR337w	VRP1	proline-rich protein verprolin	3	open frame 350 nt in +3 and -2
PAG1010I2	YLR332w	MID2	serine-rich protein, multicopy suppressor of temperature sensitivity of <i>hir1</i> null mutant. Open frame whole length in +3 and -3		
PAG1010RP	YOR240w		weak similarity to unknown <i>S.pombe</i> protein	1	
PAG1010UP	YGR115c		questionable ORF	1	
PAG1011I1	YLR374c		questionable ORF	4	

PAG1011I2	YKR054c	DYN1	dynein heavy chain, cytosolic	1	additional Hit see PAG1011RP and PAG1219RP
PAG1011RP	YKR054c	DYN1	dynein heavy chain, cytosolic	1	additional Hit see PAG1011I2 an PAG1219RP
PAG1011UP	YJL133w	MRS3	splicing protein and member of the mitochondrial carrier family	1	Terminator
PAG1012RP	YER074w	RP50A	ribosomal protein S24.e	1	Terminator, cannot be checked for Intron, not on sequence of PAG1012RP
PAG1012UP	YIL068c	SEC6	component of a multiprotein complex involved in fusion of post-golgi vesicles to plasma membrane	1	
PAG1013I1	YLR344w	RPL33	ribosomal protein	1	Promotor, Syntenie, see PAG1013UP, RP and I2 2nd Hit, Intron in A.g. at the same position like in S.c. (CAI S.c. 0.63)
PAG1013I2	YLR344w	RPL33	ribosomal protein	1	Terminator, Syntenie, PAG1013UP, RP and I1
PAG1013RP	YLR345w		similarity to 6-phosphofructo-2-kinase (EC 2.7.1.105)	1	Syntenie, see PAG1013UP, I1 and I2 2nd Hit
PAG1013UP	YLR343w		homology to Candida albicans pH responsive	1	Syntenie, see PAG1013RP,

					I1 and I2 2nd Hit	
PAG1014RP	YDR376w	ARH1	protein similarity to human adrenodoxin reductase	1	Syntenie, see PAG1014UP	
PAG1014UP	YDR375c	BCS1	MT protein of the CDC48/PAS1/SEC18 (AAA) family of ATPases	1	Terminator, Syntenie, see PAG1014RP	
PAG1016RP	YIR002C		similarity to ATP-dependent RNA helicases	1		
PAG1016UP	YJR078w		indoleamine 2,3-dioxygenase homolog	1		
PAG1017I1	YER082c		hypothetical protein	1		
PAG1017I2	YER082c		hypothetical protein	1		
PAG1017RP	YIL075c	SEN3	tRNA processing	1		
PAG1017UP	YKL216w	URA1	dihydroorotate dehydrogenase (EC 1.3.99.11)	2		
PAG1018RP	YKL018w		hypothetical protein	1		
PAG1018UP	YIR019c	STA1	extracellular glucoamylase	3	open frame whole length in +1 and -3	
PAG1019RP	YKR084c	HBS1	elongation factor 1 alpha-like protein	2		
PAG1019UP	YKR092c	SRP40	weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA POL I and III	3	open frame whole length in +1	
PAG1020RP	YOL130w		strong homology to YFL050c (ALR2,aluminium resistance protein)	1		
PAG1020UP	YNL310c		hypothetical protein	1		
PAG1021I1	YIL019w		hypothetical protein	1	Terminator, Syntenie	
PAG1021I2	YIL019w		hypothetical protein	1	syntenie	
PAG1021RP	YIL022w	TIM44	MT inner membrane protein required in transport across the inner membrane	1	syntenie	
PAG1021UP	YIL019w		hypothetical protein	1	syntenie	

PAG1022RP			3	open frame whole length in -1
PAG1022UP	YDR331w	weak similarity to S.japonicum hemoglobinase	3	open frame > 350 in +1
PAG1023I1	YCR092c	DNA-repair protein	2	
PAG1023I2	YCR092c	DNA-repair protein	1	
PAG1023RP	YCR092c	DNA-repair protein	1	
PAG1023UP	YNR047w	similarity to microtubule-associated serine/threonine protein kinases	1	
PAG1024RP	YBR119w	U1 snRNP-specific A protein (snRNA- associated protein)	2	most likely intron, no ATG in correct frame found slightly different position compared to S.c.
PAG1024UP	YER105c	nuclear pore protein (nucleoporin)	3	open frame whole length in +3 and -2
PAG1025RP	YIL118w	similarity to RAS proteins; belongs to RHO sub- family	1	
PAG1025UP	YNL061w	homolog to human proliferation-associated nuclear antigen, p120	1	
PAG1026RP	YIL096c	hypothetical protein	1	Terminator
PAG1026UP	YNL039w	transcription factor TFIIB, B" component of RNA polymerase III	2	
PAG1027RP	YOL122c	suppressor of mitochondrial matrix protease (MAS1) mutant	1	
PAG1027UP	YOR359w	hypothetical protein	4	

PAG1028RP	YNL308c	similarity to unknown protein on S.pombe CHR I cosmid c22G7	1	Syntenie, see PAG1028UP
PAG1028UP	YNL309w	Sin3p-binding protein (transcription regulatory protein)	2	Syntenie, see PAG1028RP, (classification in Hom_Class 2 according to Syntenie)
PAG1029RP	YOR205c	hypothetical protein	2	
PAG1029UP	YGL141w	similarity with hypothetical protein 1 - human (A38919)	2	
PAG1030RP	YHR205w	cAMP-dependent protein kinase homolog	1	Syntenie, see PAG1030UP
PAG1030UP	YHR204w	similarity to alpha-mannosidases	1	Syntenie, see PAG1030RP
PAG1031RP	YKL012w	similarity to C.elegans hypothetical protein ZK1098.1 and to Myo2p	1	Promotor, Syntenie, see PAG1031UP
PAG1031UP	YKL011c	cruciform-cutting endonuclease 1	2	Syntenie, see PAG1031RP, (classification in Hom_Class 2 according to Syntenie)
PAG1032RP	YKL209c	ABC transporter responsible for export of A factor mating pheromone	4	
PAG1032UP	YDL133w	putative membrane protein	1	Terminator
PAG1033RP	YBR274w	probable serine/threonine-specific protein kinase (EC 2.7.1.-)	1	
PAG1033UP	YDL037c	putative glucan 1,4-alpha-glucosidase (EC 3.2.1.3)	3	open frame whole length in -2

PAG1034RP	YGL114W	hypothetical protein	1	
PAG1034UP	YOR246c	similarity to reductases	4	
PAG1035I1	YLR337W	proline-rich protein verprolin	3	open frame 300 nt in -3
PAG1035I2	YNL281W	hypothetical protein	3	open frame > 350 nt in -1
PAG1035RP	YJR090c	required for glucose repression and for glucose and cation transport	3	open frames > 350 nt in -1
PAG1035UP	YBL079W	nuclear pore (nucleoporin)	1	see PAG1035UP for additional Hit to YBL079w
PAG1036RP	YLR266c	similarity to transcription factors	3	open frames 350 nt in -3, 300 nt in +2
PAG1036UP	YDR370c	hypothetical protein	2	
PAG1037RP	YLR430W	positive effector of tRNA-splicing endonuclease	1	
PAG1038RP	YNL068c	homolog of Drosophila forkhead protein	3	open frame whole length in -3
PAG1038UP	YLR389c	protease involved in a-factor processing	1	
PAG1039RP	YDR443c	component of RNA-POL holoenzyme and komberg's mediator (SRB) subcomplex	1	nearly whole gene on clone
PAG1039UP	YDR443c	component of ma polymerase holoenzyme and komberg's mediator (SRB) subcomplex	1	Promotor, nearly whole gene on clone
PAG1040RP	YAL040c	G1/S-specific cyclin	4	tRNA (Val1), pos. 134 - 207, perfect match to S.c. tRNA(Val1A), 1 mismatch to tRNA(Val1B), no intron
PAG1040UP	YPR097W	hypothetical protein	2	



PAG1041RP	YJL054w	hypothetical protein	2	
PAG1041UP	YLR337w	proline-rich protein verprolin	4	
PAG1042RP	YGL035c	transcriptional repressor involved in glucose-repression	3	open frame > 300 nt in -2
PAG1042UP	YKR075c	weak similarity to negative regulator Sm1p/Hex2p	3	open frame 300 nt in +1
PAG1043RP	YDR456w	similarity to NA <sup>+</sup> -H <sup>+</sup> antiporters	2	
PAG1043UP	YML029w	putative membrane protein	2	
PAG1044I1	YDL076c			
PAG1044I2	YDL076c			
PAG1044RP	YDL077c	hypothetical protein	2	syntenie
PAG1044UP	YDL075w	ribosomal protein L31.e.c12	1	Promotor; Intron, in A.g. at same position compared to S.c. (CAI S.c. 0.60);syntenie
PAG1045RP	YBL096c	hypothetical protein	4	
PAG1045UP	YDL195w	component of the COPII coat of ER-golgi vesicles	4	
PAG1046RP	YHR132c	carboxypeptidase homolog	1	
PAG1046UP	YBR149w		3	open frame 350 nt in +1
PAG1047RP	YLR377c	fructose-1,6-bisphosphatase, gluconeogenic enzyme	1	Syntenie, see PAG1047UP
PAG1047UP	YLR378c	member of the protein permease family of the major		

Accession	Gene	Protein	Function	Notes
PAG1048RP	YBL023c	MCM2	member of the Mcm2p, Mcm3p, Cdc46p family	1
PAG1048UP	YER139c		similarity to YD9609.20 (similarity to amino acid permeases)	1
PAG1049RP	YLR050c		similarity to human MAC30 C-terminus	2
PAG1049UP	YFL018c	LPD1	dihydrolipoamide dehydrogenase precursor	1
PAG1050RP	YGL139w		similarity with hypothetical protein (chromosome XVI) YPL221w	1
PAG1050UP	YIL090w		hypothetical protein	1
PAG1052I1	YPL221w		homology to hypothetical protein (CHR VII) and probable membrane protein YAL053w	2
PAG1052I2	YPL221w		homology to hypothetical protein (CHR VII) and probable membrane protein YAL053w	1
PAG1052RP	YGL139w		similarity with hypothetical protein (chromosome XVI) YPL221w	1
PAG1052UP	YGL137w	SEC27	coatomer complex beta chain (beta'-cop) of secretory pathway vesicles	1

PAG1053RP	YJL197W	UBP12	ubiquitin specific protease	3	Intron possible, same position like in S.c. (CAI S.c. 0.21) open frame whole length in -1
PAG1053UP	YGR255c		hypothetical protein	1	Terminator
PAG1054RP	YBL023c	MCM2	contains N-term down to codon 106, Member of the CDC46p/ MCM2p/MCM3p family that acts as a complex at ARS's to initiate replication	1	former class III
PAG1054UP	YDL120W		hypothetical protein	3	open frame 350 nt in +3, +2, and -2
PAG1055RP	YBL023c	MCM2	member of the Mcm2p,Mcm3p,Cdc46p family	2	
PAG1055UP	YDR065W		hypothetical protein	3	open frame 350nt in +3 and -2
PAG1056RP	YBR290W	BSD2	metal homeostasis protein and probable metal ion transporter	1	
PAG1056UP	YNL228W		questionable ORF	4	
PAG1057RP	YDR143c	SAN1	protein that may antagonize the function of Cdc68p (general chromatin factor) and Sir4p	2	
PAG1057UP	YIL169c		homology to glucan 1,4-alpha-glucosidase	3	open frame 400 nt in +3
PAG1058I1	YDR151c	CTH1	protein of the inducible CCCH zinc-finger family	1	Syntenie, see PAG1058UP
PAG1058I2	YOR306c		similarity to human X-linked PEST-containing transporter	4	
PAG1058RP	YDR150W	NUM1	nuclear migration protein	4	

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PAG1058UP	YDR152w			hypothetical protein	1	Syntenie, see PAG1058I1
PAG1059RP	YLR289w	GUF1		similarity to E. coli elongation factor-type GTP-binding protein lepa	1	Syntenie, see PAG1059UP 1st and 2nd Hit
PAG1059UP	YLR291c	GCD7		translation initiation factor eif2b, 43 KD (beta) subunit	1	Terminator + Promotor (300 nt, for Terminator see PAG1059UP 2nd Hit), Syntenie
	YLR292c	SEC72		involved in recognition of signal peptides	1	Terminator + Promotor (300 nt, for Terminator see PAG1059UP 1st Hit), Syntenie
PAG1060RP	YER157w			unknown function	1	syntenie same as PAG1637
PAG1060UP	YER155c	BEM2		GTPase-activating protein	1	same as PAG1637
PAG1061RP	YGR276c			weak similarity with GOR protein - Pan troglodytes	1	same as PAG1112
PAG1062RP	YMR297w	PRC1		carboxypeptidase y (CPY) (YSCY), serine-type protease	1	
PAG1062UP				ORF not regarded, homolog to Gly-X carboxypeptidase, pseudogene in S288C, three ORF's are separated by two in-frame STOP-codons	3	open frame 300 nt in -1, many stops in other frames
PAG1063RP	YPL004c			homology to hypothetical protein (chromosome VII)	1	

PAG1063UP	YFL002c	SPB4	putative ATP-dependent RNA helicase	1	
PAG1064RP	YBR180w		similarity to drug resistance proteins	1	
PAG1064UP	YNL185c		similarity to ribosomal protein L11	4	
PAG1065RP	YPL040c	ISM1	mitochondrial isoleucine--tRNA ligase (EC 6.1.1.5)	2	Syntenie, see PAG1065UP
PAG1065UP	YPL037c	EGD1	protein with a negative role in gal gene expression	1	Terminator, Syntenie, see PAG1065RP
PAG1069RP	YPL265w	DIP5	dicarboxylic amino acid permease	1	former class III
PAG1069UP	YGR211w		hypothetical protein	1	
PAG1071CRP	YLR405w		similarity to <i>Azospirillum brasilense</i> nifR3 protein	3	(Chimera or) repated region, hybridizes to A.g. chr. II and III open frame> 350 nt in +2 and -3
PAG1071CUP	YDL164c	CDC9	DNA ligase	3	(Chimera or) repated region (see pG1071CRP), hybridizes to A.g. chr. II and III , open frame whole length in -3
PAG1073RP					Mito
PAG1073UP					Mito
PAG1074RP					Mito
PAG1074UP					Mito
PAG1075RP					Mito
PAG1075UP					Mito

PAG1076RP						Mito	
PAG1076UP						Mito	
PAG1077RP						Mito	
PAG1077UP						Mito	
PAG1078I1	YJL024c	YKS7	sigma-2 adaptin homolog	1	Intron possible, 5' splice site not found		
PAG1078I2	YJL024c	YKS7	sigma-2 adaptin homolog	1	Terminator, for Intron see PAG1089I1		
PAG1078RP	YCR081w	SRB8	component of RNA polymerase holoenzyme and SRB subcomplex	4			
PAG1078UP	YGR175c	ERG1	squalene monooxygenase	1	Terminator		
PAG1079RP	YNL133c		hypothetical protein	2	tRNA (Phe), pos. 446 - 538, Syntenie of YNL133c and tRNA (Phe), 18 nt Intron in S.c., anticodon (gene)=GAA, same as PAG1200		
PAG1079UP	YHR069c		homology to unknown S.pombe and human proteins	1	same as PAG1200		
PAG1080UP	YLL009c	COX17	interacts genetically with SCO1 and SCO2 in cytochrome oxidase assembly	1	Promotor, whole gene on clone, (CAI S.c. 0.09))		
PAG1081RP	YOR378w		homology to aminotriazole resistance protein	3	open frame whole length in +3		
PAG1081UP	YCR075c	ERS1	Intracellular protein transport	2			

PAG1082RP	YGR055w	MUP1	high affinity methionine permease	1	
PAG1082UP	YLR357w		similarity to hypothetical protein (chromosome VII)	2	
PAG1083RP	YNL283c		similarity to mammalian mucin and yeast chitinase	3	open frame whole lenght in -2, many stops in other frames
PAG1083UP	YDR158w	HOM2	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	1	Promotor (CAI S.c. 0.43)
PAG1201RP	YDL140c	RPO21	RNA polymerase II, largest subunit (B220)	1	Promotor (CAI S.c. 0.21)
PAG1201UP	YLR218c		hypothetical protein	2	
PAG1202RP	YPR003c		hypothetical protein	2	
PAG1202UP	YPL108w		hypothetical protein	1	
PAG1203RP	YMR076c		similarity to E. nidulans bimD protein, includes C-term + terminator	1	two genes covered by RP-SRS;syntenie
PAG1203UP	YMR075w		promoter terminator combination,		
	YMR076c		similarity to Emericella nidulans bimD protein	1	syntenie;covers codons 170-372
PAG1204RP	YGR282c	BGL2	endo-beta-1,3-glucanase of the cell wall	1	Promotor, Syntenie, see PAG1204UP
PAG1204UP	YGR284c		similarity with mouse Surf-4 protein	1	Syntenie, see PAG1204RP
PAG1205RP	YJR104c	SOD1	superoxide dismutase (EC 1.15.1.1) (Cu-Zn)	1	divergent Terminator (123 nt)
	YBL039c	URA7	CTP synthase 1;last step in pyrimidine biosynthesis pathway	1	divergent Terminator (123 nt)

PAG1205UP	YHR150w	unknown function	1	former class III
PAG1206RP	YDR353w	putative thioredoxin reductase (NADPH)	1	Promotor
PAG1206UP	YHR103w	homology to hypothetical protein D9476.7	1	
PAG1207RP	YPL072w	hypothetical protein	2	Syntenie, see PAG1107UP.Classification in Hom_Class 2 according to Syntenie
PAG1207UP	YPL074w	probable regulatory subunit of 26S proteasome complex	1	Syntenie, see PAG1107RP
PAG1208RP				Mito
PAG1208UP				Mito
PAG1209RP	YDL073w	putative mitochondrial protein	2	
PAG1210RP	YLR094c	hypothetical protein	1	Terminator, Syntenie, see PAG1210UP
PAG1210UP	YLR095c	hypothetical protein	2	Syntenie, see PAG1210RP
PAG1211RP	YHR072w	lanosterol synthase (EC 5.4.99.7)	1	
PAG1211UP	YDR317w	hypothetical protein	2	
PAG1212RP	YBR180w	similarity to drug resistance proteins	1	
PAG1212UP	YDL202w	hypothetical protein	2	
PAG1213RP	YJR005w	clathrin-associated protein complex beta chain, large subunit	2	
PAG1213UP	YLR007w	hypothetical protein	1	open frames whole length in +1 and -3,former class III
PAG1214RP	YIR008c	DNA polymerase alpha subunit 48KD (DNA	3	open frame whole length in
	PRI1			



PAG1214UP	YLL031c	primase)	-2
PAG1215RP	YIR035c	similarity to YJL062p	4
		similarity to YIR036p and YIL124p	1
			Promotor, "Syntenie", see PAG1215UP.
	YIR036c	similarity to short-chain alcohol dehydrogenase	1
		family, YIR035p and YIL124p	PAG1215UP
PAG1215UP	YIR035c	similarity to YIR036p and YIL124p	1
			Promotor, "Syntenie", see PAG1215RP.
	YIR036c	similarity to short-chain alcohol dehydrogenase	
		family	
		YIR035p and YIL124p	1
			Promotor, "Syntenie", see PAG1215RP
PAG1216RP	YIL047c	protein for which truncation and overexpression	3
		can suppress \$ lethality of G-alpha protein	
		deficiency	
PAG1216UP	YJR032w	peptidylprolyl isomerase homolog	4
PAG1218RP	YAL053w	homology to hypothetical proteins on	1
		chromosomes VII, XV and XVI	
PAG1218UP	YOR367w	homology to human SM22 homolog	2
PAG1219RP	YKR054c	dynein heavy chain, cytosolic	2
			Syntenie, see PAG1219UP, additional hit see PAG1011I2 and RP
PAG1219UP	YKR056w	endo-exonuclease	1
PAG1220RP	YBR082c	unknown function	2
			Syntenie, see PAG1219RP

PAG1220UP	YDR044w	HEM13	coproporphyrinogen III oxidase	1	
PAG1221RP	YGL227w		hypothetical protein	2	Terminator
PAG1221UP	YER043c	SAH1	S-adenosyl-L-homocysteine hydrolase	1	
PAG1222RP	YLR403w	SFP1	involved in nuclear protein localization	1	Terminator, Syntenie, see PAG1222UP
PAG1222UP	YLR401c		hypothetical protein	1	Syntenie, see PAG1222RP
PAG1223RP	YGR002c		hypothetical protein	1	syntenie
PAG1223UP	YGL003c		unknown function, has MT-energy transfer proteins signature,		
			has cytochrome c oxidase subunit I, copper B binding region signature	1	former class III.SYNTENIE
PAG1224RP	YML127w		hypothetical protein	1	
PAG1224UP	YLL067c		homology to other subtelomeric encoded proteins	3	open frame > 300 nt in -1
PAG1225RP	YNL087w		probably membrane protein	1	
PAG1225UP	YKR092c	SRP40	weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III	3	open frames > 500 nt in +2 (S-rich) and >450 nt in -1
PAG1226RP	YOR181w	LAS17	proline-rich protein	3	open frame whole length in +2
PAG1226UP	YFL049w		weak similarity to Npl6p (nuclear protein localization factor)	2	
PAG1227RP	YDR262w		hypothetical protein	2	
PAG1227UP	YGR160w		questionable ORF	4	

PAG1228RP	YFL008w	SMC1	chromosome segregation protein	1	Promotor (CAI S.c. 0.16)
PAG1228UP	YAL017w	FUN31	probable serine/threonine protein kinase	1	
PAG1230RP	YNL317w		similarity to Arabidopsis thaliana PRL1 protein	1	
PAG1230UP	YOL138c		hypothetical protein	1	
PAG1231RP	YMR176w		hypothetical protein	3	open frame > 350 nt in -1
PAG1231UP	YPL027w		hypothetical protein	3	open frame > 400 nt in +1
PAG1232RP	YGL027c	CWH41	Involved in beta-1,6-glucan assembly	1	open frames 300 nt in +1
PAG1232UP	YBL014c	RRN6	component of a multiprotein complex essential for		
			initiation of RNA-POL I	2	
PAG1233RP	YKR092c	SRP40	weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III	3	open frames whole length in +2 and nearly whole length in -3
PAG1233UP	YML102w		similarity to human chromatin assembly factor I p60 chain	2	
PAG1235RP	YDL122w	UBP1	ubiquitin-specific protease	1	
PAG1235UP	YGL156w	AMS1	alpha-mannosidase	1	
PAG1236RP	YDR373w		homology to human BDR-1 protein and other calcium binding proteins	1	Promotor
PAG1236UP	YOR124c	UBP2	ubiquitin-specific proteinase (EC 3.4.-.-)	1	
PAG1238RP	YPL195w	YKS4	putative alpha/gamma adaptin	1	
PAG1238UP	YGL080w		similarity with R07E5.13 protein (clone R07E5) - C. elegans	1	Promotor
PAG1240RP					Mito

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PAG1249RP	YOR244w	similarity to SAS2 protein ( involved in silencing at HMR)	1	Syntenie, see PAG1249UP
PAG1249UP	YOR243c	hypothetical protein	1	Syntenie, see PAG1249RP
PAG1250RP				Mito
PAG1250UP				Mito
PAG1251RP	YCR076c	glycine-rich	3	open frames > 450 nt in +1 and > 400 nt in -3
PAG1251UP	YMR259c	hypothetical protein	2	Terminator
PAG1252RP	YFR015c	UDP glucose--starch glucosyltransferase	1	
PAG1252UP	YFR014c	Ca2+/calmodulin-dependent serine/threonine protein kinase type I	1	
PAG1253RP	YGL122c	NAB2	3	open frame > 500 nt in +2
PAG1253UP	YIL130w	similarity to probable membrane protein YJL206c and Put3p	1	
PAG1254RP	YJR016c	dihydroxy-acid dehydratase (EC 4.2.1.9)	1	Terminator
PAG1254UP	M_D113	hypothetical protein	4	
PAG1255RP	YDR300c	glutamate 5-kinase	1	
PAG1256RP	YGL195w	component of a protein complex required for activation of Gcn2p protein kinase	1	Syntenie, see PAG1256UP
PAG1256UP	YGL194c	high similarity with RPD3 protein (transcription modifier protein)	1	Syntenie, see PAG1256RP
PAG1257RP	YGL147c	ribosomal protein RPL9	1	Terminator
PAG1257UP	YDL117w	hypothetical protein	2	Terminator
PAG1258RP	YOL023w	mitochondrial translation initiation factor	1	

PAG1258UP	YPL115c	BEM3	GTPase-activating protein for Cdc42p and Rho1p	1	
PAG1259RP	YBR087w	RFC5	replication factor C subunit 5 (40kDa)	1	Promotor (CAI S.c. 0.15)
PAG1259UP	YBL036c		similarity to Caenorhabditis elegans cosmid F09E5	1	
PAG1260RP	YDR306c		hypothetical protein	2	Promotor, Syntenie, see PAG1260UP, next to tRNA (Val) in S.c.
PAG1260UP	YDR304c	CPR5	cyclophilin of the ER	1	Promotor, Syntenie, see PAG1260RP
PAG1261RP	YLR333c	RPS31B	ribosomal protein S25.e.c12	1	Terminator
PAG1261UP	YLR336c		hypothetical protein	2	Terminator
PAG1262RP	YER069w	ARG5,6	acetylglutamate kinase	1	Syntenie, see PAG1262UP
PAG1262UP	YER068w	MOT2	transcriptional repressor	1	Promotor, Syntenie, see PAG1262RP
PAG1263RP	YJR090c	GRR1	required for glucose repression and for glucose and cation transport	1	
PAG1263UP	YIR019c	STA1	extracellular glucosylase	3	open frame > 400 nt in -1
PAG1264RP	YBL051c		similarity to Schizosaccharomyces pombe protein Z66568_C	4	
PAG1264UP	YHR202w		hypothetical protein	1	
PAG1265RP	YHR143w		similarity to a-agglutinin core protein AGA1	3	open frame 450 nt in -1, same as PAG1176
PAG1265UP	YNL083w		hypothetical protein	1	same as PAG1176

Accession	Gene	Protein	Function	Notes
PAG1266RP	YGL163c	RAD54	DNA-dependent ATPase of the Snf2p family	1
PAG1266UP	YNL066w	SUN4	homology to Candida wickerhamii beta-glucosidase (EC 3.2.1.21)	3 open frame > 400 nt in +3, check Hom_Class, better 2 (25%/95 aa)
PAG1267RP	YLL040c		hypothetical protein	4
PAG1267UP	YGR054w		hypothetical protein	3 open frame nearly whole length in +1
PAG1268RP	YGL142c		hypothetical protein	1
PAG1268UP	YDL108w	KIN28	cyclin-dependentSER/THR protein kinase component	
			of transcription initiation factor TFIIF	1 Terminator + Promotor (177 nt, see 2nd Hit for Promotor), Syntenie
	YDL107w	MSS2	serine/threonine protein kinase	2 Terminator + Promotor (177 nt, see 1st Hit for Terminator), ATG not inframe Syntenie
PAG1269RP	YCL057w	PRD1	saccharolysin;proteinase yscD	2 Terminator
PAG1269UP	YPL101w		hypothetical protein	1
PAG1270RP	YLR106c		putative membrane protein	2 longest yeast gene, only 1 gene on clone
PAG1270UP	YLR106c		putative membrane protein	1 longest yeast gene, only 1 gene on clone
PAG1271RP				Mito

	PAG1271UP			Mito	
	PAG1272RP	YDR083w	hypothetical protein	1 Terminator	
	PAG1272UP	YIR019c	extracellular glucosylase	3 open frame whole length in +3 (?)	
	PAG1273RP	YCR098c	similarity to Pho84p, Itr1p, Itr2p (myo-inositol transporter) and to E. coli citrate transport protein	1	
	PAG1273UP	YGR160w	questionable ORF	4	
	PAG1274RP	YOR338w	similarity to FUN19 protein	4	
	PAG1274UP	YOR347c	similarity to pyruvate kinase Pyk1p	1 Terminator	
	PAG1275RP	YKL079w	member of the kinesin family that can interact with or substitute for Myo2p	3 open frame whole length in -3	
	PAG1275UP	TEF4	elongation factor eEF-1 gamma chain	2 Intron possible, same position like in S.c., unusual 5'-splice site	
	PAG1277RP	YKR043c	similarity to phosphoglycerate mutase (EC 5.4.2.1)	1	
	PAG1277UP	YNR044w	A-agglutinin anchor subunit	3 open frame > 500 nt in -1	
	PAG1278RP	YDL042c	protein involved in maintenance of silencing of HMR, HML and telomeres	2 Terminator	
	PAG1278UP	YOL067c	basic helix-loop-helix (BHLH) transcription factor see 2nd Hit (CAI S.c. 0.12)	1 Divergent Promotor of 215 nt, for 2nd Promotor	
		YTL007w	similarity to human S4 component of 26S	2 divergent Promotor of 215	



Accession	Gene	Protein	Function	Notes
PAG1279RP	YCR032w	protease	probable acetic acid export pump	nt, for 1st Promotor see 1st Hit
PAG1279UP	YCR032w		probable acetic acid export pump	2 only 1 gene on clone
PAG1280RP	YBR156c		weak similarity to myosins	2 Terminator, only 1 gene on clone
PAG1280UP	YPR026w	ATH1	required for vacuolar acid trehalase activity	3 open frame whole length in -2, two separated short blocks with high homology
PAG1281RP	YER172c	BRR2	RNA helicase-related protein	1
PAG1281UP	YER171w	RAD3	DNA helicase/ATPase	1 Syntenie, see PAG1281UP
PAG1282RP	YBL019w		hypothetical protein	1 Syntenie, see PAG1281RP
PAG1282UP	YBL022c	PIM1	serine protease required for intramitochondrial proteolysis	1 Syntenie, see PAG1282UP
PAG1283RP	YPL217c		hypothetical protein	2 Syntenie, see PAG1282RP
PAG1283UP	YPL219w		similarity to hypothetical protein (chromosome VII)	1 Promotor, Syntenie, see PAG1283UP 2nd Hit
PAG1284RP	YDL126c	CDC48	microsomal protein of CDC48/PAS1/SEC18 (AAA) family of ATPases	1 Terminator, Syntenie, see PAG1283RP
PAG1284UP	YOR348c	PUT4	proline and gamma-aminobutyrate permease	
PAG1285RP	YGR058c		with sim to ROD1(which is a protein that mediates resistance to o-dinitrobenzene)	1 former class III
PAG1285UP	YMR137c	PSO2	DNA repair protein for interstrand crosslinks	2 Terminator

PAG1286RP	YBR204c	similarity to peroxisomal serine-active lipase	3	open frame > 400 nt in -3,
PAG1286UP	YIR019c	extracellular glucoamylase	3	open frames > 500 nt in +1 and -3
PAG1287RP	YBL004w	hypothetical protein	1	
PAG1287UP	YDL003w	similarity to S.pombe rad21	2	
PAG1289UP	YKR072c	stimulates G1 cyclin expression	1	
PAG1289RP	YGR061c	5'-phosphoribosylformyl glycine synthetase	4	
PAG1291UP	YKL211c	contains anthranilate synthase (EC 4.1.3.27); glutamine amidotransferase (EC 2.6.1.-); indole-3-glycerol-phosphate synthase (EC 4.1.1.48)	1	
PAG1292RP				Mito
PAG1292UP				Mito
PAG1293RP	YGL062w	pyruvate carboxylase 1	1	
PAG1293UP	YPL187w	MFalpha1; mating pheromone alpha-1 precursor	3	open frames 300 nt in +2 and > 400 nt in +1, check Hom_Class: mating pheromone in S.c. is processed a lot
PAG1294RP	YLR147c	snRNA-associated protein of the SM class required for pre-mRNA splicing, snRNP D3 homolog	1	open frame > 300 nt in +3, former class III
PAG1294UP	YDR167w	similarity to human TBD-associated factor 30	1	Promotor + Terminator (171

						Hlt, Syntenie (CAI S.c. 0.10)	Pormotor + Terminator (171 nt), for Terminator see 1st Hlt, Syntenie
YDR168w	CDC37	cell cycle protein necessary for passage through START	1				
PAG1295RP	CPS1	Gly-X carboxypeptidase (EC 3.4.17.4) precursor	2				
PAG1295UP		hypothetical protein	2				
PAG1296RP		hypothetical protein	1				
PAG1296UP	PRE4	proteasome subunit	1				
PAG1297RP	SUP44	ribosomal protein SUP44/RPS4	1			Promotor (CAI S.c. 0.80)	
PAG1297UP		hypothetical protein	2				
PAG1299RP	IFH1	controlling pre-rRNA processing machinery in conjunction with Fhl1p	3			open frame > 350 nt ln -1	
PAG1299UP	FUN31	probable serine/threonine protein kinase	1				
PAG1300RP		hypothetical protein	3			open frames > 350 nt ln +1 and -2	
PAG1300UP		similarly to YHR090p (similarity to human zinc finger/leucine zipper protein) and YM9916.14 (Chr. XV)	1				
PAG1301RP	CHA1	L-serine/L-threonine deaminase	1			Syntenie, see PAG1301UP	
PAG1301UP		partial identity to hypothetical protein 1 (URK1 5' region)	2			Syntenie, see PAG1301RP	
PAG1302RP		weak similarity with calcium-binding protein	1				

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YLL035w	hypothetical protein	2	divergent Terminator (100 nt), for 1st Terminator see 1st Hlt, Syntenie, see PAG1308RP 1st Hit
PAG1308UP	single-stranded zinc-finger DNA binding protein required for replication in mitochondria	2	Homology due to zinc-finger?
PAG1309RP	copper-transporting P-type ATPase of the cation transport (E1-E2) ATPase family	1	Syntenie, see PAG1309UP, see PAG1165UP for additional Hit to YDR270w
PAG1309UP	mitochondrial tryptophanyl-tRNA synthetase	1	divergent Terminator (40 nt) -> see PAG1309UP 3rd Hlt, Syntenie -> see PAG1309RP
YOR038c	histone transcription regulator	1	divergent Terminator (40 nt) -> see PAG1309UP 1st Hit
YLR245c	homology to cytidine deaminases (EC 3.5.4.5)	1	
YDR060w	unknown function	1	former class III
YBR081c	probable transcription factor, suppressor of Ty transcription	1	open frame 500 nt in -2, former class III
YDR523c	Ser/Thr protein kinase; limited homology only	2	
PAG1312UP	phosphatidylinositol 3-kinase required for G1 progression	3	open frame whole length in +1
YGL211w	hypothetical protein	1	
PAG1313UP	weak similarity to human BRCA2 early onset	1	former class III

PAG1314RP	YGR023w	breast cancer gene	3	open frame > 350 nt in -3
PAG1314UP	YJR151c	similarity with Mid2p and Kai1p	4	
PAG1315RP	YPR181c	similar to proteins of the Srp1p/Tip1p family	1	Syntenie, see PAG1315UP
PAG1315UP	YPR184w	component of COPII coat of ER-golgi vesicles	1	Promotor, Syntenie, see PAG1315RP
		protein with strong similarity to glycogen debranching enzyme (4-alpha- glucanotransferase)	2	
PAG1316RP	YLR440c	hypothetical protein	1	Promotor
PAG1316UP	YLR441c	ribosomal protein S3a.e	1	Syntenie, see PAG1317up
PAG1317RP	YJL085w	hypothetical protein	1	Syntenie, see PAG1317RP
PAG1317UP	YJL087c	tRNA ligase (EC 6.1.1.-)	3	open frames > 300 nt in -2
PAG1318RP	YIL159w	similarity to BNI1 protein	3	open frames > 450 nt in -3 and > 600 nt in +2
PAG1318UP	YER073w	probable aldehyde dehydrogenase (NAD+)	1	Syntenie, see PAG1319UP
PAG1319RP	YMR277w	hypothetical protein	1	Syntenie, see PAG1319RP
PAG1319UP	YMR276w	ubiquitin-like protein	1	
PAG1320RP	YOR207c	DNA-directed RNA polymerase (EC 2.7.7.6) III	1	
		second-largest chain	4	
PAG1320UP	YMR147w	hypothetical protein	1	Syntenie, see PAG1321UP
PAG1321RP	YBL020w	involved in nuclear division	1	1st and 2nd Hit
PAG1321UP	YBL018c	hypothetical protein	1	divergent Terminator (38 nt), Syntenie, see PAG1321RP and

[illegible]

PAG1327RP	YER011w	TIR1	cold-shock induced protein of the Tir1p, Tip1p family	4	
PAG1327UP	YLR337w	VRP1	proline-rich protein verprolin	4	
PAG1328RP	YNL201c		involved in regulation of carbon metabolism	2	Syntenie, see PAG1328UP, Classification in Hom_Class 2 according to Syntenie
PAG1328UP	YNL200c		hypothetical protein	1	Syntenie, see PAG1328RP
PAG1330RP	YLL039c	UBI4	ubiquitin precursor	1	100 % Identity on AA-level, 78.3% on DNA, Syntenie, see PAG1330UP
PAG1330UP	YLL036c	PRP19	non-snRNP spliceosome component	1	Most probable Intron in A.g. but NOT in S.c. Syntenie, see PAG1330RP
PAG1331RP	YDR150w	NUM1	nuclear migration protein	2	open frame > 450 nt in -2, 30% ident./140 aa, check Hom_Class: better 3?
PAG1331UP	YNR044w	AGA1	A-agglutinin anchor subunit	3	open frames > 400 nt in +2> 350 nt in +3 and > 350 nt in +3
PAG1332RP	YKL014c		hypothetical protein	3	open frame nearly whole length in +1
PAG1332UP	YJL194w	CDC6	involved in initiation of DNA replication and spindle function	2	Terminator



PAG1334RP	YHR217c	similarity to hypothetical protein (chromosome IV)	3	open frame whole length in -2 and +2
PAG1334UP	YMR038c	homocitrate dehydrogenase	1	
PAG1335RP	YKL129c	myosin type I	3	open frames whole length in -2 and 300 nt in +3
PAG1335UP	YOR008c	similarity to N0583	4	
PAG1336RP	YJR092w	required for formation of axial but not bipolar budding pattern	1	Terminator, Syntenie, see PAG1336UP
PAG1336UP	YJR095w	protein of the mitochondrial carrier (MCF) family	1	Promotor, Syntenie, see PAG1336RP
PAG1337RP				Mito
PAG1337UP				Mito
PAG1338RP	M_A394	hypothetical transmembrane protein	4	
PAG1338UP	YCR065w	transcription factor	2	
PAG1339RP	YDL244w	nearly identical to Thi5p (involved in pyrimidine biosynthesis pathway), YJR156p, and YNL332w (nmt1 homolog to fission yeast and Aspergillus parasiticus)	1	Promotor, YNL332w near telomere
PAG1339UP	YKL213c	protein involved in ubiquitin proteolysis	1	Terminator
PAG1340RP	YMR004w	required for sorting proteins to the vacuole	1	Terminator, Syntenie (?), see PAG1340UP
PAG1340UP	YMR003w	hypothetical protein	2	Terminator, Syntenie (?), see PAG1340RP
PAG1341RP	YPL242c	hypothetical protein	4	

PAG1341UP	YFL036w	RPO41	mitochondrial DNA-directed RNA polymerase	1	
PAG1342RP	YNR030w		weak similarity to SMP3 protein (functions in the protein kinase C pathway)	2	
PAG1342UP	YPR088c	SRP54	signal recognition particle 54K protein homolog	1	
PAG1343RP	YKL134c	(MIP1)	mitochondrial intermediate peptidase (EC 3.4.24.-) precursor	1	
PAG1343UP	YLR109w		similarity to Candida boldinii peroxisomal membrane protein 20K A	4	UGG tRNA (Pro), pos. 434-545, intron pos.470-509 (40 nt), intron in S.c. 32nt, w/o intron only 1 difference
PAG1344RP					Mito
PAG1344UP					Mito
PAG1345RP	YPL042c	SSN3	cyclin-dependent serine/threonine protein kinase of the RNA polymerase II holoenzyme complex and kornberg's mediator (SRB) subcomplex		
PAG1345UP	YPL040c	ISM1	mitochondrial isoleucine--tRNA ligase (EC 6.1.1.5)	1	Syntenie, see PAG1345UP
PAG1347RP	YBR221c	PDB1	pyruvate dehydrogenase (lipoamide) beta chain precursor	1	Syntenie, see PAG1345RP
PAG1347UP	YGL126w	SCS3	probably involved in the synthesis of inositol phospholipids	2	Promotor (CAI S.c. 0.34)

PAG1349RP	YEL011w	GLC3	1,4-glucan branching enzyme (glycogen branching enzyme)	1	Promotor (CAI S.c. 0.13)
PAG1349UP	YCR017c		putative membrane protein	1	
PAG1350RP	YPR105c		hypothetical protein	2	Promotor, Syntenie, see PAG1350UP
PAG1350UP	YPR106w		similarity to protein kinases Gcn2p, galactosyltransferase-associated protein kinase P58/GTAP, and the raf proto-oncogene	2	Syntenie, see PAG1350RP
PAG1351RP					Mito
PAG1351UP					Mito
PAG1352RP	YFL033c		similarity with to S.pombe CEK1 serine/threonine protein kinase	2	
PAG1353RP	YDR456w		similarity to NA <sup>+</sup> -H <sup>+</sup> antiporters	2	Terminator
	YML031w	NDC1	component of the nuclear envelope	2	Terminator, Syntenie, see PAG1335UP 1st Hit
PAG1353UP	YML029w		putative membrane protein	2	Terminator, Syntenie, see PAG1353RP 2nd Hit
PAG1354UP	YOR017w	PET127	probable mitochondrial translation factor	2	
PAG1355RP	YCR092c	MSH3	DNA-repair protein	2	Syntenie, see PAG1355UP, order wrong
PAG1355UP	YCR094w		homology to hypothetical protein YNL323w and EST from rice	2	Syntenie, see PAG1355RP, order wrong
PAG1356RP	YKR092c	SRP40	weak suppressor of a mutant of the subunit	3	open frame whole length in

				AC40 of DNA dependent RNA polymerase I and III	-3
PAG1356UP				SP entry: UAPC_EMENI purine permease	2
PAG1357RP	YPL158c			hypothetical protein	3 open frame whole length in -2
PAG1357UP	YPL155c	KIP2		kinesin-related protein	1
PAG1359RP	YIL130w			similarity to probable membrane protein YJL206c (probable regulatory zinc-finger protein) and Put3p (positive activator of the proline utilization pathway)	4
PAG1359UP	YER163c			hypothetical protein	1
PAG1360RP	YCR057c	PWP2		periodic tryptophan protein	1
PAG1360UP	YLR342w	GLS1		component of beta-1,3-glucan synthase	1
PAG1362RP	YOR340c	RPA43		essential subunit of RNA polymerase I	1 Terminator
PAG1362UP	YCR065w	HCM1		transcription factor	3 open frames > 350 nt in +3 and > 300 nt in -3
PAG1363RP	YLR454w			similarity to hypothetical protein YPR117w	1
PAG1363UP	YDL037c			putative glucan 1,4-alpha-glucosidase (EC 3.2.1.3)	3 open frame whole length in +2
PAG1364RP	YDL108w	KIN28		cyclin-dependent serine/threonine protein kinase component of transcription initiation factor TFIIH	1 Terminator, cannot be checked for Intron, not on

## sequence of PAG1363RP

PAG1364UP	YGL142c	1	hypothetical protein	3	open frame whole length in +3 (?)
PAG1365RP	YIL011w		similarity to YIL176p, YIR041p and other members of the Srp1p/Tip1p family		
PAG1365UP	YHR144c	1	deoxycytidylate deaminase (EC 3.5.4.12)	1	
PAG1366RP	YLR413w	3	homology to hypothetical protein YKL187c	3	open frame whole length in +2
PAG1366UP	YKL188c	1	similarity to human adrenoleukodystrophy (ALD) protein and yeast peroxisomal protein Pal1p	1	
PAG1367RP	YHR089c	1	associated with snoRNA and involved in 35S rRNA processing	1	
PAG1367UP	YBR115c	1	L-aminoacidipate-semialdehyde dehydrogenase	1	
PAG1368RP	YDL171c	1	putative glutamate synthase	1	
PAG1368UP	YNR012w	1	uridine kinase	1	
PAG1369RP	YPR175w	1	DNA-directed DNA polymerase II chain B	1	Terminator, Syntenie, see PAG1369UP, same as PAG1144
PAG1369UP	YPR179c	1	hypothetical protein	1	Syntenie, see PAG1369RP, same as PAG1144

[illegible]

						Mito
PAG1381UP						
PAG1382RP	YAL036w	PYK1	pyruvate kinase, activity is regulated by glucose levels, inducer:glucose	1	CDC19	
PAG1382UP	YOR346w	REV1	similarity with E. coli mutagenic repair protein umuC	1		
PAG1384RP	YAL042w	FUN9	similarity to hypothetical S.pombe protein	1	Syntenie, see PAG1384UP	
PAG1384UP	YAL043c	PTA1	pre-tRNA processing protein	1	Syntenie, see PAG1384RP	
PAG1385RP	YGR207c	ETF-b	electron-transferring flavoprotein, beta chain	2	Terminator, Syntenie, see PAG1385UP	
PAG1385UP	YGR205w		hypothetical protein	1	Terminator, Syntenie, see PAG1385RP	
PAG1386RP	YIL093c		hypothetical protein	1		
PAG1386UP	YNL023c		similarity to Drosophila melanogaster shuttle craft protein probable transcription factor, has something to do with prolyl-isomerase?	1		
PAG1387RP	YDR371w		similarity to chitinases	2		
PAG1387UP	YPL150w		probable serine/threonine kinase	3	open frames > 450 nt int -3, >350 nt in +1 and +2	
PAG1388RP	YFL013c		hypothetical protein	4		
PAG1388UP	YPR160w	GPH1	glycogen phosphorylase (EC 2.4.1.1)	1	Terminator	
PAG1389RP	YDR327w		homology to hypothetical protein YHR080c	1	Syntenie, see PAG1389UP	
PAG1389UP	YDR328c	SKP1	kinetochore protein complex CBF3, subunit D	1	Terminator, Syntenie, see	

Accession	Gene	Protein	Function	Notes
PAG1390RP				PAG1389RP
PAG1390UP				Mito
PAG1391RP				Mito
PAG1391UP	YPR189w	SKI3	antiviral protein	1 Syntenie, see PAG1391UP
PAG1392RP	YPR190c	RPC82	DNA-directed RNA polymerase III chain	1 Syntenie, see PAG1391RP
	YLR274w	CDC46	acts in a complex at ARS's to initiate dna replication	1
PAG1393RP	YGL240w		hypothetical protein	1 Syntenie, see PAG1393UP
PAG1393UP	YGL241w		similarity to Cse1p (probable kinetochore protein, 17% identity over 1053 amino acids)	1 Syntenie, see PAG1393RP
PAG1394RP	YBR176w		homology to E.coli 3-methyl-2-oxobutanoate	
PAG1394UP	YPL101w		hydroxymethyltransferase	1
PAG1396RP	YNR023w		hypothetical protein	1
			similarity to YCR052p	1 Terminator, Syntenie, see PAG1396UP
PAG1396UP	YNR021w		probable membrane protein	2 Syntenie, see PAG1396RP
PAG1397RP	YGR098c	ESP1	required for normal spindle structure	2 only 1 gene on clone
PAG1397UP	YGR098c	ESP1	required for normal spindle structure	1 only 1 gene on clone
PAG1398UP	YMR291w		putative protein kinase	2
PAG1399RP	YDR338c		similarity to hypothetical protein YHR032w	1
PAG1399UP	YJL158c		member of the Pir1p/Hsp150p/Pir3p family	1 Terminator
	YKL163w	PIR3	member of the Pir1p/Pir2p/Pir3p family	1 Terminator
PAG1399UP	YKL164c	PIR1	required for tolerance to heat shock	1 Terminator



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Strain	Gene	Phenotype	Chimeric Plasmid
PAG1406RP	YHR007C	ERG11	Cytochrome P450 L1 (14DM) (Lanosterol 14-alpha-demethylase)
PAG1406UP	YPL026c	SHA3	Ser/Thr-protein kinase, suppressor of Hta1p mutations that cause aberrant transcription
PAG1408RP	MITO-DNA		
PAG1408UP	YBR072w	HSP26	YEAST HEAT SHOCK PROTEIN 26 expressed during entry to stationary phase and induced by osmostress
PAG1409RP	YPR154W		YPR153W:unknown function, gene may be spliced; YPR154W:protein with sim to several SH3 domain-containing proteins including myosin ID and IC heavy chains, human growth factor receptor-bound grb2 protein, C.elegans sex muscle abnormal protein 5
PAG1409UP	YPR153W YPR156c		YPR155c:NCA2:protein required for CTRL of MT synthesis of ATP6 and ATP8; Hlt no 1:YGR138C (putative drug transport r) neglected due to synteny
PAG1410RP	YOR116c		YOR116c: RPO31: RNA-POLIII largest subunit

PAG1410UP	YOR117w:	YOR117w: YTA1: Syntenie: subunit of 26S proteasome complex	1	syntenie
PAG1412RP	YJR153w	and member of the ATPase family	1	
PAG1412UP		sim to polygalacturonases	4	
PAG1413RP	YDR150w	NUM1 nuclear migration	1	syntenie ;should contain the N-term of NUM1
PAG1413UP	YDR152w	unknown function	1	Syntenie
				YDR151c:CTH1:protein of the mammalian growth factor induced proteins, len 325 aa
PAG1414RP	YLR272c	unknown function	1	
PAG1414UP			4	
PAG1415RP	YGR271w	seems to be an RNA-helicase related protein;	1	just one gene on this plasmid
PAG1415UP	YGR271w	has sim to Yer172p; has A(P-loop)	1	UP-SRS covers 1917aa to 1676aa
PAG1416RP	YLR430w	SEN1 positive effector of tRNA-splicing endonuclease, required for intron cleavage for all ten precursor tRNA families	1	codons1790 up to 1971:C-term including terminator should be on this plasmid;syntenie
PAG1416UP	YLR432w	protein highly similar to to PUR5p and inosine-	1	syntenie

5'-monophosphate of human and E.coli, has  
sim to YML056c (which was actually hit no 1)

PAG1417RP	YPR183W	Dolichol-phosphate mannosyltransferase	1	syntenie.SMX3:YPR182W: SnRNA associated protein
PAG1417UP	YPR181C	SEC23	1	syntenie
PAG1418RP	YCL060C	Protein transport protein	1	syntenie
PAG1418UP	YCL061C	protein with sim to SDL1 L-serine dehydratase unknown function	1	syntenie
PAG1419RP	YLR219W		2	
PAG1419UP			4	
PAG1420RP	YJR107W	sim to acylglycerol lipase	1	
PAG1420UP	YJR014W	YJR014w: unknown function YGR198w: unknown function	1	two genes covered by UP- SRS
PAG1421RP	YNL075W	unknown function	1	
PAG1421UP		only sim with Ser/Thr rich sequences	4	
PAG1422RP	YGL091C	NBP35	1	syntenie
	YGL092W	NUP145	1	
PAG1422UP	YGL092W	NUP145	1	Hit no 1 to YGL172w corresponds to NUP49 and was disregarded due to syntenie
PAG1423RP	YDR189W:	SLY1		SLY1: YDR189w: member of the SEC1-family,

Gene	Accession	Protein	Function	Notes
PAG1423UP	YDR191W	HST4	involved in vesicle trafficking between the ER and Golgi	1 syntenie
PAG1424UP	YDR191W	HST4	sim to SIR2	1 has A(P-loop)
PAG1425RP	YLR187W		YLR187W unknown function, sim to YNL278W	4 4 1 YNL278w was hit no
PAG1425UP	YNL279W		probable membrane protein	5;gives weak indication of syntenie or a probable homology region for chromosomal rearrangements
PAG1426RP	YDR196c		unknown function, has A(P-loop)	1 weak syntenie 1 two genes covered with RP-SRS
PAG1426UP	YDR194c	MSS16	CBS2:translational activator of COB mRNA, non-essential	1 syntenie; neighboring-clone to SLY1
PAG1427RP	YLR214W	FRE1	ferric (and cupric) reductase, acts on ferric iron	1 syntenie; two genes with RP-SRS
PAG1427UP	YDL143W	CCT4	Component of chaperonin containing T-complex	1 syntenie 1 end of syntenie

YLR215C	1	same gene sequenced with RP-SRS	5
YDL060W	1	syntenie, whole gene on plasmid	10
YDL060W	1	start of gene, syntenie. Two genes covered by UP-SRS	15
YDL061c	1	syntenie. Two genes covered by UP-SRS; identical to YLR388w	20
YS29B			
YDL061c	4	ribosomal protein	25
YBR260c	1	protein with weak sim to human bcr (break point cluster) protein	30
YLR213C		YLR213C : unknown fnction, has WAP-type 'four disulfide core'	35
		domain signature	40
YDL144C	1	unknown function	45
YDL145c	1	YDL145c: RET1: N-Term has 4 WD-beta transducin repeats.	50
		Coatomer complex alpha chain	55
YHR178W	1	protein with sim to transcription factors, has Zn(2)-Cys(6) fungal-type binuclear cluster domain in the N-terminal	

Gene	Accession	Protein	Function	Notes
PAG1431UP	YMR270C	RRN9	component of the upstream activation factor (UAF)-complex, involved in activation of RNA polymerase I promoter; non-essential	1
PAG1432RP			sim to proline rich sequences	4
PAG1432UP	YDR330W		Small region of similarity near C-terminus to Undulin extracellular matrix glycoprotein	1
PAG1433RP	YBR141c		unknown function	1 involved in maintenance of M dsRNA killer plasmid
PAG1433UP	YBR143c	SUP45	SUP45:recessive omnipotent suppressor, translational release factor eRF1	1 syntente
PAG1434RP				4
PAG1434UP	YCR065W	HCM1	HCM1 hom to forkhead. Has a transcriptional activation domain of Drosophila fkh homeotic gene	1
PAG1435UP				4
PAG1436RP	YCR093W	CDC39	nuclear protein that negatively affects basal transcription from many promoters, mutants activate the pheromone response pathway at the level of the G-proteins	1 N-term up to aa570 on plasmid
PAG1436UP	YKL215c		protein with sim to Pseudomonas	1

PAG1437RP	YOR224C	RPB8	hydanoinases hyuA-hyuB RPB8: Shared subunit of RNA-POL I, II, III, essential protein with sim to nitrogen fixation proteins	1	syntenie. Two genes with RP-SRS Hit no3 was YPL135w: LPI10: protein with sim to H. influenza nitrogen fixation protein HIU32721-12 which was equally good as hit no 2. Taken this we reach syntenie to PAG1437UP
PAG1437UP	YPL133c	LPI12	protein with sim to transcription factors, has Zn(2)-Cys(6) fungal type binuclear cluster domain in the N-terminal region	1	syntenie
PAG1438RP	YJR132w	NMD5	Nam7p/Upf1p interacting protein. Nam7p: protein involved in decay of mRNA containing nonsense codons	1	
PAG1438UP	YBR079c		protein homologous to surface antigens from trophoblast endothelial activated lymphocytes and P.falciparum unknown function	1	
PAG1439RP	YGR276c			1	
PAG1440RP	YGL137w	SEC27	Coatomer complex beta chain of secretory pathway vesicles required for transport from ER	1	syntenie. Two genes with RP-SRS. C-term must be



Accession	Protein Name	Function	Notes
PAG1440UP	YGL136c	protein with sim to E.coli ftsJ protein	1
	YGL134w	unknown function	1
PAG1442RP	YLR149c	unknown function	1
PAG1442UP	YLR150w	MPT4: protein with specific affinity for guanine rich quadruplex nucleic acids and multicopy suppressor of pop2;G4 quadruplex nucleic acid binding protein; multicopy suppressor of tom1 and pop2 mutations	1
PAG1443RP	YGL141w	unknown function	2
PAG1443UP	YMR171c	ALD2 Aldehyde dehydrogenase2	1
PAG1444RP	YFR042W	unknown function	1
PAG1444UP	YGL232w	protein with sim to dihydropteroate synthase	1
PAG1445RP			4
PAG1445UP	YOR281c	protein with weak sim to phosphatases	1
PAG1446RP	YHR077C	NMD2 protein involved in decay of mRNA containing nonsense codons	1

Gene	Accession	Protein	Function	Notes
YHR076w	1	unknown	1	syntenic. Two genes with RP-SRS
PAG1446UP	1	NMD2	1	N-TERM OF GENE
YHR077c	1	Required for vacuole segregation and vacuolar protein sorting	1	syntenic End of syntenic
YDR323C	1	VAC1	1	
PAG1447RP	1	YPR061c	1	YPR062w: len 158aa; protein with sim to members of the cytidine and deoxycytidylate deaminase family.
				YPR063c: len 140aa, unknown. YPR064w: unknown, len 139aa questionable ORF; SYNTENIC
PAG1447UP	1	YPR065w	1	ROX1
				Heme dependent transcriptional repressor of hypoxic genes including CYC7; N-terminal domain with sim to HMG-box proteins
PAG1448RP	1	YKL025c	1	unknown function
PAG1448UP	1	YIR036C	1	CHR IX: Short-chain alcohol dehydrogenase family signature; YIR036C and YIR035c: sim to human corticosteroid 11-beta-dehydrogenase and short-chain alcohol dehydrogenase family

PAG1449RP	YPL041c	unknown function	1	syntenie; YPL040c:ISM1:Isoleucyl- tRNA synthetase of mitochondria; YPL042c: SSN3: cyclin dependent Ser/Thr protein kinase of the RNA Pol II holoenzyme
PAG1449UP	YPL043w	nucleolar protein required for ribosome biogenesis	1	syntenie
PAG1450RP	YMR109w	protein with sim to myosin heavy chain homolog YKL 129 (76% id over 1090 AA)	1	syntenie
PAG1450UP	YMR108w	ILV2 Acetolactate synthase, first step in the valine and isoleucine biosynthesis pathway	1	
PAG1452RP	YBR269c	unknown function	1	syntenie
PAG1452UP	YBR268w	MRPL37 Mito protein of the large ribosomal subunit	1	syntenie
	YJL062w	unknown function	1	end of syntenie. Two genes with UP-SRS
PAG1453RP	MITO-DNA		1	
PAG1453UP	MITO-DNA		1	
PAG1454RP	YBR229c	protein with sim to alpha 1,4 glucosidase.	1	syntenie
PAG1454UP	YBR225w	YBR225w-Ybr229c Syntenie. YBR225w, YBR226c both of unknown function. 227c: protein with sim to E.coli ATP-	1	syntenie. Two genes with

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PAG1458UP	YGR099w	protein with sim to mannosyltransferase, has strong sim to Pmt3p; has 6 predicted transmembrane domain unknown function	1	SYNTENIE YJR087w:len 116: unknown; YJR086W:len 107:STE18: Guanine nucleotide binding protein gamma subunit of the pheromone - pathway
PAG1459RP	YJR088c	unknown function	1	syntenie
PAG1459UP	YJR085c	unknown function	1	syntenie
PAG1460RP	YFL049W	sim to NPL6:Nuclear protein localization factor	1	syntenie
PAG1460UP	YFL047w	unknown function	1	syntenie; YFL048c: EMP47: Golgi membrane protein with C-terminal KXKXX ER- retrieval motif, len 445aa
PAG1461RP	YIL017c	with sim to adenylate cyclase	1	
PAG1461UP	YBR256c	Riboflavin Synthase, last step of riboflavin synthesis, converts 6,7- dimethyl-8-ribitylumazine to riboflavin	1	
PAG1462RP	MITO-DNA	align		
PAG1462UP	MITO-DNA	align		
PAG1463RP	YDR232w	5-Aminolevulinate synthase, first step in heme biosynthesis pathway (pyridoxal-5'-phosphate is essential cofactor)	1	

PAG1463UP	YBR057c	MUM2	protein with sim to ubiquitin C-terminal hydrolase	1	
PAG1464RP	YOL119c		with weak sim to mammalian monocarboxylate transporter proteins	1	syntenie; YOL118c:unknown, len 102 YOL117w: unknown, len 645
PAG1464UP	YOL116w	MSN1	transcriptional activator for genes regulated through SNF1p, multicopy	2	syntenie
PAG1465RP	YFL046W		suppressor of invertase defect in snf1 mutants	1	syntenie
	YFL045c	SEC53	unknown function	1	syntenie; end of syntenie
PAG1465UP	YLR078c	BOS1	Phosphomannomutase, involved in the synthesis of GDP-mannose and dolichol-phosphate-mannose		defined; two genes covered by RP-SRS
PAG1466RP			Vesicular transport protein Synaptobrevin (-SNARE) homolog	1	
PAG1466UP	YMR196w		involved in ER to Golgi transport	4	
PAG1467RP	YIL144w		unknown function	1	complete gene should be on this plasmid
			protein with sim to myosin heavy chain, possible coiled coil	1	syntenie; YIL145c: len 345aa: with sim to E.coli pantoate beta-alanine ligase (pantothenate

PAG1467UP	YIL146C	unknown function	1	synthetase)	
PAG1468RP	YER133W	protein SER/THR phosphatase PP1 required for glucose repression,	1	syntenie	
PAG1468UP	YGL200c	probably functions antagonistically to SNF1p component of the COPII coat of certain ER derived vesicles	1		
PAG1469RP	YHR098c	protein with unknown function	1	Syntenie	
PAG1469UP	YHR097c	unknown function	1	syntenie	
PAG1470RP	YOR172W	protein with sim to transcription factors, has Zn(2)-Cys(6) fungal-type binuclear cluster domain in the N-terminal region	1	identical to	
PAG1470UP	YNR043W	Mevalonate kinase, generates mevalonate-5-phosphate from mevalonate, needed for ARS-CEN plasmid stability (regulation of autonomous replication)	1	identical to	1155,1470,1527,1535,1546,1595
PAG1471RP	YHR096c	Highly similar to hexose transporters HXT2 and HXT4 ( <i>S. cerevisiae</i> )	1	syntenie due to the transporter genes ; continued syntenie with plasmid PAG1469RP/UP	
PAG1471UP	YHR094C	HEX1:Hexokinase II, converts hexoses to	1	chosen due to syntenie, the	

		hexose phosphates in glycolysis and plays a regulatory role in glucose repression	other hits(YJL214W:HXT8;YDR345C; YLR081W) had no higher sim.
PAG1472RP	YDR016c	unknown function	1 weak case of synteny
PAG1472UP	YDR014w	hypothetical protein	2 weak synteny
PAG1473RP	YMR097c	has ATP/GTP-binding site motif	1 synteny
PAG1473UP	YMR094w	kinetochore protein Cbf3, subunit c	1 synteny; YMR096w: len 297aa, sim to YFL059p and YNL333p. YMR095c: len 224aa, sim to YML334p
PAG1474RP	YOR070c	unknown	1
PAG1474UP	YKR081c	unknown	1
PAG1475RP			4
PAG1475UP	YPR190c	RNA-POL III, third largest subunit	1
	YGR049w	Similar to Scm4p (SCM4_YEAST), possible Cdc4p-interacting protein.	1
PAG1476RP	YML091c	Ribonuclease P of MT, generates mature tRNA molecules by cleaving their 5' ends	
			1
PAG1476UP	YML126c	3-hydroxy-3-methylglutaryl coenzyme A synthase, functions in mevalonate synthesis	
			1 located near TUB3/YML124c



PAG1477RP	YER093c	unknown function	1	syntenie	
	YNL116w	unknown	1		
PAG1477UP	YER091c	Homocysteine methyltransferase, methionine synthase; 5-methyltetrahydropteroyl triglutamate--homocysteinemethyltransferase-	1	syntenie.YER092w:len 125:unknown	
PAG1478RP	YER022w	component of RNA-POLII holoenzyme and Kornberg's mediator (SRB)			
PAG1478UP	YER021w	subcomplex, required for basal transcription	1	syntenie	
PAG1479RP	YJR091c	Component of 26S proteasome complex	1	syntenie	
PAG1479UP	JSN1	protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150	4	almost all of the ORF on this plasmid starting from codon 20	
PAG1480RP	YMR167w	Mismatch repair protein and homolog of E.coli MutL involved in repair of small insertions	1	syntenie; YMR168c:CBF3b, len 608aa YMR169c:ALD3, len 506aa	
PAG1480UP	YMR170c	Aldehyde dehydrogenase	1	syntenie	
PAG1482RP	YLR214w	Ferric (and cupric) reductase, acts on ferric iron chelates external to the cell	1	syntenie	
PAG1482UP	YLR215c	unknown function	1	syntenie	
PAG1483RP	YDL171c	Glutamate synthase, involved with glutamine synthase in glutamate biosynthesis	1		

PAG1483UP	YNR013c	protein with sim to Pho87p and YJL198p, member of the phosphate permease family, 12 TMD	1	
PAG1484RP	YNR006w	protein involved in vacuolar sorting	1	
PAG1484UP	YPL256c	G1/S-specific cyclin, interacts with CDC28p		
		protein kinase to control the events at START	1	
PAG1485RP		pre-tRNA-leu	1	redundant
PAG1485UP	YGL170c	with sim to phosphoribulokinase precursor (phosphopentokinase)	2	
PAG1486RP	YNL161w	SER/THR protein kinase of unknown function; related protein from N.crassa is required for hyphal elongation, has sim to DBF2, DBF20, YPK1, YPK2, and TPK2, strong sim to cAMP-dependent protein kinases like cot-1 and human myotonic dystrophy kinase MDK	1	
PAG1486UP	YHR142w	unknown function, has 7 potential TMD	1	
PAG1487RP	YOR036w	PEP12:Syntaxin(t-SNARE) involved in Golgi to vacuole transport, len 288aa	1	disturbed syntenie . Two genes covered with RP-SRS
	YDR267C	protein with sim to SEC13 and other proteins with WD-40 repeats; has sim to transcription factors	1	disturbed syntenie
PAG1487UP	YOR038c	HIR2:Histone transcription regulator, required	1	disturbed syntenie

PAG1488RP	YIR007W	YIB7	sim to endoglucanases	1	
PAG1488UP	YOL027C		unknown, sim to YPR125p	1	
PAG1489RP	YBR001c	NTH2	alpha, alpha-trehalase, converts alpha, alpha-trehalose to glucose, promoter contains the stress-regulated CCCCT-elements (STRE) common to stress-induced genes, repressors:	1	CEN- PLASMID, HISTONES: SYN
			glucose		TENIE
PAG1489UP	YBL003c	HTA2	Histone H2a	1	syntenie
PAG1490RP	YMR167w	MLH1	mismatch repair protein and homolog of E.coli MUTL	1	syntenie: YMR170c: ALD5.Y MR169c: ALD3
					YMR168c: CBF3B
PAG1490UP	YMR170c	ALD5	Aldehyde dehydrogenase	1	syntenie
PAG1491RP				4	
PAG1491UP	YNL082w	PMS1	protein required for mismatch repair, homologous to MutL	2	
			unknown function		
PAG1492RP	YKR070w		unknown function	1	two genes covered by RP- SRS
			unknown function	1	two genes covered by RP- SRS
PAG1492UP	YLR292c	SEC72	SEC72: Component of ER protein-translocation complex that includes		

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Gene	Accession	Protein	Description	Count	Notes
PAG1497UP	YPL016w	ADR6	SWI1; Component of the SWI/SNF global transcription activator complex, acts to assist gene-specific activators	1	end of gene covered by RP-SRS
PAG1498RP	YOR021c		unknown function	1	
PAG1499UP	YPR133c		unknown function	1	
PAG1500RP	YOL094c	RFC4	replication factor c	1	
PAG1500UP				4	
PAG1501RP	MITO-DNA		align		
PAG1501UP	MITO-DNA		align		
PAG1502RP	YLR056w	ERG3	ERG3:C-5 sterol desaturase, an iron non-heme oxygen-required enzyme of the ergosterol biosynthesis pathway, ER retention signal	1	syntenic;
PAG1502UP	YPL055c	SPT8	member of the TBP class of SPT proteins that alter transcription start site selection, functionally related to SPT3p and TBP	1	syntenic
PAG1503RP	YNL297c		unknown	1	syntenic
PAG1503UP	YNL294c		unknown, has 6 potential TMD	1	YPL296w: q-ORF, len 104, YPL295w: len 524, unknown
PAG1504RP	MITO-DNA				
PAG1504UP	MITO-DNA				
PAG1505RP	YOR007c		sim to protein phosphatases	1	
PAG1505UP	YML002W		unknown function	1	syntenic. Two genes

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Accession	Gene	Protein	Function	Notes
PAG1514RP	YNL126w		sim to YJL207p	1 same as PAG1699
PAG1514UP	YHR121w		unknown function	1 same as PAG1699
PAG1515RP	YFR007w		unknown function	1
PAG1515UP	YGR021w		unknown function	1
PAG1516RP	YPL072w	LPF12	unknown function	1 syntenic
PAG1516UP	YPL074w	YTA6	strong sim to YTA4p, member of the CDC48/PAS1/SEC18(AAA) family of ATPases and probable regulatory subunit of the 26S proteasome complex	1 syntenic; there is no YPL073
PAG1517RP	YPR190C	RPC82	RNA-POL III, third largest subunit	1 syntenic
	YPR189W	SKI3	end of gene on this SRS Antiviral protein with tetratricopeptide (TPR) repeats, part of a system to protect cells from dsRNA viruses	1 two genes covered by RP-SRS. Syntenic
PAG1517UP	YPR189W	SKI3	sequence begins at codon 504	1 syntenic
PAG1519RP	YBR112c	SSN6	general repressor of trans-cription that is brought to target promoters by sequence specific DNA-binding proteins, has tetratricopeptide TPR repeats	1
PAG1519UP	YPR070W		unknown function	1
PAG1520RP	YDL100c		with sim to E.coli arsenical pump-driving ATPase, has amino- transferases class-V pyridoxalphosphate attachment site	1
PAG1520UP	YMR157c		unknown function	1
PAG1521RP	YDL145c	RET1	RPC128:RNA-POL III, second largest subunit	1

PAG1521UP	YLR213c	unknown:has WAP-type 'four-disulfide core' domain signature	1	
PAG1522RP			4	
PAG1522UP	YPR015c	YPR013c:with sim to mouse REX1 encoded transcription factor, contains C2H2-type zinc finger domain; YPR015c :same type of zinc finger	1	
PAG1523RP	YML006C	unknown function, has prenyl group binding site (CAAX)-motif	1	
PAG1523UP	YDR421W	unknown function, has a (P-loop)	1	
PAG1524RP	YPR049C	unknown function, has a probable coiled coil	1	syntenie
PAG1524UP	YPR048W	protein with sim to NADPH-cytochrome P450 reductase, has a MT energy transfer proteins signature	1	syntenie. Two genes covered by UP-SRS
	YPR047w	also YLR168c:protein possibly involved in intra-mitochondrial sorting	1	syntenie overthree genes
PAG1525RP			4	
PAG1525UP	YOR362c	proteasome subunit Y13	1	two genes covered on UP-SRS
	YAL047c	unknown function	1	two genes covered by UP-SRS
PAG1526RP	YJL111w	component of chaperonin-containing T-complex	1	
PAG1526UP	YNL135c	(FKB1) FK506-binding protein, homolog of human FKBP12, human FKBP12 is functional	1	



PAG1527RP	YOR172w	ERG19	1	identical to 1155,1470,1527,1535,1546 ,1595	in yeast, has peptidyl-prolyl isomerase activity; produces lethal complex with rapamycin with sim to transcription factors
PAG1527UP	YNR043w	ERG19	1	identical to 1155,1470,1527,1535,1546 ,1595	Mevalonate diphosphate-decarboxylase, functions in the polyisoprene biosynthesis pathway
PAG1528RP	YLR430w	SEN1	1	one gene on plasmid; covering codons 1356 to1588	positive effector of tRNA-splicing endonuclease, required for intron cleavage for all ten precursor tRNA families
PAG1528UP	YLR430w	SEN1	1	one gene on plasmid covering codons 132 to 365	
PAG1529RP	YLR187w		1	syntenie	unknown functionhas strong sim to YNL278w
PAG1529UP	YLR188w	MDL1	1	syntenie	ATP-binding cassette (ABC)-transporter family member, equivalent to a "half-molecule" ABC protein plus an ATP-binding domain, has sim to mammalian multidrug resistance protein and peptide transporter TAP
PAG1530RP	YGR277c		1	syntenie, same as PAG1538	sim to CTR1 (cholin permease)=HNM1; has multiple membrane spanning domains
PAG1530UP	YGR279C		1	syntenie.YGR278w:unknow n, same as PAG1538	unknown function
PAG1531RP	YCL057w	PRD1	1		Proteinase yscD, saccharolysin, homologous to

PAG1531UP						4	
PAG1532RP	YIL144w			protein with sim to myosin heavy chain, possibly coiled-coil	1	1	syntenie
PAG1532UP	YIL145c			sim to E.coli PANTOATE-BETA-ALANINE LIGASE	1	1	syntenie
PAG1533RP	YJR052w	RAD7		nucleotide excision repair protein involved in G2 repair of inactive genes	1	1	
PAG1533UP	YPR194c			unknown, has sim to S.pombe C-terminal region of ips4	2	2	
PAG1534RP	YOR165w			unknown function	1	1	syntenie
PAG1534UP	YOR163w			unknown function	1	1	syntenie.YOR164c:unknown function
PAG1535RP	YOR172w			sim to ts factor	1	1	identical to 1155,1470,1527,1535,1546,1595
PAG1535UP	YNR043w	ERG19			1	1	identical to 1155,1470,1527,1535,1546,1595
PAG1536RP	YJR085c			unknown function	1	1	
PAG1536UP	YPR040w			unknown function, has sim to a C.elegans protein	1	1	
PAG1537RP	YER164w			with sim to mouse chromodomain-helicase-			

Accession	Gene Name	Protein Name	Function	Similarity	Notes
PAG1537UP	YGR277c	YGR277c	DNA-binding protein, contains putative Myb DNA-binding domain	1	
PAG1538RP	YGR277c	YGR277c	protein with sim to CTR1:copper transport protein, required for high-affinity uptake of copper (=HNM1)	4	YGR278w: unknown, len 577aa.syntenie same as PAG1530
PAG1538UP	YGR279c	YGR279c	unknown, but related to YMR305p	1	syntenie.same as PAG1530
PAG1540RP	YML061C	PIF1	single-stranded DNA-dependent ATPase and 5'-3' DNA helicase required for maintenance and repair of MT-DNA, also functions in nucleus to regulate telomere length	1	syntenie
PAG1540UP	YML060w	OGG1	DNA glycosylase, excises 7,8-dihydro-8-oxoguanine and Fapy residues from DNA	1	syntenie
PAG1541RP	YDR035w	ARO3	2-dehydro-3-deoxyphosphoepoxide aldolase, phenylalanine inhibited	1	
PAG1541UP	trNA-Asp		closest to YDR035w is a copy at YDR058	1	
PAG1542RP	YIR019c	STA1	Glucosylase (alpha-1,4-glucan glucosidase), extracellular enzyme	2	weak similarity based on Ser/thr residues
PAG1542UP	YMR241W		protein with sim to MT-carrier family proteins, has prokaryotic		
PAG1544RP	YDR316w		membrane lipoprotein lipid attachment site	1	
			unknown function; Weak similarity to E. coli hypothetical 28.1 kD protein in udp-fah region	1	

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Accession	Gene	Protein	Function	Notes
PAG1548UP	YER062c	HOR2	DL-glycerol phosphatase, strong sim to GPP1	1 syntenie
PAG1549RP	YNL162w	RPL41A		1 syntenie
PAG1549UP	YNL163c	EF4	translation elongation factor EF4	1 syntenie
PAG1550RP	YLR440C		unknown function, has carbamoyl-phosphate synthase subdomain	
PAG1550UP	YML060w	OGG1	signatures	1 redundant clone?
PAG1551RP			DNA-glycosylase	1 redundant?
PAG1551UP	YLR095c		unknown function	4
PAG1552RP	YDL008w		unknown function	1
				1 end of syntenie; two genes covered from RP-SRS
PAG1552UP	YBR011c	IPP1	Inorganic pyrophosphatase, cytoplasmic	1 syntenie
	YBR009c	HHF1	Histone H4	1 syntenie; YBR010w=HHT1 which is Histone H3
PAG1554RP	YGR277c			1 redundant? Syntenie
PAG1554UP	YGR279c			1 syntenie, redundant?
PAG1555RP	YDL080w		unknown function	1 syntenie; redundant?
PAG1555UP	YDL081c	RPS29B	YEAST 40S RIBOSOMAL PROTEIN YS29B.	1 syntenie
PAG1558RP	YPR070w		unknown	1

PAG1556UP	YBR112c	SSN6	1	redundant?	
PAG1557RP			4		
PAG1557UP	YCL057w	PRD1	1	=NCPR1:YHR042w: NADP-cytochrome P450 reductase	
PAG1559RP	YBR119w	MUD1	1	U1snRNP A protein (snRNA -associated protein with 2 RNA recognition (RRM) domains, helps to fold U1 RNA and maintain it in an active configuration	two genes on RP-SRS; Syntenie
PAG1559UP	YBR120c	CBP6	1	translational activator of COB mRNA	syntenie
	YPR082c		1	Weak similarity to hypothetical E. coli protein (PIR accession number S47687)	
PAG1560RP	YDL185w	VMA1		VMA1Vacuolar H(+)-ATPase catalytic subunit, 69 kD subunit	
PAG1560UP	YDL186w		1	of V1 sector, self splicing protein	syntenie
PAG1561RP	YDL185w	VMA1	1	unknown	syntenie
			1	vacuolar H(+)-ATPase catalytic subunit, self splicing protein	syntenie; whole gene
PAG1561UP	YDL186w		1	unknown function	syntenie
PAG1562RP	YDR100w		1	possible membrane protein	
PAG1562UP	YER176w		2	protein with sim to UPF1, a putative helicase	weak homology to the C-terminal 21 aa
PAG1563RP	YGL120c			protein with strong sim to PRP22; related to putative mRNA processing	

	protein	1	Syntenie; YGL121c:unknown
PAG1563UP	Nuclear poly(A)-binding protein, required for proper polyadenylation of pre-mRNA and for mRNA export	1	syntenie
PAG1565RP	YJR156c:protein with strong sim to THI5 and YNL332wYDL244w:has99,7% identity to THI5;YNL332w:THI5: YFL058w: biosynthetic enzyme involved in pyrimidine biosynthesis pathway above the hydroxymethyl-pyrimidine precursor leading to the thiamine moiety. S.pombe homolog nmt1	1	syntenie
PAG1565UP	protein with sim to acylglycerol lipase	1	syntenie
PAG1566RP	C-8 sterol isomerase, enzyme of the ergosterol biosynthesis pathway: null mutant is lethal in the absence of exogenous ergosterol	1	syntenie; YMR203w: TOM40-MT integral membrane protein involved in protein import, forms the outer membrane import-channel.YMr204c: unknown, len 420
PAG1566UP	Phosphofructokinase beta subunit, converts fructose -6-phospat into fructose -1-6-bisphospat: key regulatory step in glycolysis	1	syntenie; YMR203w: TOM40-MT integral membrane protein involved in protein import, forms the outer membrane import-channel.YMr204c: unknown, len 420
PAG1568RP	subunit of eIF3 initiation complex, required for	1	syntenie; YMR203w: TOM40-MT integral membrane protein involved in protein import, forms the outer membrane import-channel.YMr204c: unknown, len 420

				initiation of protein synthesis, has an RNA recognition domain	1	syntenie
PAG1568up	YOR362c	PRE10		Proteasome subunit YC1	1	syntenie
PAG1569RP	YDR238c	SEC26		coatmer complex beta chain (beta-COP) of secretory pathway		
				vesicles,required for transport from ER to Golgi	1	syntenie
PAG1569UP	YDR236c			unknown	1	syntenie
PAG1570RP	YKL054c			unknown function, glutamic acid rich	1	
PAG1570UP	YOL048c			unknown function	1	
PAG1571RP	YLR077w			unknown, has regulator of chromosome condensation signature		
				(RCC1)	1	syntenie
PAG1571UP	YLR075w	GRC5		ribosomal protein of the 60S subunit (rat L10), len 221	1	syntenie;YLR076c:unknown . len 140 overlapping ORF's anyway
PAG1572RP	MITO-DNA					
PAG1572UP	MITO-DNA					
PAG1573RP	YJR066w	TOR1		Phosphatidylinositol kinase (PI kinase) homolog involved in cell growth and sensitivity to the immunosuppressant rapamycin, kinase domain is essential for G1 cell cycle functions; depletion causes starvation response but not through RAS/cAMP pathway	1	hit no 1 (YKL203c: TOR2) neglected due to syntenie
PAG1573UP	YJR065c	ACT4		actin related protein , essential, len 449	1	syntenie



PAG1574RP	YML070w	(=ACT3) unknown function, has sim to dihydroxyacetone kinase	1	syntenie
PAG1574UP	YML069w	YML069w:has sim to HMG1 proteins	1	syntenie
PAG1575RP	YOR009w	weak sim based on Ser-residues	2	
PAG1575UP	YNR044w	weak sim based on Ser-residues	2	
PAG1576RP	YML125c	protein with sim to NADH-cytochrome b5 reductase	1	syntenie, same as PAG1688
PAG1576UP	YML124c	TUB1:YML085c: tubulin alpha-1 chain, required for mitosis and karyogamyTUB3:YML124c: tubulin alpha-3 chain, non-essential, null mutant has poor spore viability; TUB1 and TUB3 each have an intron in CODON 9	1	syntenie.C-term of TUB3 on plasmid
PAG1577RP	YJR117w	protein with weak sim to tetracycline resistance proteins	1	relaxed syntenie
PAG1577UP	YJR106w	unknown function, with sim to a C.elegans protein	1	relaxed syntenie
PAG1578RP	YDL220c	protein proposed to regulate generation of single-stranded tails at telomeres; required for passage through G2/M; required in meiosis after DNA replication but before chromosome synapsis or recombination mutants are arrested At the RAD9 checkpoint;	1	
PAG1578UP	YNL192w	Chitin synthase I, has a repair function during	1	

PAG1579RP	YMR160W		cell separation; major form of chitin synthase	1	
PAG1579UP	YMR205c	PFK2	representing 90% of activity, null mutants	1	
PAG1580RP	YLR368W		resistant to calcofluor, and with lower mating	1	syntenie
PAG1580UP	YLR370c		and sporulation efficiency	1	syntenie, two genes with UP-SRS
	YLR369W		protein with strong sim to HSP	1	syntenie
PAG1581RP	MITO-DNA				
PAG1581UP	MITO-DNA				
PAG1582RP	YLL023c		unknown function	1	syntenie; two genes on RP- SRS
	YLL024c	SSA2	HSP70 family, cytoplasmic	1	syntenie
PAG1582UP	YLR314c	CDC3	Septin:Component of 10 nm filaments of mother-bud neck	1	N-Term up to codon 240 on the plasmid
PAG1583RP	YCL039W		unknown, probably a member of the beta- transducin (WD-40)		
			repeat family	1	syntenie
PAG1583UP	YCL040W	GLK1	Glucokinase, specific for aldohexoses, sim to YDR516p	1	syntenie
PAG1584RP	YKL062W	MSN4	Zinc-finger transcriptional activator for genes regulated through Snf1p		

				homologous to MSN2	1	
PAG1584UP	YMR035w	IMP2		Inner membrane protease of MT, acts in complex with Imp1p but has a different substrate specificity for removal of signal peptidase	1	
PAG1585RP	YGL162w	SUT1		protein involved in sterol uptake; expressed only in anaerobic conditions	1	syntenie
PAG1585UP	YGL163c	RAD54		DNA-dependent ATPase of the Snf2p family, required for recombination and repair of X-ray damage; required for an early step of mating-type switching; mutant cells die if mating-type switching is attempted, mutants are unable to repair double-strand breaks	1	syntenie
PAG1586RP	tRNA-Val				1	
PAG1586UP	YDR420w	HKR1		Hansenula mrakii K9 killer toxin-resistance protein	2	
PAG1587RP	YAL036c	FUN11		YAL036c:unknown, has GTP-binding motif	1	
PAG1587UP	YOR346w	REV1		protein required for mutagenesis by physical and chemical agents, has some sim with E.coli mutagenic repair protein umuC	1	
PAG1588RP					4	
PAG1589UP					4	
PAG1590RP				MITO-DNA		

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Accession	Gene	Protein	Function	Notes
PAG1596RP	YNL294c	Syntenie	YNL294c: unknown, 6 potential TMD	1
PAG1596UP	YNL297c	YNL297c: unknown, 6 potential TMD		1
PAG1597RP				4
PAG1597UP				4
PAG1598RP	MITO-DNA			
PAG1598UP	MITO-DNA			
PAG1600RP	YEL023c	unknown function		1
PAG1600UP	YJR035W	RAD26	putative helicase homologous to Cockayne syndrome B gene ERCC-6, involved in transcription-coupled repair, has putative NLS	1
PAG1601RP	YBR041W	protein of unknown function, probable ATP-binding protein, with 4 potential TMD		1
PAG1601UP	YBR043c	member of major facilitator superfamily (MFS), multidrug-resistance proteins family 1		1
PAG1602RP	YPL059W	protein with sim to Legionella pneumophila LPNTSAA_1 glutaredoxin-like protein		1

PAG1602UP	YBR162c	protein with sim to AGA1	1	1	
PAG1603RP	YJL190c	ribosomal protein	1	1	syntenie. Same as PAG1670
PAG1603UP	YJL191w	ribosomal protein	1	1	same as PAG1670
PAG1604RP	YJL069c	unknown function	1	1	same as PAG1670
PAG1604UP	YGL123w	ribosomal protein, E.coli S5, rat S2	1	1	
	YDR172w	=SUP2; omnipotent suppressor with sim to EF1-alpha, protein responsible for the (psi+) phenotype probably through a prion mechanism, required for G1/S-transition; has EF-TU homology domain, C-terminal 2/3 homologous to EF-1alpha, N-terminal domain has tandem oligopeptide repeats and has structural sim to mammalian prion protein	1	1	
PAG1605RP	YDR170c	data on length vary, but it should be larger than 1800aa	1	1	this clone contains the N- terminus down to codon 432 syntenie with upstream genes
PAG1605UP	YDR172w	=SUP35;	1	1	syntenie YDR171w:HSP42
PAG1606RP			4	4	
PAG1606UP	YNL254c	unknown function	1	1	
PAG1607RP	YBR214w	protein with sim to moc1 protein of S.pombe	1	1	
PAG1607UP			4	4	
PAG1608RP	YNL287w	Coatomer complex gamma chain (gamma-			
	SEC21				

Gene	Accession	Protein	Function	Notes
PAG1608UP	YBR025c	unknown, probable purine nucleotide-binding protein	essential	1
PAG1609RP	YJL041w	TFS1:suppressor of CDC25; has affect on the phosphorylation state of two proteins whose phosphorylation varies with the cell cycle		1
PAG1609UP				4
PAG1610RP	YNL267w	PIK1:Phosphatidylinositol4-kinase, generates PtdIns4-P; overproduction causes increased sensitivity to growth arrest by alpha factor		1
PAG1610UP	YNL268w	Lysine specific permease		1
PAG1611RP	YMR061w	component of pre-mRNA 3'-end processing factor involved in poly(A)-site choice		1
PAG1611UP	YKL075c	protein with sim to HEX2, histidine-rich protein		1
PAG1612RP	YJL004c	protein of unknown function, probable membrane protein		1
PAG1613UP	YJR019c	unknown function		1

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PAG1618RP			4	
PAG1619RP	YOR085w	OST3	1	syntenie
				member of a complex of 6 ER proteins that transfer core oligosaccharide from dolichol carrier to Asn-X-Ser/Thr motif
PAG1619UP	YOR86c		1	syntenie
PAG1620RP	YKL217w	JEN1	1	CHIMERIC-PLASMID
				unknown function
				protein with sim to E.coli osmoregulatory proP
				proline/betaine transporter and KgtP alpha-ketoglutarate transporter, member of the major facilitator superfamily
PAG1620UP	MITO-DNA			CHIMERIC-PLASMID
PAG1622RP	MITO-DNA			
PAG1622UP	MITO-DNA			
PAG1623RP	YDR150w	NUM1	1	syntenie
PAG1623UP	YDR152w		1	syntenie,
				YDR151c:CTH1:1en 325:
				protein of the inducible
				CCCH zinc-finger family
PAG1624RP	YIL093c		1	
PAG1624UP	YNL023c			unknown function
				protein with sim to human DNA binding protein
				tenascin and
				Drosophila shuttle craft protein
PAG1625RP	YLR180w	SAM1	1	high degree of identity to
				S-adenosylmethionine synthetase 1;repressors:

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PAG1628RP	YKR092c	SRP40	suppressor of mutant AC40 subunit of RNA- POL I and III, overproduction is lethal	2
PAG1629RP	YNL257c	SIP3	interacts with SNF1, contains PH-domain	1
PAG1629UP	YGR255c		protein with sim to E.coli ubiH protein	1
PAG1630RP	YLR424w		protein with sim to retrovirus-related proteases	2
PAG1630UP				4
PAG1631RP	MITO-DNA		align	
PAG1631UP	MITO-DNA		align	
PAG1632RP	YNL068c	FKH2	Homolog of Drosophila forkhead protein	1
PAG1632UP				4
PAG1633RP	MITO-DNA			
PAG1633UP	MITO-DNA			
PAG1634RP	YBL085w	BOI1	BEM1p-binding protein, has a SH3 domain and a PH domain; involved in bud formation redundant with BOI2p	1
PAG1634UP				4
PAG1635RP	YDL052c	SLC1	Fatty acyltransferase	1
				two genes covered by RP- SRS,same as PAG1664
	YLR377c	FBP1	Fructose-1,6-bisphosphatase	1
				two genes covered by RP- SRS,same as PAG1664
PAG1635UP	YDL054c		putative transmembrane protein	1
PAG1636RP	YLL055w		protein with sim to DAL5 and members of the allantoate permease	

PAG1636UP	YKL215c	1	family of the major facilitator superfamily (MFS)	1	
		1	protein with sim to Pseudomonas		
PAG1637RP	YER157w	2	hydantoinases hyuA-hyuB		syntenic, same as
			unknown function		PAG1060
PAG1637UP	YER155c	1	bud-emergence protein		codons 403 to 218
	BEM2				including N-
					term+promoter(?)syntenic
					YER156c:unknown
					function, same as PAG1060
PAG1638RP	YCL037c	1	with sim to SLF1, has a motif in common with	1	syntenic.YCL038c:unknown
			conserved sequence in LHP1 but does not		function, len 528aa37c:is
			contain a RNA recognition motif		SRO9
PAG1638UP	YCL039w	1	probably a member of the WD-40 family	1	syntenic
PAG1639RP	YKL046c	1	unknown function, has 2 predicted TMDs		
PAG1639UP	YMR020w	1	sim to corticosteroid-binding protein	1	
	FMS1	4			
PAG1640RP		1			
PAG1640UP	YLR196w	1	member of WD-40 repeat family		
PAG1642RP	YKR023w	1	unknown function	1	syntenic
PAG1642UP	YKR024c	1	unknown function, probable purine nucleotide-	1	syntenic
			binding protein		
			protein that amplifies the magnitude of		
PAG1643RP	YMR179w	1	transcriptional regulation		
	SPT21		at various loci		syntenic; YMR180c:len

[illegible]

PAG1649RP	YHR206W	SKN7	1	Transcription factor with homology to response regulator proteins of bacterial two-component systems and DNA-binding region of Hsf1p, may be involved in the response to oxidative stress. May act in parallel to PKC1-MAP kinase pathway to regulate growth at the cell surface, but is not in the same pathway as PKC1, null mutant w/O phenotype, high level of overexpression is lethal: Has a potential coiled-coil domain	1	syntene; two genes covered by UP-SRS
PAG1649UP	YER183C		1	unknown function	1	syntene; two genes covered by UP-SRS
PAG1650RP	YOR317W	FAA1	1	:long-chain fatty acid CoA ligase (fatty acid activator 1), can incorporate exogenous myristate into myristoyl-CoA and other fatty acids to the CoA derivatives	1	syntene; two genes covered by UP-SRS
PAG1650UP	YMR100W		1	unknown function	1	syntene
PAG1651RP	YNL121C	TOM70	1	MT specialized import receptor of the outer membrane, has tetrapeptide repeats	1	syntene; two genes covered by UP-SRS
PAG1651UP	YNL123W		1	unknown function	1	syntene; two genes covered by UP-SRS

	YNL122c	unknown function	1	syntenie; two genes covered by UP-SRS
PAG1652RP	YOL095c	sim to DNA helicase pcrA	1	syntenie
PAG1652UP	YOL094c	Replication Factor C , 37kD subunit	1	syntenie
PAG1653RP	YHR047c	see ATP8,ORC6;Highly similar to aminopeptidase yscII ( <i>S. cerevisiae</i> ), AMPE_MOUSE, and several other zinc metalloproteases	1	
PAG1653UP	YHR074w	Weak similarity to spore outgrowth factor B (sporulation protein OUTB, <i>B. subtilis</i> )	1	
PAG1654RP	YMR196w	unknown function	1	very end of the gene
PAG1654UP	YMR196w	unknown function	1	very start of gene, w/o promoter
PAG1655RP	YNL202w	sporulation specific protein, probably peroxisomal, ends in SKL*	1	syntenie
PAG1655UP	YNL200c	contains a possible signal-peptide, predicted to be extracellular	1	syntenie; two genes covered by UP-SRS
	YNL201c	protein involved in the regulation of carbon metabolism	1	syntenie; two genes covered by UP-SRS
PAG1656RP	YHR201c	degrades polyphosphate, converting ADP to ATP	1	
PAG1656UP	YJR141w	unknown protein	1	
PAG1657RP	YJL130c	multifunctional pyrimidine biosynthesis protein	1	from codon 1781 to the C-terminus
	URA2			

PAG1657UP	YKR051W	unknown protein	1	
PAG1659RP	YBR038W	Chitin Synthase II, responsible for primary septum disk; Mutants resistant to calcofluor white, 8 TMD, mutant is unable to grow on non-fermentable c-sources Membrane location is altered in an rho0 strain unknown function; has 12 TMD	1	syntenie
PAG1659UP	YBR037C	SCO1		
PAG1660RP	YBL004W		1	syntenie
PAG1660UP	YBL004W		1	codons 800-1033
PAG1664RP	YDL052C	SLC1	1	codons 2167-1951; C-terminus missing
PAG1664UP	YDL054C		1	syntenie, same as PAG1635
PAG1666RP	MITO-DNA			
PAG1666UP	MITO-DNA			
PAG1667RP	YMR061W	RNA14	1	syntenie; same as PAG1635
PAG1667UP	YKL075C			
PAG1669RP	YLR277C	BRR5	1	same as PAG1611
PAG1669UP	YLR281C		1	same as PAG1611
		protein required for processing of mRNA 3' end	1	syntenie
		unknown, however there are other overlapping ORF's	1	syntenie; YLR278c:protein with sim to transcription
		Pap1p		
		unknown protein		
		component of pre-mRNA 3' end processing factor involved in poly(A) site choice, interacts with Rna15p, Fip1p, and	1	



							factors, has Zn(2)- Cys(6) fungal- type binuclear cluster domain in the N- terminal region, len 1341aa syntenie; two genes covered by RP-SRS, same as PAG1603
PAG1670RP	YJL191w	CRY2	ribosomal protein rp59 (E.coli S11, rat and human S14)	1			as PAG1603
	YJL190c	RPS24A	RPS24A:ribosomal protein RPS24 (E.coli S8, mammalian S24)	1			syntenie, same as PAG1603
PAG1670UP	YJL069c		unknown protein	1			same as PAG1603
PAG1671RP	YBR112c	SSN6	has 10 TPR repeats (TPR-Tetratricopeptide)	2			
PAG1671UP	YML042w	CAT2	Carnitine-o-acetyltransferase, peroxisomal and mitochondrial, not required for growth on fatty acids, Catalytic activity: undetected in cells grown on glucose, increased on glycerol or acetate, very high on oleate	1			codons 442 to 655 promoter and terminator missing; regulatable promoter?
PAG1672RP				4			splP24197YIGID_ECOLI HYPOTHETICAL 28.3 KD PROTEIN IN T...-3 73 1.2e-10 5
PAG1672UP	YDL203c		unknown, has weak sim to SKT5	1			
PAG1673RP	YDL104c	QRI7	sim to E.coli orfX gene; may be in a cold spot for recombination	1			syntenie
	YDL105w	QRI2	unknown	1			syntenie; two genes

PAG1673UP	YMR166c	sim to members of the MCF MT carrier protein family	1	covered by RP-SRS not in syntenie to RP-SRS
PAG1674RP	YPL072w	unknown function	1	syntenie
PAG1674UP	YPL075w	required for expression of glycolytic genes. binds to DNA with high affinity but low specificity , motif CTTCC, contains a leucine zipper that is necessary and sufficient for homodimerization	1	syntenie; YPL074w:YTA6:CDG48-ATPase- family
PAG1675RP	YMR259C	unknown, has sim to YGR273p	1	
PAG1675UP	YML100w	alternate third subunit of the trehalose-6-phosphate synthase complex, probably regulatory	1	
PAG1676RP	YLR429W	unknown, with WD-40 repeats	1	syntenie
PAG1676UP	YLR426w	rotein with sim to FOX2p, E.coli 3-oxoacyl-reductase and insect-type alcohol dehydrogenase/ribitol dehydrogenase family	1	syntenie, YLR427w:len 670aa,unknown function
PAG1677RP	YNL116w	unknown function	1	
PAG1677UP	YNR044w	sim relies on Ser-residues	2	
PAG1678RP	YLR347c	karyopherin-beta, acts to target proteins with nuclear localization signals (NLS) to the nuclear pore complex	1	syntenie; YLR345w : len 509: sim to rat fructose-2,6-bisphosphatase;YLR346c :len 101: unknown

PAG1678UP	YLR344w	RPL33A	1	syntenie	
PAG1680RP	YLR107w		1	syntenie; YLR108c: unknown, len485aa; YLR109w: slm to C.boldinii peroxisomal membrane proteins A and B complete gene	
PAG1680UP	YLR110c		1	cell wall protein, probably highly O-glycosylated, null mutant fails to flocculate; repeat domains account for 70% of the protein FLO1 homolog	
PAG1681RP	YER172C	BRR2	1	RNA-helicase related protein required for pre- mRNA splicing	syntenie
PAG1681UP	YER171w	RAD3	1	DNA-helicase component of RNA polymerase transcription initiation factor TFIIF(factor b) and the nucleotide excision repairosome	syntenie
PAG1682RP	YKL214C		1	unknown function	syntenie; two genes covered byRP-SRS
PAG1682UP	YKL213c	DOA1	1	DOA1:Protein involved in ubiquitin proteolysis, has WD-40 repeats	syntenie
	YKL212w	SAC1	1	Protein involved in Golgi function and actin cytoskeletal organization, required for growth only at low temperature; mutants are inositol auxotrophs; Sac1p is not associated with actin cytoskeleton	syntenie
PAG1683RP	YDL077c		1	unknown protein	start of gene to codon 164,

PAG1683UP	YDL077c	1	same as PAG1133 very end of gene; maybe including terminator, same as PAG1133
PAG1684RP	YLR425W	1	syntenie
PAG1684UP	YLR424W	1	syntenie; somehow disturbed by overlapping hitno 1
PAG1685RP	YNL330c	1	Transcription modifier required for full repression or full activation of many genes including PHO5, STE6, SPO13, HO, TRK2, and TY2
PAG1686RP	YLR120W	1	DOM34p interacting protein, with WD-40 repeats.
PAG1687RP		4	
PAG1687UP	YOR240W	1	unknown function
PAG1688RP	YML125c	1	sim to NADH-cytochrome b5 reductase
PAG1688UP	YML124c	1	TUB3 rather than TUB1 due to syntenie
PAG1689RP	YKR059W	1	Translation initiation factor 4a eIF4A of the DEAD-box family
PAG1689UP	YJL140W	1	RNA-POLII, fourth largest subunit
	YJL139c	1	Mannosyltransferase of KRE2/KTR1/YUR1

Accession	Gene	Protein	Family	Overlap	Notes
PAG1690RP	YDL033c	sim to H. influenza protein HI0174	family	1	overlapping genes
PAG1690UP	YDL035c	unknown function; putative transmembrane protein		1	syntenie
				1	syntenie; YDL034w: unknown, len 114;
				1	overlapping with YDL035c
PAG1691RP	YHR023w	MYO1	Myosin heavy chain (myosin II), involved in septation and cell wall organization; null mutant has abnormal nuclear migration and cytokinesis, has delocalized chitin deposition, are defective in cell division, are osmosensitive,, and have an altered budding pattern, mutants show wild-type movement of actin cortical patches. Molecule is a dimer with two heads and a long coiled coil tail	1	N-Term down to codon 198
PAG1691UP				4	
PAG1692RP	MITO-DNA				
PAG1692UP	MITO-DNA				
PAG1694RP	YBR280c	sim to SRM1/PRP20		1	syntenie
PAG1694UP	YBR281c	unknown, with WD40 repeats		1	syntenie
PAG1695RP	YPR194C	unknown function		1	
PAG1695UP	YFL010c	unknown function		1	
PAG1696RP	YCL036w	unknown function		1	syntenie. Hit no1: YDR514C:unknown has sim to YCL036w

PAG1696UP	YCL035c	sim to thioltransferase	1	syntenie	
PAG1698RP	YHL002w	has one SH3-domain; Similar to several proteins with SH3 domains	1	syntenie	
PAG1698UP	YHL004w	MT ribosomal protein of the small subunit	1	YHL003c:LAG1:Longevity assurance protein, has sim to YKL008p and mammalian UOG-1 protein; has 7 TMD	
PAG1699RP	YNL126w	unknown function , has weak sim to YJL207p	1	same as PAG1514	
PAG1699UP	YHR121w	unknown protein	1	same as PAG1514	
PAG1700RP		AG-TEF	1	481 out of 491 bases ar identical	
PAG1700UP			4		

Table 2:

*Ashbya gossypii* sequences with (>100 codons) ORF's that show no homology to *S. cerevisiae*

5	PAG1002RP	open frame > 450 nt in -2
	PAG1005RP	open frame > 350 nt in -1
	PAG1005UP	open frame 300 nt in -3
	PAG1006RP	open frame > 450 nt in -3
	PAG1006UP	open frame > 350 nt in -1
10	PAG1010I1	open frame 350 nt in +3 and -2
	PAG1010I2	open frames whole length in +3 and -3
	PAG1018UP	open frames whole length in +1 and -3
	PAG1019UP	open frame whole length in +1
15	PAG1022RP	open frame whole length in -1
	PAG1022UP	open frame > 350 in +1
	PAG1024UP	open frames whole length in +3 and -2
	PAG1033UP	open frames whole length in -2
	PAG1035I1	open frame 300 nt in -3
20	PAG1035I2	open frame > 350 nt in -1
	PAG1035RP	open frames > 350 nt in -1
	PAG1036RP	open frames 350 nt in -3, 300 nt in +2
	PAG1038RP	open frame whole length in -3
25	PAG1042RP	open frame > 300 nt in -2
	PAG1042UP	open frame 300 nt in +1
	PAG1046UP	open frame 350 nt in +1
	PAG1053RP	open frame whole length in -1
	PAG1054RP	open frame whole length in -2, 350 nt in +1
30	PAG1054UP	open frames 350 nt in +3, +2, and -2
	PAG1055UP	open frames 350nt in +3 and -2
	PAG1057UP	open frame 400 nt in +3
	PAG1062UP	open frame 300 nt in -1, many stops in other frames
35	PAG1071CRP	open frames > 350 nt in +2 and -3, possible chimeric plasmid, hybridizes to A.g. chr. II and III
	PAG1071CUP	open frame whole length in -3, possible chimeric plasmid, hybridizes to A.g. chr. II and III
	PAG1081RP	open frame whole length in +3
	PAG1083RP	open frame whole length in -2, many stops in other frames
	PAG1214RP	open frame whole length in -2
40	PAG1216RP	open frame >300 nt in +2
	PAG1220RP	open frame 350 nt in +2 (S-rich)
	PAG1223UP	open frame whole length in -2, open frames > 350 nt in +2 and -3
	PAG1224UP	open frame > 300 nt in -1
45	PAG1225UP	open frames > 500 nt in +2 (S-rich) and >450 nt in -1
	PAG1226RP	open frame whole length in +2
	PAG1231RP	open frame > 350 nt in -1
	PAG1231UP	open frames > 400 nt in +1
	PAG1233RP	open frames whole length in +2 and nearly whole length in -3
50	PAG1245UP	open frames > 400 nt in -2 and > 300 nt in +1
	PAG1247RP	open frames whole length in -3, open frames > 400 in +3 and +2
	PAG1251RP	open frames > 450 nt in +1 and > 400 nt in -3
	PAG1253RP	open frame > 500 nt in +2
55	PAG1263UP	open frame > 400 nt in -1
	PAG1265RP	open frame 450 nt in -1
	PAG1266UP	open frame > 400 nt in
	PAG1267UP	open frame nearly whole length in +1

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Table 2: (continued)

Ashbya gossypii sequences with (>100 codons) ORF's that show no homology to <i>S. cerevisiae</i>	
5	PAG1272UP open frame whole length in +3
	PAG1275RP open frame whole length in -3
	PAG1277UP open frame > 500 nt in -1
	PAG1280RP open frame whole length in -2, two separated short blocks with high homology -> funct. domain?
	PAG1286RP open frame > 400 nt in -3,
10	PAG1286UP open frames > 500 nt in +1 and -3
	PAG1293UP open frames 300 nt in +2 and > 400 nt in +1
	PAG1294RP open frame > 300 nt in +3
	PAG1299RP open frame > 350 nt in -1
	PAG1300RP open frames > 350 nt in +1 and -2
15	PAG1303RP open frame > 350 nt in +2 or ending frame > 250 nt in -1
	PAG1303UP open frame whole length in -2
	PAG1305RP open frame whole length in -2
	PAG1306UP open frame whole length in +2
	PAG1311UP open frame 500 nt in -2
20	PAG1312UP open frame whole length in +1
	PAG1314RP open frame > 350 nt in -3
	PAG1318RP open frames > 300 nt in -2
	PAG1318UP open frames > 450 nt in -3 and > 600 nt in +2
25	PAG1331UP open frames > 400 nt in +2> 350 nt in +3 and > 350 nt in +3
	PAG1332RP open frame nearly whole length in +1
	PAG1334RP open frame whole length in -2 and +2
	PAG1335RP open frames whole length in -2 and 300 nt in +3
	PAG1356RP open frame whole length in -3
30	PAG1357RP open frame whole length in -2
	PAG1362UP open frames > 350 nt in +3 and > 300 nt in -3
	PAG1363UP open frame whole length in +2
	PAG1365RP open frame whole length in +3
35	PAG1366RP open frame whole length in +2
	PAG1387UP open frames > 450 nt int -3, >350 nt in +1 and +2

40

45

50

55



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## 1001RP

	GTGATTTCGTC	CGAGATTGAA	AAGTCCCTAA	CAATCAAAAA	CAACGGGAAG	GCGTACGAGG	60
	AATGGCTGGA	CCTGGGTAAT	GGGTGCCTAT	GTTGCAGTCT	GAAGGACGTA	GGGGTGAAGG	120
5	CCATCGAGGC	GATGGTTTCG	CGGTCCGCCAG	GTAAAATCGA	CTACATCATA	CTTGAGACAA	180
	GCGGGATAGC	GGACCCAGTG	CCGATCGTGA	AGATGTTCTG	GCAGGATGAG	GGTCTCAATA	240
	GCTGCATCTA	CATTGATGGG	ATTGTGACGG	TGCTGGACGC	AGAGCATGTG	ATGACATTGC	300
	TCGACGAGGT	GGCCCTCCCG	CGCCAATTGC	GCGGCGACCA	GGTGCTGATG	GAAAACCAGA	360
	TGACCCNNGG	GNATCTTCAG	GTTGCCATGG	GGGNGCGGGG	GNGTTGATTA	AATCNACCCC	420
	TGNAGGCTGN	NTAAAAATCT	TGGNNGGGAA	AANGGTGANT	ATAAGCGGCC	TTTTTCGGCN	480
10	AATNCGGGAN	TTTNGNTANN	AAAGNTNT				

## 1001UP

	TGATCCGACC	AAGAGCAGGG	CTTTGGTGCG	GTGAATCTCG	AACTCCTGCC	CCTGTGTCAG	60
15	CTCACCCCGG	CCGAAGTCCT	TCCAAAGAAG	AGCTTGTAAG	AAGTGTCTTT	CGAACCCTC	120
	GAGCTCAGCC	TTGTCCGCGA	GCGGCCGGCA	GGTCAAGGTG	ACCGTGGACA	GCCGCGGATC	180
	ATGGTAAGCC	ACGTGGGCAT	CGGGAATGTC	AGAGGCACCA	AAAGCATGGA	GATTCAAGTA	240
	CCTTGTTTAT	CTCCAGATCG	CCGAACCTGG	TCCCGATAGA	TGGGCGCGAC	TGCATTAATG	300
	CTACGCACTT	TTTCTCCAA	CCACAGCGAT	TCGTCAATCA	NGCCTCCCAG	CCNGTCGGAT	360
20	TTATCAAAAC	AACCNNGTCC	GCCATGGCNA	GTTGNAGATG	GCANGGCACT	TTNTTCCAC	420
	AGACTGGNGG	CCGGCAATGG	GGGGGGCACC	CGCGACATTA	NAATTNTGTC	AGACCNAAAC	480
	CNCAATTGNN						

## 1002I2

	GATCTTCGAG	TGGGCGAGGG	ATAGTAGCGA	CCGTGGCAGA	CATTCATCTT	GATCAATTGA	60
25	AGCGCCTGCT	CCATGTCTCT	GATGAAGTGG	GGAAATAAAT	GCCTATAGAG	TTGGTGTACA	120
	AGGGTAACGA	CTTCTCTCGA	TTGCCTATCA	AAAGACTGAA	AAGGTACGTT	CGGCAGCACA	180
	CAAAACAGCG	AGTTCGGCTG	GTGGACTGTT	CGCGTGTACT	ACGCAGTACA	CATATACCTA	240
	AGATAAAGAG	GTTTCATGAAT	AAGTGGTTAG	CCACTATATT	CAATTCATTT	GGAGGAAATA	300
30	ATACTACTAG	ACGTGGATTG	TTGGTGCCAC	TGGGTTCCAA	TCGATAGCTA	CTTCAAATTT	360
	CCCGGCTACA	CTAAAAACGG	GCGCTCTTGT	CCTTCAAGGA	TAGAACGCTT	CCGGAGTACC	420
	TCCCTGTTTC	ATGCACAAAA	GCGAACTACT	CTTGGCACCA	CCGCCGGAGG	AGACAAACTT	480
	TGGGGCAATC	CTTTGAGATT	TCGACACCAN	TGNAAGAGNT	N		

## 1002I1

	GATCTCCGCA	AATTCTCCCA	AAATGGTAAG	TCGTTATCCA	CCTTAAATGC	TTGCTCGGGT	60
	AGCTTGTTCC	CCAATAAATA	ACGTGACCCA	TCATTGAGAT	CCAATACCTG	GGGGAGCAGT	120
	TCGCTCCAAT	CGCGTACTTT	CTTTAAAAAC	GGAAATAGTT	CATGATGGAG	AGAGTACAAG	180
40	TTTATGTCCT	CACCAAAAAC	CTCACGAAGA	CCTATATCTC	CTTGATGAA	ACAAGTGTG	240
	AACACTCGTA	GTCGTTCCAG	CATGGCAGCT	GTCACCGAGG	CATCCTTCAT	GCGACCACGC	300
	GACCTTTCGA	TAATTTTCGTT	CAGCCATTGT	TGTCTCTTTT	TCTTTCGCAA	AGTACCACTG	360
	GCATTCTTTT	CCAGGGGGCA	TCTCCCGAAC	TGGGTTGGTC	AACAGAAATG	ACTGTNTGGG	420
	GNGGGGTTTG	GTGTTGGACG	ACNTTNGTG	AAGATGGGGC	ACAGTTNTGC	CGTTTTTGAG	480
	GNCAGGCAGA	TNTGAAACAA	ATTNNCGNNA	ANTTCGNTTT	CCCNACGCAC	GGGGCCCGAN	540
45	TTCAGGCAAC	CTNGACATTN	TCGAAGTACC	N			

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## 1002RP

	GATCTACTAA	GGAATTATGG	GAATCGTGTC	TTTTCTTCTT	AGAAATGAAT	TTGTTTGCAG	60
	TCGAAGACGA	GGTGGAAAGAC	GAGCGCGACT	GTTTACTCTT	GGGGAAGTTA	GTCAAACAAT	120
5	CGCTAGATTG	TATCCGCATG	GTATCACCTG	AGTTTCTATC	TATAGGAATG	CTACTATYAC	180
	GGAAGTTGCG	ATGCTGATGG	GCATGGTTGT	CATGAAAAAT	AGGATGTTGG	CTCCGGTTAG	240
	ATGACTGMCC	GAATACCTCT	TCTATGATTA	ATTCCTWCAA	GCGGGTATTG	ATTAATGTCTG	300
	ATCCTGTGGC	GTATGATGAA	ATGACTGCCG	CGTCATTGCC	GGTACGCCCT	TGGAGTGTTT	360
	GGANTTGACA	AGAANNCGCT	CTTAGGTGCC	NGGATTCCCN	GGGTGGGAAA	GATGATNGCG	420
	AATNCCAATT	TNGGTCCAAT	AGGGAATCTG	GNATTATTTG	TTATTGCAAT	NAGGATNCCC	480
10	GGGAGGGGGT	TNCNCTACGA	AGAAGGATTA	GGTTTNNC			

## 1002UP

	GATCCACGKG	AGTCGCAGCG	CCAAAGGCCG	CTGGGCGTCA	CGATGCAGGT	TATGCTGTCTG	60
15	CGTCGACAGA	GTGCGCCCCG	CTGGATGAAG	CCCATAAGAC	TATTGAGCCA	CTATATAATA	120
	CCAGCTGGTT	ACMTGATACT	ATATGGTCAT	AGCATCAATT	GTAGTAGCCA	GGGCAGTGAG	180
	GCTATAGCAG	CTGGAAAGGC	GACTCTGAAA	AGGGATTAT	GCCAAGAGCT	TCAGAAGTGG	240
	ACTCAGGCCA	CGCATCCAAC	GGATTCTTCC	TCAATTCTCTC	TATATTGAGC	CAGAGCTCCA	300
	TCTTGACCGA	GGTCCCTCAT	TCATATTTCAT	ACGAGTTACT	TGAACATCCA	ACAGGTGCCA	360
	TATTTAGKTT	GGGGGGGTAA	GTACAATANC	GNTGNNGGCC	GTGGAACCCC	GGTCCGTTCC	420
20	CNNGGTTTTG	GAATTTTNG	G				

## 1003RP

	GATCGCTCAT	GACCAAAACA	ACGAAATCCA	CTACATTTCTG	CTTGCCACTG	CTCACCCAGC	60
25	GAAGTTTGCG	GACGCTGTGA	ACGAAGCTCT	CTCCTCTTAC	GATGACTACA	ACTTCGATGA	120
	CGTTCTTCCA	GACCGTCTAA	GACGTCTAGG	TGACCTTGAG	AAGAGAATTA	AGTACGTGGA	180
	CAACACCCGAC	GTTGATGTTA	TCAAATCTAT	CATTGAGGAG	GAAGTATTA	ACATGGGCAT	240
	TTACAATCCA	TAGATGATCT	GAAGTCTAGA	TGATTTATAG	ACTATCTAGT	TAGCCTTCTA	300
	GTCCTATATA	CCTAATTCCA	ATAGGCAGGG	GGGCCTATGT	CAAGTTTAAA	TCCATTTTGC	360
	CTTCTACTGC	CGCAACGTGG	TTTTTTTGCAA	AGCCAATTTT	GCCGTCGGGG	CCAACCTCAC	420
30	CTCANTACCC	AGNTCTGNGA	GTCATCANCA	TTCCCCGCTN	TAGGCCCCAG	TGANTAGAAG	480
	TGGTCTAGGT	CGTTTCAAGA	GGAACATNAA	TNT			

## 1003UP

	GATCTTTAGA	CAATTATGAC	ATCCAAGTTT	GGTCCGTTCA	GACTGGTCAG	TTGCTTGACA	60
	CACTCTCTGG	TCACGAAGGC	CCAGTCTCTT	GCTTGCTCTT	CAGCCGGGAA	AATAGCATAC	120
	TAGCCTCTGC	CTCTTGAGAC	AAAACATATA	GAGTGTGGCC	GATATTTGGG	CGGCCCCAGC	180
	AAGTCGAGCC	TATAGAAGCA	TACTCTGATG	TGCTGGATAT	TTCCATGAGA	CCTGATGGTA	240
40	AGCAGGTCTG	TGTCTCCACG	CTGAATGGTC	AGCTGTGATT	CTTCGACGTT	TGAAACCTCA	300
	CGGCAGGTTG	GCAACAATTG	CTTGCAAGAG	GGACATCATA	TCAGGACGCC	ATTTAGAGGA	360
	CCGGTTTACT	CAAAGAACTT	CGGCAACGGC	CCAAATATTC	ACAACAATCC	ACTACAGTTC	420
	GGCGGCTTTC	AATGNTGGAG	NTGGGANAAA	ATCTNNTGGT	NTAGAATCCN	ATAAGGGTAT	480
	AANCGTCATG	TTCCANAAAT	NATC				

## 1004RP

	GATCTTAAAG	AGGCTCAGTA	TGCAGAGGCA	GTTTCCAGAA	GAAGACAGGC	TGGGCTTCGA	60
	AATCCCTCAG	CTCCCGCCGT	GGAAGAGTCC	GCAGATGAAG	CAACACACAC	AACAGGGCCA	120
5	GCAAACGCCG	CTGCGGCGGC	CGCGCTGCAT	CCTCGGTGCC	CCTTATGAAC	CGAGCAGGGC	180
	GTCGTCCACT	GGTGCAGGCC	AAAAGCGCGA	CTACGACTAC	TCCGTGTTCA	ATGAGAGCAG	240
	GCTCCTCACT	GAGAGCAAGA	TAGACCAGTA	CTTGAAGAGC	GAGGCCGCAA	CGCACAAACG	300
	CGTATTCCAC	CCGCGACCGC	CCCCACGACG	ACAGCTACCC	GCCCCGACTT	TGCAGCCCGC	360
	TCTGCTTGCG	ACAAGCTTCG	GACGANGAGG	GAGAGCCCN	CCCCCTCNC	AGAGNGCGCN	420
	TTNGNGACCC	CCCNNTGGNTG	TTCATCATCC	CCCCANTCCT	CCAGGAGAGT	TTTNGAAAGG	480
10	GCGCCCCNA	NACNCCNTAG	GATTCGTGGA	GGATGGAGTN	GGGCCCTTTT		

## 1004UP

	GATCACCAG	CCTAATGAGT	GGTGCTAGGG	TAGCGGTTAT	TACCGGTACT	AATAGGTATG	60
15	TTAATATGCC	ATCAGTGTCT	GAGCTCACGA	CTGACATATA	TTAGCAATCT	TGGCCTGAAT	120
	ATCGCATACA	GGTTGATTGA	GCAGTTTACT	GATGACAGCA	AGTTGGTTAT	CGTGGTAACA	180
	TCGCGTACGC	TGCCAAGAGT	AAGGGAGGTG	GTAGACCTAA	TCAAAACATA	CGCCGAGAAA	240
	TGTGGYAAGT	CTGGAGCAGT	AGATTTTCGAC	TACCTGCTGG	TGGATTTTAC	CGACATGGTT	300
	AGTGTGCTGG	GCGCGGCATA	CGAATTAGAA	AAACGATATG	ACGCTATACA	TTACTTCTAC	360
	GCTAACGCTG	GCAGGGTGTG	TATTCCCCGA	ATTGATTGGT	TGGGTGCACC	NGGTGTTTAC	420
20	GGGATCCNCG	GGTGTGTGAT	ATCCNCGTTA	GNCNGGGTGG	ANNAATCAGG	ATGGTNGGTT	480
	AGTTTCAAGC	ANTC					

## 1005RP

25	GATCTCCCC	AGGAACCGCG	ACGGGTACGC	AGTCGTGCTT	CTTCCCAGCG	TGGTCGTCAC	60
	GAATTCCATC	AGCATGTGGA	ACTTCAGCGC	GAACATCTCC	TCACGCAGGA	TCCGCGTCTT	120
	CCTCCTCCTC	TGCGGCCACC	GAGAGCTCCG	CCAGCTGCTG	GCACCCGGTC	AGGAAGCACT	180
	CCCGCGCGTT	CCCCTCgCG	cccacCTCCC	TGAAGCAGCC	CACCAGGAGC	CGCCACACCA	240
	TATCATCCCC	GAGCCCTTCG	TTGAGGTGGA	AGTTGTCTGC	CCTAATGCAC	CGCACAAGCA	300
30	CCTTCGGGAT	ATCCCaACCC	AAATCTCCCA	CGAGTGCagG	GTGCTCCCGG	AGCTGCTCCC	360
	AcAGCGCCTC	CAGGAAGCTC	GCCAgCCGCC	CCGCGTTACC	GcTCGCAAGC	GCCTGCTcCG	420
	CGCACAACTC	GATCCCCGCT	GCGAgCGAgA	TcTCGTcCCC	GCCTGcTCCG	CGAATAGCaC	480
	GCCCAGACTC	TCaCCTTCCG	TATTGCGTGG	cGTTTCATAg	AATcAcTCT		

## 1005UP

	GATCTTGcAG	TTAACGGTTC	TTCCATCAAG	GGACAAATGG	GCGTACCGAA	GCTCTTAGCC	60
	CAGCCAAGTA	TCCCACAGCT	GCACAATGCT	AAGGGTGAGG	TAATTGATGT	TCAGTCCCAG	120
	CCCCCGCGGG	GCTGGCGGCA	GGTGCTACTA	NAGCATGGCC	CAGAAGTATT	TGCGAAGAAG	180
40	GTGCGTgAAT	TCGATGGAAC	ATTGCTTACA	GACACTACAT	GGAGAGATGC	CCATCAATCA	240
	TTGTTGGCAA	CTAGGGTGCG	TACTTATGAC	CTAGCTGCTA	TTGCACCTAC	CACTGCACAT	300
	GCaTTAGCAG	GAgCCTTTGC	aTTAGAgTGT	TGGGGTGGCG	CTACGTTTGA	CGTTGCCATG	360
	CGGTTTTTGC	ACgAAGACcC	aTGGGAgCGC	TTGAgGACAC	TGCGGAAATT	GGTGCCAAAC	420
	ATCCCATTC	AGATGTTGCT	TCgTGGTGCC	aACgGTGTTG	CTTACTCCTC	TCTGCCTGAT	480
	AATGCGAATG	ACATTcGTCa	AACAAGCAAA	GGAgAATGGT	GTC		

## 1006RP

	NNNNNGNNNN	NNNNTGTGGG	GCGTGGTAGA	NTAGTGGGTC	TCGTAGACAA	TGGATGCCTG	60
	TAAGCATgTG	TAACGGGTAT	CGTGGAGGGG	TCCCTTCCCG	CCTCCGAAGC	CTTCTTCGGT	120
5	TTCTCAATTT	CCCATAGcAA	TGGCGACTCG	CACCAGTAAA	TCCTCCTCTG	GGTAGGCTCC	180
	GCTCATTAGT	CGAACGGTTC	TCCGTAGCCC	ATCCTCGTCC	AGTTGCGGCG	CCGCGAAAAC	240
	AAACAAACAC	TGGCCGCCCC	GATAACGTCA	GTAGcTATGT	TTCAGcAGAT	TCCGCGGAAA	300
	CCGTCCAACA	GATCGTCTGT	AACCGGTGcA	GATACGTCTG	GGcAGcGGGT	TTTAACTGCA	360
	GCCAGTGcAG	ATTTAACGTG	CGATGGAAGC	CTGCGCGCGG	TTCTGGcTGC	CCGCCGGTGG	420
	CTCCAGCGGA	GCGAGCGCGC	GCGTCGCGAT	GCGCGGcGTa	AGTCTGTgAT	CGcCGGGAGC	480
10	TGAgTAGcGC	TAGCGAAGGT	CACACGGACG	CCGGATAGTA	GaTGGAGcAA	GGGGCCTCTT	540
	TGGACGGTTT	GGTTACGAAA	TNCCGGG				

## 1006UP

15	GATCTCTGTT	CTTTTTTTAC	CTCTGAAGGT	GCCGAATGTG	TGCGCGTGAA	ACCACTCTTT	60
	CGCGATGGGA	TGTTTCCTGA	TCTCCCTCGC	GAGCTGTTTC	ATGTATTACT	TCCTTGTAAG	120
	GCAATCGCCA	CGCAGGACAG	ACCGAGCTGG	TGCCAACGGT	TTCTCCGGCG	TGCCPTTGCT	180
	GAGATGCGTT	CGCATGTTTT	GACCCAGCT	CTGGAATATG	CGCGCGGTGC	GATGCTGCGT	240
	GTGGTACGAT	GCAACGTCAG	CGATCCCGCA	GGGCGGgGGT	GCAGgGGTGT	ACTTCGATCG	300
20	TAGGCCGCTG	TAAATGCTCC	TCTGGGACGC	CGCTCCCGCC	GATCTTACTG	TCCGCCATGA	360
	ACGATGGGAC	AgAgTAGcCG	GGATGGTTCC	CTTTGcAGAT	AGGAAATCTG	GAAGAATTG	420
	GTCCCgCtCC	gcCTGATTG	TtTATACAAA	AAATTGGCCA	TACATTCCTT	G	

## 1007RP

25	GATCTTCTCG	CCGAAGTACT	GCACCATGTC	ATTTCTCTCC	GGTTCACCAT	GAACAAGGAC	60
	ATCTAGGCCG	ACCTCCTCCT	GGAAGCGGAT	GACTTCCTCA	ATCTGAGAAT	TGATGAAGTT	120
	GGTGTA CTCC	TCCGTGGAAA	TCGCCCCCTT	TGCATGCTTG	TTTCTGTTGA	TCCGAATGTC	180
	CTTAGTCTGT	GGGAAGGAAC	CGATGGTGGT	GGTTGGGAAT	AGCGGGAGCT	TGAAAATTGG	240
	CTGCTGCTCC	TTGAGACGCT	CCCCGAATGG	TGCGGCTCTC	GTGGATAGCT	TCTCGTTCAA	300
30	ACCAGCAACA	CGTTCTTGGA	CAGAAGGATC	GTTGGGTGAT	CGCAGAGGCG	GGACGCGCAG	360
	CAATCGAGTC	TGCATTGGC	TCCAATCTCAG	AGGAAAAGTC	TCGCCAGAG	CGTCCTTAGC	420
	GAGGAAACAA	ACTCATGCAG	TTCTTGGMTG	AAAAGAGAAC	CAGCCTGGCT	TNTTGTCCAA	480
	GGAGATCGTT	TCCAAGTAAC	TGGNNTTGAA	NAAGGAGC			

## 1007UP

35	GATCTTGTCG	AGCTCGCCAT	GACAGATGAG	AATCCGACAG	CACGTTTCAC	GGCATTTTAT	60
	GCGCTGGGGC	TAATTAGTAA	AACGGAGGAA	GGCTGTGAAC	TATTGGACGA	GTTGGGCTGG	120
	GACTGTTGCA	TCGATGTTCTG	TCGCCAGCCA	GTGGGTATTT	GGGTACCAA	TAACATCACC	180
40	ACCTTTCTCA	GTTATCCTCA	AGAGAGCGTC	GAGAAAACAA	CCGTTTCGGA	AGGTATCGAC	240
	CAATTTGGAC	CACGGAATTT	CGGGAGGAGG	GACTTCCCCC	CACTGGAGGG	TATCACAAAT	300
	ACAAGTTGAT	ACAATACTCT	GAAAAGGTAG	GAAAGGGATG	TCCTGACAGA	CAACCAAGAG	360
	CTTAAATCCA	TCCTCGCACA	CAGGGGTAGA	CAAGTGANTG	NAAGCGGNGA	TTGATCTTCC	420
	CATGGAGNTC	CAGGATGACC	AGCTCCCCAA	GATTTCCGTT	CGTGGGAANC	GGAATCATTT	480
45	NTACACAGNG	GA					

## 1008I2

	TCGAGACCGC	ATCAAATATC	TGTCATTATG	TAAATGTGCA	TATTATAGAC	TTCTATTTC	60
	AGTACCAGGC	AATTGTGTCC	GATAAATGAG	GTGCAATGAG	CACCCGTCAT	CACCGGACGC	120
5	GATAAATTTT	TTTTTGGGGG	TCAACCATTA	AATCTACGTG	CATCTAACGC	AAGGAGCAAT	180
	TTAGCTAACA	ACTCTTCTTA	TCTTAAGAAT	CGGGTATACC	TCCTCTTCGC	ACATCTTCGC	240
	CTTCTTTAGT	CTCGAGTCTT	AACTACGTTT	AACAATGTCA	GCCTCCGATA	AGATGTACAT	300
	GTGCTATAAC	AACATACACA	AACTGTGTCA	GCAGGTAGCT	GGCCAAATTA	TGGAGCGTGG	360
	TGACAGACCG	GACGTGATTA	TCGCCATTAC	CGGCGGCGGC	ATGATTCTCTG	CAAGAATCAT	420
	CCGGTTCGTT	CTCAAGGTCA	AGGGCCAGAA	AAACATCCCC	ATCCAGGCGA	TTGGGTCTTT	480
10	CTTTGGTACG	AGGACTTGGG	TTTGGGAAGAC	GGGACGGAAA	GCATCGGCAA	GGAAGTTATC	540
	CGGATCAAAGT	GGCTAGACTT	TGGGGGCCTT	GGGCAAACAC	TTTGGACTCA	ACTGATTGGA	600
	AGAAGGTGTT	GGATTGGCGC	CGAGTTGGNC	GANACCCNGA	CACGTCCCTA	CGGTTGTNAC	660
	CGANTTGGGG	AGGGGGNCAN					

## 1008I1

	TCGAGTCATT	TCTTGTAAGT	CAGTGCATCG	ACAAAGTCGT	CTGCTTCGCC	GTTGGCATA	60
	GTTATTTTCG	TTCCATACTC	GGCATCATCA	GCGTCCTCAA	GCGCGACCTG	AGACAACCTC	120
	TGGCGCAACT	TTGTCTGGGC	GCGAAGCATC	TCCAGGGGAC	CCCTGCATTG	ATAACAGGAT	180
20	CGGGAGCGAG	TCGGAACCTG	CCTTGAGGTT	CGCGCGAAGA	GCCTTGATTT	CCTTGTTACC	240
	CCGCGGCTGC	AAGGAATCTA	GGTGAGGAGC	ACGCAGTCGA	AGCAACCACT	TAAACCACTA	300
	ACGGATCGCT	GAGCTTTCTG	TCCAAACGTC	AGAGGCCACC	CGCTGGCTCA	CGATGACAAA	360
	ACAGTTCATT	GNANCGCNAT	GGAAGGNGAT	NCATGTGCGN	NANATCTTTT	NNTCTTTTCC	420
	TCGGACCANG	NGTNANAAC	NACAGTCCCT	GACGANTTCC	TCACCTANGT	CNCCGCAGGG	480
	GATNNTTTCA	ACGCCGCNCC	GTCTNNCCCC	CTCNCNCTCG	NNNACCTTCT	TTGTTNNNGG	540
25	TTTTCTTTTN	CCNNCNCNCC	TNNTNCCNAC	TTNGGTTTTT	NNACNCCNTC	NNNAC	

## 1008RP

	GATCTGTCTT	GGACGATATC	AACGTCTATG	CCATCTTCCA	AACCGTCTTT	TCCACATTGC	60
30	AACAAAATGA	CTCTACAAAA	TACCAGTTAG	TCCTAGAAAA	TATGTCACAG	GACGAACAGA	120
	TGCACCTAGC	ACATATTACA	TCGTTATGAG	CACCATAAAT	CTCATAGTCT	TCCTACTTTA	180
	TCTTTAATAT	TAATAGTATG	TGTATGCCAA	TCGGCGCGTT	ATGCCCGGGT	AACAGTAGTT	240
	TCTTTTCTTN	GAACATCTGA	AAAATTTTCA	CCGATGAGCT	CTCTTGTTGC	AATGGCGCAT	300
	CGAGCTACAA	GTGCAGGTGT	ACCATTCACA	TCCCTATCGG	NATTCGGCTG	TTGNTAGAGC	360
	TGTTAAATATG	ATTGCTTCAG	AAGATACGAG	GTCCCTGGGA	GTTTTCGGCC	CGATGAACGN	420
35	GGTCGCATTG	CAAGCCAATG	CGTGGAAGG	ACTCATTGAA	TTTTCANNGA	CCNGNAGAAT	480
	TAANGGNAAA	GTCANCNGTA	ACCNATTGT				

## 1008UP

	GATCAAGCGG	GAATTTTCGGC	GCAAAATGCAC	GTTAATGCTC	ATATTGTTAA	CAAGCTCGGG	60
	GCAGAAGTCC	GCCGTTTGGG	GCTAGAAATT	TCCACATTGA	AAGCGTTCAA	TAACACATTA	120
	GAGGAAGAGA	AAGCTCGTGC	AGAAGATGAT	ATTTTGAAGC	TGCTAGAGGA	AAATCACACT	180
	GTGCATCATT	TGAAGACTAC	CAACGAAGCG	TTGACTACCA	AGGTAGCCGA	CTATAGCAAT	240
	AGACAAGATA	CGATTCTCCA	GCTGTTGGGC	GAAAAGACGG	AACGTGTAGA	GGAACCTTGA	300
45	AAATGACGTC	GAGGACCTCA	AGCAGATGCT	GCGGATGCAA	GCACAGCAAC	TTGGCCGACA	360
	TGCAAGAGAG	GTTAAGAATT	TAGATTCCCA	TATCTTATTA	ACATTATTNA	TNCAANCGGC	420
	TTGGGTTNGT	TAATCAACTT	CNCCAGATGC	NTAGATTG	GTAGTTAGNC	ANTTTTTTCGA	480
	NGTGGNTCAA	ATGGNGGCCC					

## 1009RP

	GATCTTTCGCT	TGGGGCCGTG	CGTTCACGGT	CTTAGAAAGC	AAGCGTGCAA	GCGATGTCTT	60
	GCCTACCCCT	GGGGGGGCCC	ATAGTATCAT	CGAAGGTATT	GTTCCCTGGC	TCACATATTT	120
5	GTATAGTGCC	CCGCTTTCCCT	GGGAGAGAAT	ATGCTGTTGC	CCCACGTACT	CCCGCAGCTC	180
	GCGGGGACGA	AGTTTCTCAC	TTAAGGGCAA	ATGTGCCATT	TTCTGCAGCT	CACGCTGATC	240
	TGAGTTCACC	GCCCCGTGTG	GACGTGCCCC	CTTCCGTTGG	GGAGAGTCGT	CCATCTCTAT	300
	CACCTCACTA	TCCTCCATAT	TAACGTCCGA	GATCACAGAC	ACGCTATCCT	CATCCTCCAG	360
	CTTATGCTTG	CGCCCCAGCA	TCTCAGATAC	GGACGTGGTC	CTCGCTCCTT	TCGGCTCCTC	420
	CTGCAGGGAT	GCACTCTAGAT	GGTATGGATG	TGATGAATGG	AAAGCCTGCA	ATCTGGNAAT	480
10	GGTAAGTCTC	CCCCCCGTAT	CATTTN				

## 1009UP

	GATCATGCTA	GTTCTGCAGC	TGAGTTTTTA	AAAACGCAGT	ACTGGAGATG	TTTCGCTTTA	60
15	TGGTATCGCT	CCACTAGCGC	ACGGACTGAC	TTTGGTAAAC	GGCTTAGCAC	TGATGCCGGT	120
	ATTTGGAACG	CCCGTCCCTAA	GAAGCTTGAG	TTCGCACCAT	CAATGAAGGG	AGCGCAAGTC	180
	GAAATTTCCC	AGCCTAGAGG	CATGTCACTA	GGGTCAAATA	CGTCTTGTTT	TGGATCGCTC	240
	TGCATCATGA	TATCGACATA	GTAGTCGCAC	ATATCGATGG	AGACGACCTT	GCCGGGGTCA	300
	AATTTGTTAA	ATTGGTTCAA	TCCCTCAGGC	ACTTGGGTGA	TAACCTCAAG	TAGCGGCATT	360
	TCTTCAGGGA	AATCGCCCCG	TAGGAGGGCA	TCGAAGNCAG	AGTTNGACGA	ACCNCAGGCG	420
20	GGGGGANTCT	TTGAAGGGAG	AAAGAGGCCG	GGAANTGGTA	CCACTCCGCT	CCCCNTCANA	480
	AGTTGGCCCC	AGCCTCAATN					

## 1010I2

25	TCGAGGTGGC	GGGCGGGAAA	CCCCTGCGCA	ATCCTGGCCT	CCAGCGCCCG	GCTGACTGCG	60
	GGTACCGTCA	AGCACTTGAA	GTGGCTCCGC	TCAAGATAAT	CCACCGCCTC	GTTCGCCCCG	120
	AGCCCGCGAC	TCCCGTGAC	ATCCCGCGGG	ATCAGCTTGA	ACTCCCCCGC	GCTCAGCCAG	180
	AGTCGGTTGT	TGCCCACCGG	GTAGTCGTAC	TCCTCTGGCA	GCGCCTCGCT	GCTCATCATC	240
	AGCAGAAAGT	CGCCCTCTGT	GTCGCACATC	TTGATGAAAA	CCTCCGCGCC	CTGAGCCCGG	300
30	GAGAATCGCT	GCAGCACCCC	TGCCACCAGC	GCCTCCTCCT	CCTCGGGTTG	TCCGCGACTT	360
	CCACTCCGCC	AAGCACCATC	GCCTGCCCTC	CCGCGCCCCG	CACCGCCCCG	AGGTGCACCC	420
	GCTGTACCCC	TGNCACGGGT	AGTGGTCAAT	CCACGGCCGG	AACACTCCTC	AAGCTGAGCA	480
	TGTTCTTGGG	ATCTTTGTCT	GGACGTCATC	AAAATTGTCT	ATTTGAAAAA	CGATACAATA	540
	NAGNGGCTCN	GGGGTNGAAA	GTCACACCNA	TCACTCTGGT	TCAAAGCATG	TCTCAATNTG	600
35	CGGGGCATAA	CCAATTCNCN	GGTANGCA				

## 1010I1

	TCGAGGCGCT	TACGTGGGTC	CACCTGAAGA	TGCGGCAGAC	GGCGCACGCG	GAGCTGGTGC	60
40	GGGCGAACCC	CACCGTGTTC	CCCCTGCTGC	TGGCGAACTT	TCTCAGAAAC	GATCTGTTCG	120
	TGACCGGGGC	TGCGATGGAG	GGCCAGGAAG	CGAAGTGCAG	CGACGTGCAC	GTGCTAGTAC	180
	CGAAAACACA	CGCCGCGCTG	GCGTCTCTCC	TGCTTGACACA	TAGTCCCGTG	GCGCGGGGTG	240
	GCGATCTTGG	CATCACCCCT	GGCGACATTT	TATCGTTGTC	CCTGCAGGAT	GCACTAGACG	300
	CGGGCCAGTT	AACGACAGCT	GAACCCAAAAG	GAAAGTTAGA	GGGTGACCTA	GTAAGCGCTC	360
	TGGTACATAC	AAAACAGCTA	GAGCGCCCCG	TGGAGTTCTC	TACGACTGAA	TAAATACGGA	420
45	GGTACCGACT	TGCGGACAAA	GAGGCGTCTA	TGGATGCCTT	GGCCTGTTCG	TGGAGATTTT	480
	CTGACAGATT	TAAAGATGAC	GATGAGGTAG	AATGACATTT	CTTGTCAGGG	TCTCAAGTGG	540
	GATGAGAGGT	CGGCATTTTC	GAAGGAGNNT	GGTTTATNAN	NANATCTTGG	ATTTTCTGAG	600
	GGGGCTNAGN	TNCAAGAAAG	TCANATN				

## 1010RP

	GATCCGGCTC	GCAAAGGAGA	AGATAGAAGA	GCAGAAAGAA	TACCCGGTGC	AGGAGTTTGA	60
	CAAAAAGCTG	TATCATAGCA	ACCCCGCAAG	GTACTGGGAT	ATATTCTATA	AAAATAACAA	120
5	AGAAAACCTC	TTCAAAGACA	GGAAGTGGTT	GCAGATTGAG	TTTCCTCTC	TATACGAAGC	180
	TACCAAGAAA	GATGCTGGTT	CAGTGACTAT	CTTCGAGATT	GGGTGTGGTG	CGGGCAATAC	240
	CATGTTCCCG	ATCTTATCTG	CAAACGAAAA	CGAACACTTA	CGCGTTGTGG	GTGCGGACTT	300
	CTCCCCGAAG	GCCGTGGGAA	TTGGTAAAGA	CGTCGCAAAA	CTTTAACCCC	TCGAATGCCC	360
	ACGCGACGGT	ATGGGACTTT	AGCCAACCCT	GATGGTCTTT	TGGCCGATGG	TGTCGAGCCG	420
	CATTCCGGTCG	ANATCGNAGN	AATGATTTTN	GTTTTAGTGC	CTNGGNGCCC	ACAGGGGGCC	480
10	AGGNTNTGGT	TATTGGANAA	AGTCTTNANC	AGNGGGT			

## 1010UP

	GATCAGGACA	GTAGCAGCTT	GA CTGAGTAT	CAGCAGGAAA	AGCCTAGCTA	ATTGGCGCGA	60
15	GTACAATTAC	AAGTACCTGT	CTGACTACTT	CTTTGGGTGG	GATGCCATAT	TTTTTAGGAT	120
	GGCCTGCAAC	GGGCCGGTGG	GGGCGCCATC	CAAATTTATG	GAGTTGAAGA	GCTGTTCAAT	180
	GCCCTTTATC	CCATCTGCAC	CGTCTTTATC	GCCGAACATG	GCATGCAACT	CTTCAAGCAT	240
	GATATCTTCT	TCCTCGTGCT	CTGATCCGGC	GTTGGTCGTC	GTTTGGGCAG	TCTTCGTAGG	300
	CGCCATTTCT	GTAATGTTGA	AGCTGGTCTT	TGGTCATCTT	CAGACCTTCC	CGTCAGGAAA	360
20	TATCAAAGAA	ATCGGCTTCA	CTAATATCTA	CGCCTCACTC	TCGAAAAATG	TCCGAGGCTC	420
	TTCATCCCCA	GCTGAAGGAC	CCTGACCAGA	AAAATGTCAA	TGGTACTCAA	CGCAACTTTA	480
	ATNTTNCAAG	AN					

## 1011I2

	GATCTCTTGC	ACCAGTCCAA	ATCAGCGGGG	TCGTCCACCT	TTCTCTCCATA	TATGATTTTG	60
	CCGATGGTGT	CGCTGACAAG	CTTCCAGGGC	ACCAAATCGG	GGTCGACATG	CTCCTTGCCG	120
	TTACTGCTCT	GTTCAAATAT	GTGGTCCAAA	AACTTGCTAC	CTGCGTGGA	GTCACCATCG	180
	TGGAAGTCGT	ACTTCTTGGT	GAATCCAATA	GGCGCGAGAC	GGCACCTGGC	CATGATAATA	240
30	GAGTGGAACC	ACACGAGGAT	GAACCTTGCTA	TGAAGTTTTT	CTACTGGTTT	GACATTCTTC	300
	AGTTCTCTG	ACTGAGTCCG	CCACAGCTCG	CAGACTGTGT	TTAGAACGCC	GGGCTCACCC	360
	TCGTACGCTA	TCTTATAGTT	CTGCTGAGCA	AAGGAACCAC	TAGAGGCTTG	CTTTGGGATC	420

## 1011I1

	GATCTGCGCG	GCGGATGTTT	AGCAGCGACG	CGTATCTAAA	CAATTTGCAA	GTTGTCCAAG	60
	GCCTGACCGT	TCCAATAGAC	CGCTCTAGCT	ATTCCCAAGT	TGACAAATGG	TTTAAATCGC	120
	TAGATGCAGC	TGCAGAACGT	ACAACCTGCT	GGTTAGAGCT	GTCGGATGCT	TCGGCCCTGC	180
40	AAAACCTCTA	CGCTCACGAG	GCCAGGATGA	TCTGCAAAAA	AATCATCCAG	ACCAATGGCC	240
	CCACATCTTT	AATTCACTGA	GTGTAATGTC	CATACCTCCA	GTACTCACCA	GTCTTTTGGT	300
	TTTCTGGATG	TCAGATACCA	GACTATGTAC	TGAATAGCGA	CAACATTAGA	TATCTAAAAA	360
	GTCTGTCCGT	TTACAATCTT	AAGGTCCGGT	GAAAGAAGAG	AAACAATCTT	CGAAAACAAT	420
	ACTAAGGCGA	ATATATCAAC	GTAATATGAC	CGCTCAGGCT	TCGGATAACA	TTCCGATATC	480
	AGAGGGAGAA	GACTCCGCNG	GNGTCTTGNC	NNTCNGGCGN	AAATTGCNCA	GTNTTNATCC	540
45	CGGNAGCCNC	CCACNGGTTT	TCANACCCCT	TTTTNGNGT	TCNCGNCAAT	NAAGGGNGNC	600
	CTCCTGCANT	TACCCTANNA					

Pag1011rp

5 1 GATCCAAAGC AAGCCTCTAG TGGTTCCTTT GCTCAGCAGA AGCTATAAGA  
51 TAGCGTACGA GGGTGAGCCC GGC GTTCTAA ACACAGTCTG CGAGCTGTGG  
10 101 CGGACTCAGT CAGAGGAACT GAAGAATGTC AAACCAGTAG AAAA ACTTCA  
151 TAGCAAGTTC ATCCTCGTGT GGTTCCTC TATTATCATG GCCAGGTGCC  
201 GTCTCGCGCC TATTGGATT ACCAAGAAGT ACGACTTCCA CGATGGTGAC  
15 251 TTCCACGCAG GTAGCAAGTT TTTGGACCAC ATATTTGAAC AGAGCAGTAA  
301 CGGCAAGGAG CATGTCGACC CCGATTTGGT GCCCTGGAAA GCTTGTCAGC  
20 351 GACACCATCG GCAAATCAT ATATGGGAGG AAAGGTGGAC GACCCCGCTG  
401 ATTTGGACTG GTGCAAGANA TCTGCGCGGC GGATGTTT CAG CAGCGACGCG  
25 451 TATCTAAACA ATTCGAAGTT GTCCAAGGGC TGACCGTTCC ATAAACCGCT  
501 CTANCTATTC CCAGTATGAC AAATGGGTTA AATCNCTAAA NGCANCTGCA  
30 551 GAACGTACAA CTGCCCTGNT TANANCTGTC GGATGCTCGG CCTGCAA ACT  
601 TCTACNNCNC GAGGCCAGNA NGATNGGCAA AAAAATCTNC AGANCNANGG  
35 651 CCCCCTCCTT TAATCCCTNG ANTNTNATNT CCAACCNCCN TTNCCCCATC  
701 TTTTGNNTTT TGTTNTTAAA AACCAAATTN TC

40  
45  
50  
55



1012/RP

1 GATCCTAACC CAACTGCACA AAATTGTCAG TCATATGTTG GGAGGCAGTT  
5 51 TACCCTTCCG CCGCAAATA CATACTTCTC CTTAGGAAAC GTCCTCGCT  
101 CAGGACTGCA ACTGCATTGA CGAGCAGCAG AATAACGTAG AATAGCTTTC  
151 CCAGGCCAAA TATCATCCCT CCACGTACAG TCTATCAGCA GTGTACTGCG  
201 CTGTGCGAGA AGTGGCATTG ACAAGATAAG CAGAAGTAGT TCTAAAAATC  
251 AGTGGTCACC AACGCGAGGC TGCAAATCG TGTTGTTTAT TCCCATCTCA  
10 301 AAGCATCGCC TGAAAACAAA GGCTCACAGT TGCAGGTGCC CCCGCGTGAT  
351 AACAGATGAT AATTTATATT TTAAGTTATA TTAACACACA TATACAAAAA  
401 GATTTGGTAG TGGATTAATG ATGATTTGCT TAATCAGCGT TACGTCTTGC  
451 GGCCTTCTTA GCCAATCTCT TACCGGTACC AAAGACCTTC TTACCTCTGT  
15 501 TCTTTCTTTG CTTTCTCTGT TGTCTGGAAG CCTTCTCAGC CTTCTCAGCC  
551 ATGCCGTATC TGACCAATCT GTANGTTGGC TCGAACTTCT TGGCGTCNGC  
601 AACAGAGTTG TAGATCAAAC CGAAACCGGT GGAATTGCCA CCACCAAAC  
20 651 GGG

## 1011UP

	GATCTTCACA	CGCACTATTT	GTCCAAGGGG	CTTCAATCGT	CATTGCATTA	CACGAAGAAA	60
	CAATACTTAC	ATGAGAATGG	AACAATAATA	AACTAAGCGT	ATGGTGCCCTA	ATGATTGTCC	120
5	AGATGGGCGT	TGCTGTTTCG	GAACAGTAAA	TGCTTGGCAA	ACTCATAAGA	TGTCCACGAT	180
	ATAGCAGTTG	CAGGCATGTT	GCTGATAATT	CTGGGTTTTA	GGCCCCGAAA	GAAACCGGAC	240
	CAACCATATG	TTTTGTGGAT	TGCAGATGCA	GCCTTGCGGA	ATGTGTCAGC	CTCCTTGAAC	300
	AGCTGACTTT	GAACAGAATC	TGCACCGCGA	ATCTGCAATA	CTGTCTTCAC	GCAGTCTAGC	360
	GGTGTGGGTT	ATGGCGGCAC	ATGTTGGCGC	CCGGATATCC	CACCGCACAG	ACAATGTATC	420
	CAGGGGTTTG	TAGCTGGTTA	CTCGGATTGA	TTATTTTGGT	GGATGATTCA	ATAAATTACA	480
10	AAAATTCAAC	GCTGCGACGG	ATTGTTTCATA	GCAATAGTTG	TCCGGTTATG	ATTAGAAAAA	540
	CGCTTGAAAT	GCCCCCTCGT	GGTCAATCCG	CACGGGGCAT	CCCAGCAATG	ANCANTGGGG	600
	TGAANTGAAC	TCTTTGGTGG	GNGNNANCGG	TCCNNAGGGA	C		

## 1012UP

	GATCTTCCTC	GAGCGCACCA	CGCCGCCCCA	CACAGACTCC	GAGAACCTGC	TCTTCCTGGA	60
	GGGCACCAAA	ACATGCTTCC	AGATGTTTAC	GCAGCAGGTG	GAGGTGCGCG	CAGGCTCGGG	120
	CCAGGCGAAG	ATCCTGGTCG	GCGTCGTGCA	GCGCTTCTGC	AAGCTCCTGT	TCGAGCGCCA	180
	AAGCCACTGG	ATGCAGGCCA	TTTCGTCCGA	GGTCAAGAAG	TGCCTCCAGT	ACAACCACAA	240
20	GTATGAGAAA	GACCCCGACA	ACATCGCGCA	GGAGGAGGAG	TGCGCCGGCG	GCCTCGTCGA	300
	GTACCTCGTC	GCGGTCGCCA	ACGACCAGAT	GAAGGCCGCA	GACTACGCCG	TCGCCATCTC	360
	GCAGAAGTAC	GGCTCCATGG	TCTCCAAGGT	GCACGAGCGC	ACCATCACGA	ACCGCATCGA	420
	GGAAGACCCT	CGACGGCTTC	GCAGAGGTCG	CCAAGTGCAG	CAACAGCGGC	CTCGTCGCCC	480
	TGATCTTCGA	CGACCTGCGC	CGCCCCTACG	CCGAGATCTT	CAGCAAGGCC	TGGTACTCCG	540
	GCAACCAGGC	GCAGCAGATC	GCAGACACCC	TCTACGAGTA	CCTCGCCGAC	ATCCGCAGCC	600
25	AGATGAACCC	TTCTGCTACT	CCACCCTCGT	CGAGTCCGTC	ATCGAAGAGA		

## 1013I2

	TCGACAAGGT	GACCAAGGAG	AAGTCCAACG	GTGCCCTCCGT	GCCATTGGAC	GTCCACCCAT	60
30	CCAAGGTTGT	CATCACCAAG	TTGCACTTGG	ACAAGGACAG	AAAGGCCTTG	ATCGAGAGAA	120
	AGGGTGGCAA	GTTGGAGTAA	ATGCATTCCA	CAGGTCAGCC	AGCATATTAT	AAGTAATTAT	180
	GTTCTACCAA	CTCTCCTCGA	TATATAGTAA	GTTCAGAAAG	TCGTGTTTCA	CTAGTGTTTA	240
	TCAGTGGGGA	TAATGACTGC	TCTGGTGCTC	CGCTCGTGCG	CAGCCATTCT	TGGCGGACAG	300
	CCATGACTCC	CGCGGACCCG	TGAACAGGCG	CGAAATTCCG	TTCTCCGGGC	CGACCACCNT	360
	TGGACTCTTA	TTGATTTCTT	TCCGCCCTAA	GAAAGTAGAC	AGCGCCTACA	TATATGACAC	420
35	ATCCCTGTCT	GGGTGTTTAA	GGAGCACCGC	TCTGAAGAGC	AGGGAAAACA	CGGAGTCACT	480
	AGGCTCTGCT	ACGGCTCGAG	GTTTTTGAAG	TGAGTTTGNA	ATTATTTCGT	CNNTGAGAA	540
	TGANAGGGGT	GGAGGCCGTC	ACCCGATCAA	CAGACNANCA	GGCAATGGTN	TGAGTNGNAA	600
	CACAGCNCGG	CGAGAACGTG	GCAANCNTCN	ANGNA			

## 1013I1

	TCGACGCGGA	CAGCGTACTT	CAATCTGTAG	ACAGAAGAAA	CCTTGCCCTC	TTGGCCCTTC	60
	TTGGAGCCAC	GCACAACCAT	AATCTCGTCG	TCCTTTCTGA	TTGGTAGAGA	CTTGATGTTG	120
	TACTGCTCTC	TCAACTCCTT	GGATAGAGGA	GCAGACATGA	TCACGCGGCG	CTCGGAAGAT	180
45	GGCGCGTTGA	AGTACGCCTT	TCTGGCCTTT	CTTCTGTGCG	AGGAAACGTC	TGCAGACATG	240
	TTAGTACTGT	GCCGGGCCAC	CAACTTGTTC	CACGCACTGG	ATTATGCTAG	GTCCGCCTGC	300
	GCGCTGGGCC	GTATGCCCCAG	GTTACCACGG	ATCGCAGCGC	CAGAGACGCT	CATTCCCAAT	360
	GTTTCGGGAG	CCACCATCGT	TCTGTACAT	ACCTAGAGAT	TGCTTAGCCA	TTGCTGATTC	420
	GCCTGGTGCT	GTGTAAGAAC	CTCTGTTTCA	NNATGTGNAN	AATCTCAATN	GTCGNAACCT	480
	TTTCANNTTG	TCCCGNCTAC	GCTGNACCCN	CTNNCNNTCG	TNAANCNNCN	NNNNNNNNCN	540
50	CAANCGTTTC	GCTANNNTNN	TCCTANANAC	NNANANNNNNT	CNNCNNNNA	NCCCNNNNNN	600
	CACNNNTTTC	NACCNCCNNN	CAANNNNNNN	NNCNNNNNNN	NANCCNNNNN	NATNCNTCAT	660
	NCCCCCTTNC	NNNACTNNNN	ANCCNNNNNC	TNNNNNNNAN	NTNNNNNNNC	ATNNNAACNA	720
	NAACNCC						

## 1013RP

	ANAATGGCTG	GTAGTTATTG	TTAACCACTA	GTTTCTCCCC	GAAGTTGAAG	TACTTCACAT	60
	AACTCAGCCC	CTCCGAGGGA	CTCATCTCCT	CGTACAGAGG	CCTATTCAAC	TCAATGCGCT	120
5	GCTTGTAGTC	CTCCAATGCA	TCCTGCCTAT	TCCAACCCCT	GTNGTCTGCA	GAGGCTGCTG	180
	CCATCTCCAC	TGTGCGCGCC	CTCAGAATTG	ACTCGCTCAC	GACAGACTCA	ACGAAGAATA	240
	CTTTTACATT	AAGAGCAGCA	AACTCCTCGG	CGAGCATTCT	GCGCTCCTCG	CGCATGATGT	300
	TCATCCCATC	ATAGACAGNA	AGCTGTCCCT	GCTCGAAGAA	CTTCTTCATG	TCCGCTGGA	360
	TCTCGGCTAT	CAGCGTGCGC	CGCAGTCTGA	TCCCTTCCGG	CGTAACTGGT	CTGGTAGAGA	420
10	AGTAGTCCAG	CGGTAGNTTC	ACCATCCCCCT	GCGGGACCCG	NGNCCNNCGA	TACTCGGACA	480
	CANTGAAGGA	TTGTGTGNGC	ACCCCNAGCC	ACCCCCGTAT	TGCGTGTATT	GNCACCGNAA	540
	CAANNNTTTT	GGGTGNTCGT	TGNAGGCCAC	CCAGGACGNA	CCAAAATTTT	TCCCCGNTTG	600
	GAAANCCCCC	CAGNTCCCAN	NNNGNAAATT	GGNCCCCGGG	AATTTTITNG	CCCTNGGCNC	660
	CNCCGNCNG						

## 1013UP

	GATCGCTTAC	CAGCCCAGTA	GTGCGCCACA	GGAACTTGAG	GTGGCTATC	CGGCTGACAC	60
	GAAGTATATC	GACCCTTTGG	CAGAAATTGA	CATATGTAAA	CGGGATTTCG	CGCATTTGAA	120
	AAAGCTCGGA	GTCAATACCA	TTGCTGTTTA	CTCCATTGAT	CCAACCAAGC	CACATGACGT	180
20	TTGCATGGAG	GAGTTGAGCA	AGCTGGGAAT	CTACGTTCTC	ATCGATTAT	CAGAACCAGA	240
	CACCTCTATA	ATTAGGGAAA	CACCAACATG	GGATGTAAAA	GTATTCCAGC	GGTACAAAGA	300
	CGTAGTAGAC	TCCATGCAGA	AATACAATAA	TGTTCTGGGC	TTTTCTGCTG	GTAACGAGGT	360
	CACTAATGAC	CGCACGAACA	CAGACGCATC	GTCTTTTGTG	ACGGCGGCTA	TCAGAGATGT	420
	CAAAAACCTAC	ATCAAGCAAA	TGGGATACAG	AACTCTTCCG	GTGGTTTACT	CACCATCGAT	480
	GACCAGGAGA	CGAGGGATCA	CTGGCCTGAT	ACTCCCTTC	GGTNGCGTAT	CTNCAGANNC	540
25	TTTTGGCATA	ANTTTGTCCG	ATTGGGCCGG	CATCCACCTN	CNGACGANCG	TTCAAGAGAG	600
	NGGCTTNCNA	TTCNNGAACT	CCCCTTGCCG	CC			

## 1014RP

	GATCAAACTG	CCGTCTTGGC	GCAGCACGCG	GCCgcgCGAG	TTGGATACGC	GGTCCGCGTC	60
	AAAGGCCACG	CCgAGCGCGC	CAAACCTCCG	GAGGGGCTGG	CCGCGGTAGC	CCAGTGACGT	120
	GATAAGCACG	TCCAATTCTG	AATCCAATTG	CTCGTCCAGG	TGACGTACAA	CCTTGTTTTC	180
	AGGGGTCAGG	GAGTTTTTGC	AGACGGTCAG	CGCAGATATC	GCGCCGGCGC	CGTCCCTGCG	240
	GATGTAGAGC	GGCGTCTTGA	GATAGTCGGA	CACCCAGGCC	TTGGAGTAGC	CTTCCGCCGG	300
35	AGGAGGGTAT	TTACTCGCGG	ACTTGTCTGC	GCGGGCGGCG	TACGGCAGCA	GGTACTGCTG	360
	GCACATGTCA	ATGCGGCGTT	TCGTGCGCGG	GTCgAgCGGC	AGCgCCGcCC	ACGCCTcGGG	420
	CGTGAAGTGC	TCGGGCGCGA	TGTGGCCGCG	CACGCCGCAG	CGCTCGAGCT	CCCACATCTC	480
	GCGCAACTcC	TTGNTCGTGA	ACTTGTCTGcC	GAGGAAGTCC	CGGCGCCCGA	TGAGACGCAC	540
	CTCCTCGAGC	GGCgCGCGCC	GcAaCGCCTG	CAGCGCGTgC	gGGTTTGATG	TCGGtCTGGC	600
	CC						

## 1014UP

	GATCAGTGTT	CGGGGCGAGC	CGGAGAGcAt	ACTGCTGTCA	TGTCATATACC	AGGAGCTGCT	60
	CTCGCGGGTC	ATTGAGGAGT	CCAAGCGTTT	TGCAGACAGG	GACAGCACCA	AGCACATCAC	120
45	AGCCGAGCAC	CTAGATGAGG	CGGTGGAGGC	GTTGCTGGGA	GATGTAGACC	GAGGCGCGGA	180
	CGGGGCGATGG	CCTTGATGTA	AGTCTATGTA	CAGGATATTA	GCTTTCAAAA	TGCATGGTTG	240
	GGGTACTTCA	GCGTTTCCAC	CATGGAAAGG	GCGCTGGCGG	CGTCGTTTTT	GTTGAGCACG	300
	AAGAGGCCCT	GGAGCTGCGC	GGtCGACACT	GGGACGCCTA	GCGCGACGGC	CTTGGCGACA	360
	AACTcCGGgC	AGAGCGCCgA	GTCGTCCGGG	TAGAAGCGCA	gGAACATCTG	CTCGATCTGG	420
	TGCGGCGgTTG	CGTTCCCCAC	AAGGACCTTG	TAGTCGATgC	GGCCCGgGCG	CaGCACGGCG	480
50	GGGTGAGGGA	CCTCGGGATG	GTTGGTGGTC	ATAAAGGTGA	TCATCTTCTC	ACTGGAGGCG	540
	ACgCCGTcCA	GGGCGTTGAg	CAGCCCCGCTG	AaCGTGACGC	CGTTGGTGTA	ACCGTCGTCG	600
	TTCTTCTTgC	GCTTgACAAA	GGCGCGT				

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1016RP

	GATGTGAaTC	GATGTGTGGA	GACGAGTGTA	ACTAGACACA	AGCTGGCGAT	GCAGCGAGAT	60
	CTAACAGGAA	AGGTGCTGGt	TGGGGAGAAA	AGGTACTACG	AAGAGGTAGT	CACTAGTGTC	120
5	ACCTACAAGC	CTACACACCA	CCAACTGCGT	TACGAAAATC	TAAATACGTA	CCTCTATCCT	180
	ACAAACTACG	AGGTGcGCGA	ATtCCAATTC	AATtTTGTCC	ATCGtGCGTT	ATTCGAAAAT	240
	GTGCTCTGTG	CGATTCCCAC	AGGTaTtGGT	AAGACCTTCA	TTGCCAGTAC	GGGGATGCTC	300
	AATTACTATT	GGTGGACAGG	GGGCACAAAA	ATTATTtTTTA	CTGGTCCCAC	ACGACCACTT	360
	GTTGGGCAGG	AAATTAAAGC	ATTCCtGGGG	aTTACTGGTt	TTCCCCNTTA	TGATACGGGA	420
	ATNCTTCTTT	GACAAGAGCC	NNNNGCACAG	GGNACAGATT	TGGGNCAAAA	GAAAACGTTT	480
10	TTTTTTTCGN	NAACGCCCCC	CANTGGGGGG	GNAANTTTCC	CCNNCGAGAG	GGGGGACTTN	540
	NNTCCCCNNA	GANNNTNGGN	TTTTCTNGGG	NNTNNGNNGA	NGGNTCCACC	CCNGNCNNGG	600
	GGGGCCCACN	NCCCCCNCNN	NNGGNNTTTT	NNGNNNNNTTN	TTTTNACAAA	ANTTNC	

15 1016UP

	GATCCATCGA	ACGTCCATTT	TATACGACGA	CATTTTTTATA	CAATTTTTTAT	TTAATAATGA	60
	GGATTTGGCA	TTCCCTCAAA	CTCGCTGACT	AGAAGTTAGC	TGGTGCTAGT	AGTGTAGCTG	120
	GGCTAATGTC	GACTGAATTG	CCGTTGCCGG	TGCTGGAGGA	TTATTTTGTG	TCCGCAGCTA	180
	ATGCCTTCCT	GCCAGATGAA	TTCCCAGTGA	AAGAATTGCA	AGATGAATAC	TATCGACCTT	240
20	GGGAAACGAT	TGTGAGTAAT	CTACCCGCGC	TATTGTTGGC	GCGACAGCTG	CGGGATGTGG	300
	TGGACCAGCT	GAAGGTGCTG	GAGGTGAAGA	AGGAGCTGTT	CGACGATATT	TCGGCAGGTT	360
	CGGCGCGCAT	ATTCCGGCGTT	GGGCTTCAAC	GTCAATGCGT	ATGTGTCGAG	CTACGACGAC	420
	GCGTTCGACA	CGATT					

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1017I2

	GATCTTCTTG	GCGTCGGGCA	TCAGACAGGC	GTAACATAAT	TGATCATTC	TGGTGCGGGT	60
	GAGGCTAACT	ATGATGCATT	GGAAGTTAAT	CCTTACGAGA	CGACGAAGCA	AAGGAAAGAG	120
5	CAGGAGGTTA	GATCGCTACT	GAACAAATTA	CCTGCTGATT	CTATTGCATT	AGATCCAAAT	180
	GTGATTGGTA	CGGTCGACAA	GCGTTCTGCG	CAGATTAGAT	TGACCGCCAA	AGACCTGACC	240
	CAAATCGCAA	CTGATGAAGA	CATGAAATCT	AAGGAGAATA	GAGACATTCC	AAAAGCAAAC	300
	CCTGCTGTGA	AGAGTAAGAA	ATTCAGGTCT	GCGTACATT	CTCCGTAAGA	AGACGCAGAA	360
	TGTTGTAGAT	GAGAGGAAGT	TGAGAGTACA	GAAGCAGTTA	GAAAACGAAA	AGGNNGCCCN	420
	CTTGCGGAAG	CANCAAGCTG	CTGAGGNGAG	CTANCAGNAG	ATNCGANCTN	CCCTGNCCGAN	480
10	GCGTCAGCNA	GTCCACTCGC	NNTNNNCTCA	CCCNNTTTC	TTGCTTNNCN	GAMTTCACNC	540
	CANNNCNCCT	CCCCNNCTNN	NNCTTNCNN	NCCTTNCNN	ACCNCNNCNC	TCCCNNTTCC	600
	NANCCACNC	CCCCNCCNC	NNCCCCNNCN	CCNNNNNNAN	NCNNNNCCCC	CTCTNCCCCN	660
	NCCCCCCNT	NCC					

1017I1

	GATCTTCAAA	TGGGACAAAT	GCAAGGCTAT	TGATCTTATT	CCCAGCAAAC	AAGTGCGACA	60
	TGTATGGTGT	ATTTTGTGTG	GGCAACCGAC	TGCTGGTGAA	AACGGGCTTA	AAATCTGAGC	120
	TAGTTTAAA	GGCATCCTTC	CAAAGTGTC	CATGTGGTCC	TCTCGACACT	GCAAGCAAGC	180
20	CCATGTCAGA	GATTTTCACA	TTGCTTGCTG	GTATAGGCAG	GTTTTCAACG	GAATGTAAC	240
	CCTTGAAGTT	CCTGATATCC	CACAGTCTCA	TGGACTTATC	TGCTCCGGTN	TGTAGCCATA	300
	TAGTAACCTT	GCCTATCTAC	CGCGACACCA	GTGACGGGCC	CGGTACC		

1017RP

	GATCAAGGTT	GAAAACGAGC	AGCGTGATAA	AAAAGAGCAT	GACGCCGATG	TCCCTGAAGA	60
	GGAATTTAAG	ATTAAATATA	CCTCGACCTA	CTATAAGGTT	GAGAAATATGA	CGCGTGAGT	120
	ACCACAGCAA	TTAAATATA	TTGCATTTCC	AAAGGATGAG	AGATTTACTC	CCGCTCGCAA	180
	GTTTAAGGGT	AGCAATGGCG	TTATAGTGCT	ATCGGACAAA	ACTCCTGACG	AGCCGGTCTGA	240
	AGTAATCAAA	ACCGCTAGAC	AGGAAAAAGA	GACGGATGCT	CCTCTGCCTG	CTCCCTTCAA	300
30	GGTTCAGGAT	GACTTAGAAT	TCTGAACCTGA	TAATTAGGAA	GCGTCGATTA	TGTTTCATTAG	360
	GAAAAAGGGT	ATTTTTCCTA	GAAACGAAAAG	AACTTACTGA	TGCGAGCTCT	CTCTAAACAA	420
	GTATATTATG	AGGTGATTTA	TTTCAACTGA	ATCTGGCTAA	CGCCCGGCAA	CTAGGTCTTA	480
	TCTTCTTGTA	GTCACCCTAG	AGGTGGTGGT	CCCCAANCAG	CNC		

1017UP

	GATCTCCATC	CACGTTTTTG	CCTCGTTCCCT	GAGCTCCTCT	GTGACTTCAT	CCTTGATACG	60
	CGCAATTAAG	CCAGGGCCTC	TGTATGCGTA	CGCAGTGTAG	AGTTGCACAA	AGTGCGCCCC	120
	CGCTTTGGCA	AACTCGATGG	CATCCTGGCC	ACTACTGATA	CCACCACATC	CAACCAAAAC	180
	CAGGTTCTGT	TCCTTTGTGT	ATTGGTGTAT	CGTGCGCAAA	GCTTTTAGCG	CAAATGGTTT	240
40	CACGGGCTTG	GCGGACAAGC	CGCTGCCTG	GTTTTTCAGC	TCCTCATCGA	CAGTGACAG	300
	CGAGTCTGGC	CTTTGGATAG	TAGTGTTTGG	AAACGATGAT	ACCCCAATA	CTCGATTTTC	360
	TTGGGCCGCC	TCTGCGATCG	ATTGGAATCC	TGGCTCGGTC	AAATCCGGTG	CGATTTTAAC	420
	AGGAAAGTTG	GTTATGGTTA	CTGGACCAAG	AAAATGCCNC	CGTGGNCAAA	GATTGGGTTA	480
	GCANAACAAG	NTN					

## 1018RP

	GATCATCGTC	GAGGAGTACA	CGCACTCGCT	CTgcgCGTGC	GTGAACTTCG	CCGCGTGACA	60
	CCCGtaCTTC	TTCGACGCCA	CCGTGTTTCTAG	GAACCGGCAC	CCGGCCGCGT	CGTACAGGTG	120
5	CATGTTGTTCG	CACGCCGTTG	CGCTCAGAAG	GTACTGTCCA	TGGTCGTCTGA	ACGACAGCGA	180
	CGTGATCGGG	CCCTGTTCCCT	TCTGCGCCAC	CTTGAAAGAC	TTGACCGCCC	GGAACCCCGC	240
	CAATGTGTCT	TTGTTGATCC	CGATACTCAT	CCCCGCTCGTC	TTGCAGCTTC	CGGTCCTTGG	300
	CCCTCTCGCC	GCTGCTCTGC	ACTGCTGGCT	AGCAGAGCTC	ACCAAAATTT	TTATAGCCAT	360
	GGCCAGGCCA	AACTTcaCTA	ACTGGGGAAC	CACACGACCA	CAGCAAGCAA	TGCCCTCAGT	420
	ATGTcgGtCG	GtCGCACCGT	CCTGGGATCG	CTACTAACCC	GCACAGCTCA	AGCAGATGGT	480
10	GCACTTCAGC	GCCgACCTCG	CGCTGGtGGC	GATGGtGCTG	GCC		

## 1018UP

	GATCGCGTGT	ACGACTTCAT	GCGGATGCac	tACGTTATCA	CCCAGATGGT	GGTGCGGCGC	60
15	GACTTTCCGT	TCATGCGCGA	CTACCTGGAG	GTCCTGGCGC	GCCGGCTCGA	GCAACACGAG	120
	TTGTGCGATG	CCCCCATGTC	TGCCGCTGTG	CAACGGGACC	ACATTGCCCG	ATACACCGAG	180
	CTGCTGATGC	TGTATGCGCG	GAAGTCTGGG	GATGAGAAAA	TGCTGGCGGA	GCTCTTTGCC	240
	TCCTTGGTCC	ATAGTCTGCC	TCGCGGGATG	GGCGGAGCCA	CTCTTCGTCA	GCCATTGCAT	300
	GAAGTCATGA	CGTACCTGAT	CAGCGAAAAC	CAGCCGCAAC	AGGTGCTGAA	ACTGGTGGCG	360
	GGCATGCGCA	AGGCGGAGCC	CAATCGGCGG	CCGGGCAAAAT	CCTCCGTTCC	AGGCACCTTG	420
20	GCGCTGGTTG	TTTCCGCGTT	GCGACAGTTC	AACAATCCTA	ATCTCGTCTG	GAGCTTTATT	480
	GTGCAGGCAT	ACAGAAAGAC	GCAAACGAGA	GTGCTGCTGG	GACAACTCgG	GCTATGGTCT	540
	CTGGCATTTC	ATGGCCGCGC	TGTTGCGCTC	TCTcCCGAGG	CGGCGAAgTC	GCCGCAgGAG	600
	CTGGCGCAGa	TATCGcCTGT	GGACCTGCCG	AAGGAGCTAA	TACTGAAGTC	CGtACCTgac	660
	AGCTGATAAT	GTGCgAGCTC	TATCAGCGAA	TCTATcCgAG	AAgcgATCGc	AGGTGCCCGc	720
25	GGAgGAgTAC	CgCGAGATTT	AATCCAgCTa	TTTGCGCTTT	AcCAGGACTT		

## 1019RP

	GATCCATGAC	CCATGCTAGG	TGGAAGGAGC	CCTTACCCGC	TAACTCGGAC	TCCCTCTTCA	60
30	ATTGCCTTAT	CAGTTTGGTA	TCCACAGCAC	CCACGTCGTA	CAACAACCGC	CCCATCAGCG	120
	TAGACTTGCC	CGCATCCACA	TGGCCTAGAA	CAACAAACGA	CATATGGGGC	TTCTTCTCAC	180
	GTACATATCG	AATGGGTTCG	AATGGGTTC	GCGGGTTAGT	GGGCTGCACA	ACCTTCTTGG	240
	CCGACGGCTG	TTCGCCCTCC	TTCCGCCGCG	AATCCTCCTC	CTCGTCCCTG	TAGTTCTTCG	300
	GGGCGCGCTC	CTTGTTGTTG	AATTTTCAGAT	CGGCCACCTT	CTCGGCCACC	TGCTTAATCT	360
	CAAAGGCTCG	CTTCTGGGAT	TCCAAACACA	CGTCATCCGG	CGAGGGCTTC	ATGAAATTGG	420
35	CACTGGCCTG	CTTCTTAGCT	GCTTTATAGT	TGTTAGGATA	AAAAACTGAG	AACACCTCCT	480
	CCACTCGCCT	CTTGAGCTGG	GTTTTGCGTG	GTTCGCGCA	TCCTGTCTGT	CTCGAGAGGA	540
	GCACGCTCGA	CAGCTGCAGT	GCAgGGCGCG	CTGCagGCTT	GAAGGACGGc	TGACGCTGCA	600
	GAAGAgCCCC	CagGGcCATc	CACTGGTCTT	GcCgtgCCTc	CGTCCCTTGC	GGGCGCGCTG	660
	cAACAgGCTT	TGcCTcAGCG	TCGcCGCGCG	ACTGcTTCGC	AgAGACgACA	GCGTcTGCAT	720
40	cAgCgACgCG	CCCCG					

## 1019UP

	GATCGCAGAT	TCATCATCGC	TGTTATACca	gGCTCTATCT	TCCTCGAGGT	CCTCGGGACC	60
45	AAACCGGGCG	CTCTCTTGTG	TGCCAAGAGG	TGCAGGACCC	TCGGCGCGAT	CCTCGGCCAG	120
	CAGAGTGGCA	ATCTGGTCTT	CATCCGCTAT	CGCTGTACGC	TTAGGCACAA	AAGCCAGTTT	180
	TTCCGTTTTC	TCGCCGTGAT	CATCCTGCTC	GAGCGTGCTC	TTCTGATCTC	TGCGACCCCTC	240
	TGCAAACTCT	TTGAGCTGCC	TTGCTGCTGC	CTTGTCAGT	CGCTTAAATC	TCAGCGGTTT	300
	CTGTTTCTGG	CCACCGCTCC	CCAAGCTCTG	GTCCGGCTCC	AGTGCTGTTT	CCAGTTCGTC	360
	GTCCGAATCT	TCGAAGCTCA	gCGCGACCAA	GTTTCTGGAT	GTGTTTCCCT	TCACGCGCTC	420
50	CCCGTCAAGG	ACAGCCTTCA	CCGTGGTGT	TGTGCGCTCC	TCCTGCGTAC	TcCGCAGGGA	480
	TACTAGCAGC	TcATGCAGGA	ACTTCTCtC	CCCTTAAACT	TGCCAAGCGC	CATGCagCTC	540
	TTAgTGAAct	TCACTGGATC	GTATGCATGC	ACGCGCGCTA	TATTGCATAT	CGGCTGcACA	600
	AACTTTCTGT	GACATTGGAT	gCGGATGTTG	GTGGATCACT	CCTTcAGCCG	GGGtCATCGT	660
	CTTAgCTCCT	ACCGTACTTG	cTcTCTcAgA	TgCatGATGt	GTaCCATcGc	ATcTTcAGcT	720
55	tGaCAGACTT	CCATATACGt					

## 1020RP

	GATCGTTCCT	GTTCCTGCGG	GCAAAGTTCA	GAATTGACCT	AGTGCCAGAC	ATGACAGTAT	60
	CGTTCAAAC	CCTCGGAGAG	TTAGCCTTGG	ATATCCACCA	TGAAGACAAA	AACCAGAGAC	120
5	CAACaGCGGA	TCCTACCAAA	ATGGcCAGAA	TACCGAAAAA	CCAGTGCAAT	TCTCCGGTTG	180
	CTTCACCTGG	GACAGTGACG	TTCATCCCAA	ATAGACCCGT	AACAAGATTC	AAAGGAACTA	240
	ACATTGTTCC	AATCATAGTG	ACCTTTCCCA	ACaTTTCaGT	AACaCGATTG	TTACACCGGA	300
	AGGACtCAAC	TTGCAATTGT	GCCAAGTAGT	TACCAtGTGA	ACGGGAGAAA	ATCTTCTCAT	360
	agGACAgTAA	aTTTTGAAAC	aTCGGGAGGA	CaTGGTCCCTG	AAATATCTCCC	AAATAGAGCG	420
	CtATATCAgC	TCTTGGTTgA	gTGCGCTGGA	CaTGATGAtG	TTGTATGTTT	GAGCCTAgCC	480
10	TGGCagAcAg	AgGGTcgTgT	cCGCTAgCCT	GCAAgTTCgC	aaTGTTTtATC	tCGAGGT	

## 1020UP

15	GATCAGCACC	GTGCCCTTCG	TGTACGCCCTG	CTTGGACATG	GTGTGCGACG	ACCGTGTGTCT	60
	GCATTTCTTA	CACGTGAAAG	CAATCATCAT	CATCGGCTTG	TCCACCTTTTA	TAGACCCGAT	120
	ATGCCGAAAC	TCATCTGCAA	TAgGCGGTTT	CTGGCTGTTT	TGCAGCTGCG	GCGAACCCTG	180
	GTGGAACCGA	TGAgCTACCA	AATGCCCCCC	AAACACCGGA	CCCAGCACGT	ACTGCATGCA	240
	GTTACGGCTT	GGGCGGAGTA	AACCAGCAAT	CCTGAGAgGC	CCCATCGAAC	GTCTAAGCAT	300
	TTTAAACAGT	TATACGTaGT	CAGCGGTTTT	CCTAAAACAG	GACATGAgAg	TGCGTCGAAA	360
20	GAAgGcGTCA	TCTCAAATTT	TTCAACTTTA	GAAGCGCTGC	CCGAAAAAgC	ACCGTCaCCA	420
	TTTATCTATT	ACAAGATGAA	CagTTAGTGG	TGCCGGCaAT	TGTGTcAGAt	ATATgTcTCT	480
	GGACATGGAT	ACAAGACACT	CTCgCCaCaG	AAgGAGCAGG	AgATAgCaTC	gAAAATCTTG	540
	CagAAGGCTG	AgCTGGcTCA	gAT				

## 1021I2

25	GATCTGCGCC	GGATGGCTGC	GAGTTGAGCG	CGGCGAAGAT	GTGTGACTCC	TGCAGAAAAAC	60
	GCTGGAGCTC	GATGTCCTGT	TCCAGCAGCT	GCTTCTCGTC	GCGGTGCGCC	GCGGCAGATT	120
	TCGGCGCGGG	CTCGGTCTCT	AGGCCCGGCG	CCTTGCCGCT	GCGGATGCGG	CGCAGTTCTC	180
30	GTGGAGAAGG	CCCGCTGTAG	GCATCTGACG	GCGCGCGGAA	CGAGATCACG	CGCGGCGTAT	240
	GGGCCGCTTC	GTCTGTCGGAG	CTGGCTGAGG	CGCCGTCCAT	TTCCGACTGC	TCGTCTGGATT	300
	CAGACTGTCC	GGAGCGCGCG	TCGCCCTCGC	TCTCCGGGTC	ACTGTCTGCTC	TCGGAGGCGC	360
	TGGTGCTTGT	GTCTGCTGCTT	TGTGCAGCAC	GGGTCTTGTC	TACATATCCC	ATATCCTCTA	420
	GGGAGCCAAA	CTGGGCCTCG	AAGGCCCTCC	CCTGGGNCCC	GACNTGCTTG	NATTTATCTT	480
	CAATTGTTCG	TCATCCNNGG	GGGTTCCTTG	GCCCCANGAA	GTNTNTNANC	AGGAANCCCT	540
35	AGNANNANGG	TTTTCAAATT	CC				

## 1021I1

40	GATCTCACCC	TGCGCACCAT	CGACAACCCT	GCATACGCCG	GCGGTGAGGT	CATCGGCAAG	60
	GCCCCTGCCC	GCACACTCGA	GATGCGCCTC	AATGCCCTGT	CCGCTACCAA	TGGCGCGGCA	120
	CGAACCCTCG	AAACCGTGCC	TATGAACATA	CGCAAAGGCA	TGGTTTCCAA	GCACCGCAGT	180
	CGCATCCGGG	AGCACGAGCA	GCTGGCCCCG	GACTCCGGCA	CCGTCTTCGC	CAAGGTCCGT	240
	CGCGGAGAGT	TCCGGAAGAT	AGACGCAACC	TACAAAAAAG	ACATCGAGCG	TCGCATTGGC	300
	ACGACCATCA	AGGCTGCAGA	CCGTGCCCGC	AAGAAACACC	GCGATC		

## 1021RP

	GATCCTCGAG	TTTGTGCGCG	GCGGGTCCCG	CTCATTTACC	TAATCCTGTC	TATAGTAAAC	60
	ACGTTGTTGT	ATCTACATAG	CGCACCTGTT	GTAACTTACG	CTGCACGCAT	GCGCGGGCGC	120
5	ACGTCCCCCA	CCAGCGCCCG	GTAGAACGCC	TGGCCCCGCG	GCCGCCCGCC	CAGCATGCAC	180
	AGGCGCAGCC	ACGGTTTCAT	CGTGATCAGC	AGGCCAGTCC	ACAGCGGGCC	CTGCACCAGC	240
	GGGATCAGCA	GGACGTCCCG	CACCACCACC	TTGGCGACGA	CCAGTGCCTG	GATCCCCGTC	300
	TCGCCGTCCG	CCGTGCGCTC	GCCCTCCTTC	TGTGCCCGCA	GGTGTGCTG	GCGCGCGCTT	360
	TCCTTCGCCA	GCGCTGCGCG	GAACGTCTTT	TTCGAACCTG	ACGTCCGGTA	TCGTTATTGC	420
	TTGGGGTCCA	TTGGAACGGC	TGTTCCGGGT	CAGAGGGAGG	ATTCTTCCGC	TGGTTTGGTT	480
10	TTTACGAAGA	CGACCTTCGG	TGAGAATGTC	AGTTTGGCCA	CTNGGCAGCC	CCAGGAAGGA	540
	CCGNGAATTC	AAACCACCTG	AGTNGGGCGN	CGNGTAAAA	ACGCTAAGTT	AGTGCNNTGC	600
	ANACCCNCCT	C					

## 1021UP

	GATCGCGGTG	TTTCTTGCGG	GCACGGTCTG	CAGCCTTGAT	GGTCGTGCCA	ATGCGACGCT	60
	CGATGTCTTT	TTTGTAGGTT	GCGTCTATCT	TCCGGAACCTC	TCCGCGACGG	ACCTTGCGCA	120
	GGACGGTGCC	GGAGTCCCGG	GCCAGCTGCT	CGTGCTCCCG	GATGCGACTG	CGGTGCTTGG	180
	AAACCATGCC	TTTGCGTATG	TTCATAGGCA	CGGTTTCGAG	GGTTCGTGCC	GCGCCATTGG	240
20	TAGCGGACAG	GGCATTGAGG	CGCATCTCGA	GTGTGCGGGC	ACGGGCCCTG	CCGATGACCT	300
	CACCGCCGGC	GTATGCAGGG	TTGTCTGATG	TGCGCAGGGT	GAGATC		

## 1022RP

25	ANNNNNNGNN	NNNANGGTGG	GGCGTGTTNG	AaTAGTGGGT	CTtTCTGcCG	GGGTCTGTGC	60
	AGAAAACGAG	ATTCTGGGGA	GTATCTGAAA	TECTTTGTTG	CGCCGAGCCG	tCTGGGTCTG	120
	CGTCAAGCGA	CAGCGAGTTt	GCGACAGGAA	CTGAAGCTAA	TTTCGTTGCT	GGAGGTGTTT	180
	TGGGGCTTCG	CGTTTTcCAGC	CTTTCAGGAA	ATCTAGAGGG	GCTGTGTGCT	TTGAGGCTGA	240
	AATCAGGGGA	ATAGCCTGAA	TTTGCGAGCG	TGAATTGAGC	GGTTATATGG	AACTGTGGTA	300
	CATCGNCACA	CTGTaCCACG	AGGACAGCGA	ATATCTGACA	GTAGGGcGTC	CTtCGtAAGA	360
30	ACACAGtGTA	TCGCGTgAGA	TAGGTGTtGA	TTGAGTCTAG	CGTgCTAGGT	ACTCTTtAAC	420
	TTtCAGtCGG	tGTTTTttt					

## 1022UP

35	GATCCAGCAG	ACGTTTTAAT	CACCGATTTT	TTCCGGTAACA	TTCAAAATAT	AATTCTCGAT	60
	GACAGTGAGA	TAGATGGTGA	AACTCCAGCT	GGACTTACGG	AATCTGGCCG	GACTCGCAAT	120
	CTGCTAGAAT	TCGCAAAAGC	GAAATTTTTT	GGCANTGTAG	ACGCAGAGAC	TAATGGCACG	180
	CATAAAAACG	TGATTCCAAG	CTATCCAGTG	GTAAATGAGG	ATTTACTAAG	TGGGGNANCA	240
	AATGCATCCA	CAAACAAAAT	GATAAAATTG	TGGGGGATTA	TCATCTTCCt	GGcACTAACG	300
40	TCATTAATGA	TGAAGTACGC	CAACACTGAA	AACATATCGG	GTAGTCGAGc	ACTATTATgT	360
	TTCTCTTAGA	AAAATGCTTC	AtGCTTCATG	GAATTAAGGc	GGcaACAAGT	GCAAGGTTAa	420
	GAACGGaaTT	TTaCTATaGG	CGCGAAATTT	GtaTaTaTTa	T		



## 1023I2

	GTCGAGGGAA	GTAACCAATA	TATTCACGAG	GGCTACCTAT	GGCATCAATG	AGACGTTCCG	60
	AACCAAAGAT	CGTCGGGTCC	TGGGTGATAG	CGCTTCTGTG	TGGGGTCTTG	TGTGCAAGCG	120
5	ACAACCTTCA	TACACGCGAT	ACTTCCTGGT	TAGTGTTAAT	CTCAACAGCG	GTGAAGTTAT	180
	CTTCGATGAC	TTCAAAGAGG	AGCGTTTTCT	GACGGAGGCT	TTGGAGACGC	GAATAAAATA	240
	CACAAACCCG	AGTGAAGTTG	TGGTCGGAGA	TGGCCTTGCG	TCAGAAATCG	AAAAGGTGTT	300
	TCATACTTCA	GATTCCGATA	TCACTCTAAA	TAGGATCGAG	CTCGTCGGGT	TGTATGAAGA	360
	AATCTTTCAGT	GAGCCGCACC	CAGCCTTTAG	GGGCAACGTT	CCTCTGCAAA	CAGCGCTCAT	420
	GCTGGTGCAT	GGCTACCTAA	CAAACTTCAA	AAATGAGAGT	TTACTCTTCT	TCAAGGAAAA	480
10	CTTTAAACCA	TTCTGCTCGA	AGACGCACAT	GATTCTTCCC	TTCTAGCGCT	ATTGGAAGCT	540
	TAGATATTTT	GGGGACAGTA	CAGATAGGAG	CAGTAAAGGT	CCCCTGTTAT	GGGTNTTAGG	600
	TCAANCTAGA	ANAACTAGGG	TTAAGGACTT	GGAGGACTGG	NTTGAAAGGC	CTTNTAATTT	660
	GGTCAAGTCA	ANAGAGTTGN	GGNNGCCAAN	GATTACACNAG	GNGGGNATTN	TCATGGCTCG	720
	GAATT						

## 1023I1

	GTCGAGAAAA	CAGAGCTTGA	GGTCCCCTG	TTCTTTTTCA	CTGCGGATGT	CTCTGTCTGC	60
	TCCACGACCC	CCACTTTTCA	ATTGTGGTGC	ATCAAGCGCT	GCAAGTGGAC	TTCGAGACGG	120
20	GTGTCTGGGA	TGGTGACAGTA	CGCAAACCTC	TTGTGCTTGT	GATCAGCGGG	GTCGTCTCTG	180
	TGTACCGTAA	GCTTGCCGGG	CACCAGCTTG	ATC			

## 1023RP

	TGCCCCGGCAA	GCTTACGGTA	CACGAGACAG	ACCCCCGCTGA	TCACAAGCAC	AAGAAGTTTG	60
	NGTACTGCAC	CATCCCAGAC	ACCCGTCTCG	AAGTCCACTT	GCAGCGCTTG	ATGCACCACA	120
	ATCTGAAAGT	GGGGGTCTGT	GAGCAGACAG	AGACATCCGC	AGTGAAAAAG	AACAGTGGGA	180
	CCTCAAGCTC	TGTTTTCTCG	ACGCTAGGGA	TAACAGGGTA	ATACAGATAT	CAGATCTAAG	240
	CTTGCTCTGT	CCCCGCCGGG	TCACCCGGCC	AGCGACATGG	AGGCCAGAA	TACCTCCTT	300
	GACAGTCTTG	ACGTGCGCAG	CTCAGGGGCA	TGATGTGACT	GTCGCCCCGT	ACATTTAGCC	360
30	CATACATCCC	CATGTATAAT	CATTTCATC	CATACATTTT	GGATGGNCGC	ACGGCGCGAA	420
	GCAAAAAATTA	CGGGTCCCTG	CTGNAGACCT	GCGAGCAGGG	AAACGCTCCC	CTCACAGACG	480
	CGTTNGATTC	TTCCCCACGG	CGNGCCCN TG	TNGAGAAATN	AAAGGTTAGG	ATTNGCAATG	540
	AGGTNCTCCT	TTCANNTNCT	CCCTTTTNAA	ATCNNTGTNG	GTCAAGTCNT	CANATCAAAT	600
	TCCCAACATT	AACACCN TGG	TTAGGGAAAGT	TCANNTTTCN	GGGGCCNNGA	TTANTTCN	

## 1023UP

	GATCTCAAAC	CTGAGAATAT	TCTACTTCAT	CAATCTGGTC	ACGTTATGCT	TTCTGATTTT	60
	GACCTGTCAG	TACAGGCAAA	AGGAACCAGA	AATCCTCAGG	TTAAGGGAAA	TGCCCCAGTCT	120
40	TCGCTTGTCG	ACACAAAAGT	TTGTTC TGAT	GGCTTCAGGA	CTAATTC TTT	TGTTGGAACG	180
	GAAGAGTACA	TTGCACCTGA	GGTCATCAGG	GGAAATGGCC	ATACAGCATC	CGTGGATTGG	240
	TGGACATTGG	GTATACTTAC	TTACGAAATG	CTCTTTGGGT	TCACTCCTTT	CAAGGGCGAC	300
	AACACAAATC	AAACGTTCTC	CAATATTTTG	GAAGAA TGAC	GTTTATTTCC	CAAACAATTA	360
	CGATATATCT	CGCACTTGCA	AGGACTTGGA	TTAAAAAGTT	ATTGGGTCAA	GAAAGAGAGT	420
	AAGCGACTTG	GTCAAAGTTT	GGCGCCAAGT	GAGATTAAAA	AAGCATCCCT	TTCTTTTAAAG	480
	ACCCGTCCAG	TGGGCGGTTA	TTGGAGGGAA	CCAGGAACCT	CCCTTTTATC	CCCGTATTGA	540
45	CGGGAGATGG	GTACGACTTT	GGAAAGNTAT	CACATTAAAG	GATGTTAAAA	AGGCCGGGAA	600
	TCCGGCCAC	CCGGGTTAGT	CTCATATTCA	AAGGCGNGGT	TCNNCN		

## 1024RP

	ATNNNNNGNN	CANNNGTGGG	GCGGAGCGAN	TAGTGGGTCA	GCANGGTGCG	CTCGGTGTgT	60
	GCGCAGCCGT	TGGcATGCTC	GCGGATCCTC	GCGTCCAATA	TACCAGAATG	CATCATGCTT	120
5	CGCTGGCTCT	ATATTGACCT	GGTGGCCATA	TATGAAAAGG	CGGTCCCTGA	AGTTTtGTAG	180
	AAACTCGTCT	GCCTGAGATG	GCGTAGCGAA	CCCAAGGAAG	CATTTATTGC	GGCATTTACG	240
	AGGCCTGGAA	ACACTAACTA	CCCCGTACTT	CTCATCTAGC	AGTGAAGGG	GCACGTCTGC	300
	GGAAGGAAGC	GGCTCTGGCA	ACGTTTTCTC	CgCCGATAGA	GCATATGGGT	TATCCTtGTT	360
	GATGGACTTC	AACAGTTGTC	GAGCATATT	TATCCTGGAG	GCATTTGACG	CTGGCAAATT	420
	TGACAGGTAG	ACACTGgATG	GCGGcGTTAG	tATCGAATCG	ACAGcAGtAT	AGtGACCAGc	480
10	ATTCACATAC	GACCgGACGC	ATgATaTTAC	TTcCTTGNGN	ACTTAANTTN	CCCAATCTTN	540
	NGCCAGATTN	ATTTTCG					

## 1024UP

15	GATCTAAATT	CCCACGCCGC	TGCGGCGGTT	TCTCTGCGAG	TCTTTGcCGT	GAAGCACGAC	60
	ATAATCGAGC	CCAAACACAG	CAAGATCGCA	GAGAATCAAG	CTTATGTAAG	TCTCACGTGA	120
	CTCGANGCGT	GCAGAACGGT	ACGGGTGTGC	ACTGCAGGTG	CCACGCCATG	TCTCACATGG	180
	TTGTaACACG	GcGCGACCGC	GGTTCGGAAT	ATCAAACAAA	CATATgTTTG	CCGCAAAAGG	240
	GACTGGTTCC	CGCAGCTGcC	ACCCgCAGGG	GCACAgcGCG	GcAATGCAGA	GTCGCGTTAG	300
20	GGtGCCgTCG	CcCCGATGGG	GCAGtGTCGC	CGCC			

## 1025RP

25	GATCAGCCCC	TTGCCGCCGC	CGCCGTTGTA	CTTCTGGTTC	TGGATGGACC	CCGGCGTGAT	60
	GGCGCTCTCG	TTGCCGTACT	CGTCGCTGCT	GCGCAAGTCG	CACTTCAGCG	CCACTAGCAC	120
	CAGCTTCACG	CCCTCGCAGT	GGTCCGCAAT	TTCGCTCACC	CACTTGTTCT	TGACGTTCTC	180
	CAGCGAGTCC	CGCGAGTCCA	CCGAGAAACA	CAGCATAATC	GTGTGTGTGT	CCGAGTACGA	240
	CAGCGATCGC	AACCGGTCAA	ACTCCTCCTG	CCCAGCAGTG	TCCCACAGGC	TCAGCGTGAT	300
	TGTCTGGTTG	TCCACGAAGA	TGTCATGGAT	GTAGTTTTTC	AATACCGTGG	GCTCGTACAC	360
	CTTCGGAAAG	TACCTCGCGT	GAACACGTTT	AACAGCGACg	TCTTCCCACA	AGCACCCTCT	420
30	CCGAgGATGA	CGATCTTGCG	CTCGATAgGA	TGCTTCGACG	AcGAgCTCGA	CCACACAGAg	480
	GCATCTTGTG	TTTGTAgAgC	TGGTGGTGGG	AGCTcCtCTG	ATGCCAGTCC	ACGCTACaAA	540
	TACAGCGTTT	GAgAcgAAAT	AcTAgCTGCT	ACTGTCCTtT	CTCTCTGACG	AgGTGCACGG	600
	cGCATCCCCG	TTATAACTGT	C				

## 1025UP

40	GATCCCCATG	AGAATGAGCG	CATCTTGGAT	ATGGCGGCGG	CACCCGGTGG	TAAAACCACC	60
	TATATATCTG	CCATGATGAA	GAACACTGGT	TGTGTCTTTG	CAAATGACGC	CAACAAGGCA	120
	AGAACGAAGT	CCTTGATTGC	GAATATTAC	CGTCTCGGCT	GCACGAATAC	AATTGTCTGC	180
	AACTACGACG	CCCGCGAATT	CCCTAAGGTT	ATCGGTGGAT	TTGACAGAAAT	TCTACTTGAT	240
	GCCCCTTGCT	CAGGTACAGG	TGTTATCGGC	AAAGATCAAT	CTGTGAAAGT	AAATCGTACT	300
	GAGAAGGACT	TTATGCAAAAT	TCCACACCTG	CAAAAGCAAC	TGATATTATC	TGCAATTGAC	360
	TCTGTTGACA	GCAACTCCaA	GCACGGcGgT	GTCATTGTCT	ACTCTACTTG	TTCCGTTGCG	420
	GTTGAAGAAA	ACgAgGCCGT	GGTCGAATAC	gCCTACGGAA	gAgACCTAaT	GTCAgCTGTT	480
45	GAAACCGGCT	gGcTATTGGT	AAGGAAGGCT	CaCTAgCTaC	GA		

## 1026RP

	GATCCAATTG	CTGGTCATAC	AtaCGCATTA	ACAGATTTTA	TTACTATGTA	TCCAACGTGA	60
	ATTGCTaTAT	GTACCTTATT	ATCGGTTTCA	TAAAgATGCT	TTAATTTCCT	ATTCTGAATC	120
5	GGAGTCgTtT	GACCGGCGCT	TAgaCTGGTT	ATGCCTCtTG	CCATCGTTTT	TCTCGAAAAT	180
	GAAAAATCTA	GCTTCACGCT	CgGCTGCAGG	CTTAgtTCGTa	TCTTGCTCAT	TGTTAGTTCT	240
	CCTAtGACgG	TATCctGGGA	AgGTATCCCA	cTGGAAtTTg	TgCgACCTCT	CAAGCTTtaA	300
	aCCATgCTCC	TTGGCaaAGTA	cCTtAgGCTG	CCaAGAATCg	TaTgGATCAC	CGGCAAAATag	360
	GGACAAAATG	ATCctCCCCA	TATCATCAGA	TGATtGtctCT	TtttCCTACT	tCatATCCGG	420
10	AAAGATGGGC	AACAACtACC	ttCTTATTTCG	cCAGcTTGAT	AGttGtttAC	AGcTATCAAA	480
	AATATCCCga	TaGAGcTCTG	aGcTCTCT				

## 1026UP

	GATCTAGCAG	ACTAGACTCT	CTATCGCATC	AAGTTTCTGT	TTTCAAGTCT	GGGTTTCTTG	60
	AGCAACCTGG	TGCCCCCTATA	CCTGTGTGTCAG	ACGCACAGCG	AAGCAGACGT	CTATCGACGA	120
	TGTCGAACtT	ACAGACGAAA	AAACAGCGCC	CGCCAGCTAT	TCCAGAGGCA	GACGTATCAC	180
	TCCAGGCTAT	CAAGAAGCGG	CGCATGTCCG	CCAGGTCTTC	TACCTCCCGT	AAGTCGGGTT	240
	CTGCCACGCG	TATTAGTGT	GTGCCACGGG	CCGCAGCTTC	AGAGTCATAT	GTGGTTCCAC	300
	CTGCTGGTGC	TCCTCTGAAG	AAAGAGTCTG	CGGATGACTT	ATTTCAAACG	ACTGCTTCCT	360
20	TTTATGAACG	TTACACTATT	TCCACACTGA	AAGAAATACC	GAAAAACATT	GCAGATGAGG	420
	ActCTGCcCG	ATATACCGTt	aACGAgGATA	GCaTCaCTAT	GGCTGAcCTT	TGCaaACCTC	480
	TATtCcCGAT	AGGTGAAGTa	tCTGATAATT	TCACCGGGCG	AAAGAAGcTG	CAAAAGCCAA	540
	GATGGAAGCT	CGGAAGAAGC	GCCGcGAaCT	CCGACAGATg	GcTaAgCGTc	AATC	

## 1027RP

	CATATCGACG	TACTCTGGCG	TTTGTTCCTC	TTCGTCAGCA	GGAACGCCGT	CCGGCATAGG	60
	CTTACTGACT	TtCACAGACA	TGATTCTTTt	GCTGCAAGTA	AAGTATATTA	ATGGCGCTGT	120
	CAAAAATGGT	AATAGTACGG	AAAGAGCAAC	CTGAGAAGCG	TCCAGGGCCT	GCGATAAGCC	180
30	GTTTTTACCT	AGAGCAGTGG	ATACAGCTAA	TGTtGGAATC	AATGCAATGG	CTCGTGTGAC	240
	AATTCTCCGT	TTCCATGGGG	TTATAGTCCA	GCGTaTaTGG	CCTCCGCATA	CTATTTGTCC	300
	AGCTATGGTA	CAGACAATNC	CTGCCGATTG	GCCCGAGATT	AAGAGTGCGA	GCATGAATAT	360
	GGTACCTGCC	GCTGGTGCCA	AAGTGTtGGA	TAATAGGTGG	tGTATCGtGT	ATAGATCCgC	420
	ATCGATGGcT	TCCGGGGTAT	CATACAGtGc	GcTA			

## 1027UP

	GATCAACGAG	TAAAAATGCC	AGGTGTTTTCC	GTTAGGTACG	TGTCATGAGT	GCTAGTTTAT	60
	GGTTTGGTAC	GGCTGCTGGG	GGGCGCTTTC	TGGGAGGTTT	CAGCGCTCAT	ACGTTATGTG	120
	AAGATGCTTC	GATCGNGAGG	GTTGCGAGAA	GGAATGGGAA	TGTGCCAAGC	AGGACTTGGT	180
40	GATTGGTTCC	AGAACGTCGC	TGACTGTGTC	AAATATGAAA	TCATTGGGCG	AAACTTAGCT	240
	TGCTACGGAG	TCCAGCATGC	AGAACGTGCG	GCCGAAGCTA	GCTGAGGCTC	GATGAGACGG	300
	TGGCGGAAAT	CCTTCGATCC	CAGGCCAAAG	CAGACGTACC	TACCAGCTTT	TAATGTGCCC	360
	GCCTACTAAC	ATGATATACA	GAGACGTTCC	AGCTCAAGAG	TTCATCAACG	CTTACGCTTC	420
	TTTTCTTGCA	AAGACAAGGT	AAGTTG				

## 1028RP

5 GATCATGCAA ACGGAGAGAA GGAGAAGAAG TCTAAGAAAG AGGGCACTAA AGAGAAGAAA 60  
 GCCaAAAAGC AGGAGAAAAA GGAACCTGAGA AACATCATTTG AGGAGTCCGT TGAGCAAAAT 120  
 AAGCTAGCAC TGATAGAAAA GGTGGAGGAA GAAAGAGGCC GCACGAAGGA GAAAGACCTT 180  
 GACATCaAGT TCAGGTaTCG GGAAGTTTCG CCaGAAAGTT TTGGCTTGAC CACCCGTGAG 240  
 ATATTTTATGG CTGACGACGC TGCCTTGAAT GAGTaTATTG GCCTCAAGAA ATTTGCACCA 300  
 TATAGAGCAA AGGAGTTGCG CaACAAAGAT AAAAGGAAGG TCaTGAaGC TAAGCGTCTA 360  
 AAAGAATGGA gGAAAAaGT GTTCaATAAC GAAAAATGGGT TGGCCGATGA gGATgAgGcC 420  
 CTTGATACCC AgGCgGCTCC TAAAAAGGAg AAAAgCcgTT CTAAGCaCAA GACAAGTAaG 480  
 10 TAATATTACC GTCTTTATGT aCgTTCTGCC gTAATTATAT TTTGCTATaC aTaTaTATTA 540  
 ATTTAAACTT T

## 1028UP

15 GATCCGCGCC CGGCACAGGC CTGGCAGCAC CCATCGCCGC ATGCTGTGCC TAAGATGTCT 60  
 CAGAATTACG CGGCCGCTCA GCGCGGCGCC AGCCCCCTCA TGCTTTTGGG CCAGGAAGCC 120  
 TTCCACGAGC TGGCGGACTC GCCTGGCATG TCAATGTACA TGTCGCCCCA GACCCATAGG 180  
 CTCAAGGGCA ATGGCGGGTA CCTGTTGCCG ACCGCTTCTA TCTCCGACCC TTCGGTGCTC 240  
 GGTGACACCG GCCGCCCTCC GTCTTCTCAG TCATTGACAT CGCACCTTCT GCGTACCCCC 300  
 AACTTTAACA TGAATGACTA TGTGCATAAC CTTTTTCAGCC CCTCACCAAG AATAGaCCG 360  
 20 CCAGGTaGCT CTGGGAATAT ATaGGGcCTC GCACACATTT AGCGCACAGT ATACTaGCTA 420  
 ATCCTACATT CTCTGTCATA gTAATGCCTA TGTCAGCACA CCTGCCGTAT AATTTcATTA 480  
 TTTCTGTtTT CATAAATGCT GAcATATGTc ACGTGGCTGG ATCaGCaCgT gATGGCAAAA 540  
 TTCTTATGAA TGAgCCTGTT CATCTCGTCA gACAATACAT TATACACgCa TCCaTCTCTC 600  
 GGTATGAaC GGACTCTCTC ACaCTGGA

## 1029RP

30 GATCGTAACA CTCTGGAGAA GTGGAAAGAG CTAGTCCCTC CGAGCTGTAA ACGATGCATG 60  
 GATGCGCTTC ATCACAACCG GTACGACACC GCGGAGTTTC CGGAGCACAC GCTCGAGGAT 120  
 GTGGGAAAAG GGGTTCCGCG CGATGCAGTG GTATACCATA TTGCGCCACT GTGGCAATTT 180  
 CCGATGGGAC TGGATCGGCG CGTGCTGCAG AGCTCAAAGA AGGTTTGTGT GCTATTCTCG 240  
 AAGATCGATA TGGTGGTGCA GAGACCGTCG CACATGCCGC AGGACGTAGG TGCATTTTCT 300  
 CAGAGCTTGC TTTATCATGA CCTGCATGTC AAGATCACGA ACTTCCGCTT CTTTTCTGCG 360  
 CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT 420  
 GCGGGGCCAA ACGCGGGCAA GTCGTcATTG ATCAATGCCC TGATGAAGAC TGTtGTTTAC 480  
 35 GAAAGTCGGC GTCTCGTATC CTCAAAGCAG TCCTCTGCGA CCCCTGCCGA CCTGCCTCCA 540  
 AAAGCGCATT TGGACATCCA TTCTGCGGGT GTGAGCACA TACCgAACTT CACTCGCCAA 600  
 CCCAGCAATA CGATATAAAG GGCAAGATCT CCACGATTTT CAGGCTACCG CACAT

## 1029UP

40 GATCTCGTGG TGTTTTGCAA CTTGGTGCGT GACGCGATAT CTCAGGCTTT GCGTGCTGAG 60  
 CATGATTATG AGGTGAACAA GATGCGCCGC GCGCTCTCCT TACTCCAAAA GCTGTATATT 120  
 AGGGATAGAA GGACCAATTT CCTCTCCGCG GCCAAGGGGG ACGACTTCTG GGTcATTGCG 180  
 GATACCACGG TGAAAACTG CGACATTACA TCTCTCCTTC TTTACTTTGA TGAGTTCTAC 240  
 AGAGAACAGT TGGATTTGTT CCTGGCGCAG GGCCGTGCTC GGCACGAGGT CCCCAGCGGC 300  
 45 GATCTCGTAG CGTGGGAAAA CGATATAAAA GTAAAGTTCT TTAGCGAGAA GTCATCGAAG 360  
 CACGCTTcGT GGGGTTCCTT TGCCCTGCGG AAATTcGAAC TCGTACTGCG CGCTCCGTTT 420  
 CTGTtGCCCT TTCGCGAGCG GGTcGCCTAC TTTGAAACGC TGATACACCA CGACCGACGG 480  
 CGGTTGcAGG GACGCCACAC AGGACCAGCC TTGCGCCTGC CCGACCTGTA CTTCCCCTCG 540  
 TCGCGGCGGC AGCGTGCGAT TATCTCCAGG AACAACATCC TGGaAGATGC ATACSAGGCG 600  
 50 TATTATCCGC TGGGCGAAGA CTTTAAGGAC CAGCTGGC

## 1030RP

	GATCTGCTTG	TTGCGCAACG	CTTCCCAATC	GATgTCGCTG	AGAAAGGGGT	GGGCGCGGAC	60
	CTCTGCGCCG	TCGTTGACCG	CACCGAGGCG	GTGCTTGGGA	TTGCGGTTCA	AAAGGCCCTT	120
5	GACAAAGGAG	CGACCTTCCG	GCGATAGCAC	GTCCCTGGGG	AATTTGACCT	TGCCAAACGC	180
	AATCTTCTGG	TACATCTTCT	GGTTGTCCCTC	TGCAAAAAAA	GGCGACCAGC	CACAGCACAT	240
	CTCGAATATC	AAGACGCCCA	GCGACCAGAA	GTCAACCAAT	TTCGTGTAGC	CGGTCTCATC	300
	GAGCAGCAGC	TCGGGCGCTA	GATACTCGGT	GGTACCAGCAG	AACGTATTGG	TGCGATCCTT	360
	TAGGTCCGCT	TTTGAGAGGC	CGAAGTCACA	TAGTGCAGATA	TTGCCGtTGG	CGTCTAAAG	420
	GATGTTTTCT	GGCTTGAGGT	CGCGGTACAC	GATATCAATTA	TCGtGAAGGT	ATTCCAACGC	480
10	AAGCACCAAC	TCGGCAATGT	AGAACTTTGC	CCGCTcCTcC	GCGAACCAGC	CTTCTTTCTG	540
	AAGGTGCCAG	AAAAGCTcAC	CAcCGNTCAG	GAAGTcAGTC	ACCAAGTATA	AGTCtGtGGG	600
	CGTTTgAAAA	GAAAATTTCA	ACCAaCAATG	AAGGGACaCg	ACTTTgAgCA	gTaCgAACgA	660
	GATGTTgcGC	TCACCAATAG	TATGtGCA				

## 1030UP

	GATCGATTCC	CTGAGCATGT	TTTTCCCTAT	GCTGCAGGTT	TTACATGGTG	ACATTGCGGA	60
	TGCCGAAGTA	AAGAACCTTA	TGTCTTTGAA	ACTCTGGAAC	ACTTACGGCG	GAATTCCTGA	120
	ACGCTGGCTA	TTCACTACTC	TCTACAAGAA	ACAGCAAGTT	ACCGTAAATG	ATACCGTGCA	180
20	GCTCGAGTGG	TATCCTTTAC	GGCCAGAGTT	TGTAGAATCA	ACCTATTCCC	TTTACAGGGC	240
	CACTAAAGAC	GCATTTTATC	TGAATATCGG	ACGAAGCATC	CTCCAGGCTC	TATCAACGCG	300
	CTTTAAACAG	AAATGTGGGT	TTGCGGGCAT	ACAAAACGTC	ATAACGGGAG	AGCCACATGA	360
	TAGGATGGAA	TCGTTCTGTTT	TGGGCGAGAC	CTTAAATATAT	CTCTATCTCC	TCTTTGACGT	420
	ATCCAATGAA	TTGCATACAC	AAAAACGCAC	TAACCAAATA	TTTAGCACTG	AGGCGCATcC	480
	ACTGTGGtTG	ACTGCCTCGA	TGAAGgCTCG	CTACGAAAAG	AACAAGTaCT	GTGAAAACGA	540
	CgTGTATATA	CAGAACTTGC	GTcGcCTACA	gGAGCTTgaC	CAGCTGAAAA	GcCgtGCCAA	600
25	TTCATTCACT	GcAGAGGaAG	cCATGATaCC	AGCTTCAGAt	TTCAAAACAG	AAGACTcCgA	660
	GGAGtCTTTG	AAGGACCGCG	TTGcAgcGCC	AtaCTaGAGG	CCTACACGTa	GAtaCgACaC	720
	gTTGCTGGaA	cATGCAGACC	TTTCGCGACA	A			

## 1031RP

	GATCTTAGTA	ATGATCACGT	GATTGGATTA	CCGCTTGTGC	GTTTTGCTCT	CCGCAAAGCG	60
	ACATTTACAC	GGGAAAAGCG	GTGAACTCCC	GCCGAAACCC	AAATACTCGT	ACACTATGAC	120
	TATAGACGAC	AATGTCGATG	ACGTGAGCAC	AGTTTAACTC	TAGTGTACAA	TCACGTGCAC	180
	ATACCTTCTC	TGCCACCCAC	ACATTAACCA	TTTATTTGTG	GTCACGTGAA	ATGAATCGAT	240
35	GCATTTTATA	ACTGCAGGTT	AGTTGAGCCA	TCTCGCCAAC	GATGTCCTGC	GACAGCATTC	300
	GGGGCACGGC	GCGTCATGAG	TGATTGGAAG	GAGGCACAGG	ACTCCACGGG	GCGTGTTTAC	360
	TACTATAATT	CGAAGGGGGA	AACGTCATGG	AATAAGCCCA	ACGACACGCC	AGTTGAGCTG	420
	GAACCGCGAC	TCGAAGAATG	TGGCTGGAAA	GTGGCAACGA	CGGAGGACGG	TAACGTGTAC	480
	TATTACAACA	GGGAAACTGG	CGAAAGCAGG	TGGGAGAAGC	CGGAGTTGGA	GCCAGCCGAG	540
	GAAGTGCCCC	GGGAAGARGA	CGAACGCGCG	CCGGAGGARG	AGAAGAACGA	GCCGTCCGCT	600
40	GCTGARGAGC	CCGGGGTCCG	GATCGAACTG	CTGCTCAACT	CAAAAC		

## 1031UP

	GATCANCGAN	CAGCACGGAC	AAATATAACA	GCAGCACGGG	CATTTGTCTA	GTCGGCTGGT	60
45	GYYYTGtGTC	CACCGTGACG	CTGGCGCTGG	GCTGGAGTGC	AAAAACCGGA	GCCACAAGCG	120
	TGCGCGTCCG	ACGGGGAAAG	CTGCGATCGT	GGCAGCAGCA	GAGAATGGGT	GCGGGAGTGC	180
	YAGAGCGGTG	CTGGGAGCGC	GCGGACGCGC	GCACGCTGCG	CGCGGCCGCG	CTGATGCTGG	240
	GCGCGGCATA	CCGAATCAAG	AAGGCACACG	CGCGGGCGCA	GCTGGCGATG	CAGGTGGCGC	300
	GGCTGCSCCG	CCTGCGTGAC	GTGCGGCTGC	GCCGCGGGCG	CGTCCCCTG	CTGGCKGTAC	360
50	ACCCCGGTCT	GGTGAAC TTC	GCGTAC				

## 1032RP

	GATCTTTAAC	CTCTGGACTT	CAATCTTCTG	GGTaaaAGCA	CAAGTTTAGA	GATGTATGAT	60
	CCAAGCACCA	AACTACAGTC	TCGAGACAGC	AAAATAATCC	TACTTATATA	AACTGAACGT	120
5	TGCAATTCTT	TAAAAAATTT	ACTAACTTCG	ATTAATGCGG	CGCCGGTGAG	CGCCTCTGTT	180
	ATTAGCTGAG	TCATGCTGAG	GGTTTGGCTA	GGAAGCATCC	GCTCTTACTA	CGTATTTACC	240
	AAGGCACAGG	AAAATGTGGT	GGTATTCTTG	ATTTTCGGCGG	CGTTTTGTAC	ATTACTCCAT	300
	AGCTCATGGT	CAGCAATCCC	GTTCAATGGA	CATTTGCTCA	ATCGTGAGTC	TTCCACTGGA	360
	CTTGAAATCC	CGCAGGGATT	TTTCGGCTCCT	GGCTCAACCA	GGTCGCCCGG	ACACCTACAG	420
	CCGAAAAAAT	TGCTGCTTGG	ACTAGGTCCG	CTGACGTGGA	CATGCGAGAT	GACTTTAAAG	480
10	TGATACATTA	AAACCAGGGC	TGTATGAACT	CAGCAAAGGT	CTCTTTTATA	CAGTGTGCAT	540
	ATAATATTTC	GGGCGCTTGC	AATTACCTCA	TGCCAGGTac	TCGTAAGATT	CGCCGTCCGC	600
	GAGCGCTGTA	gGtATTCCCTT	GCTAATTAAAG	tTGTCgATgG	CCTTCTTGAT	AGAGAtaCCt	660
	TTGCATTTGA	CCGTtGTgAG	AtTCgGCTAT	GCATTCGTCA	CCAAAGTgGC	ATGAGAgAcG	720
	ACCCGTTTGC	TTTCATAATT	CTGaCgATaC	AAGCTTCAGA	ACaATTGCTT	TCTTG	

## 1032UP

	GATCCCGAAA	ATAGACTACA	TCTGCCgcaa	gCAGCGCGCC	CTATCTGCAT	TTCTCTTCTt	60
	GGTGGTTGTC	ATGTGGGTCA	TCACGTTTAC	CAITAGCATT	CTAAGGGTAG	TGGAACGGGT	120
	GAGTTCACCT	TCACCCAGAT	AAAAGTTAAC	AGGACAAGTG	AAAAAAAACG	GGGATAAAGG	180
20	CATCAGTTAT	GTAATAAAGA	GCTATACGGC	AATAAACATT	TAAGTAACTA	CCATGGTATC	240
	TCCAGGGTAT	TACTAGGTTT	CCCTGAAGTT	TCCAATGTGC	CTTCGTTACC	CGGTGTTTAT	300
	GCAGGCTAGC	GCGACAAGAA	AAATGCGGTC	CCACCCATT	CACGATTAGC	GGTGGCAAAA	360
	GTCCATAAAG	TTAGGCAAAAT	AAACACATAA	CCATCCCTCA	AAAAGCGCTT	GAGCAAGGCT	420
	ATCGGGGGTC	AGAGCAGGTG	TAATATACAT	TAGAAGTGAG	CGATGAACGA	TAAATTGCCG	480
	AGAGCAGATG	ACTTGGAAAGC	CACTTGGAAAC	TTTGTGGAGC	CCGGtATCGG	GCAGATCCtG	540
25	GGCCGGGATG	GGTCGCCCCA	TGCAGGGCGA	GTGCAGAAAC	TGCTGtCAGC	TGCgATGTaC	600
	ATGGATGTCT	ACACGGcTAT	CTaCAACTAC	TGCGTCAACA	AGTCGCGGtC	CACCGGGCAT	660
	TTTCAGtCgG	ACTCGGCGCA	ACGGCAGTCG	AACCAGtCAT	CGAtCCTGGt	CGGAGGGAGA	720

## 1033RP

	GATCTTGTGCG	AACAGGTCGC	CCCCGTCCGC	CAGcTcCATC	GCGATCCATA	GGTACTCAGC	60
	TGACACATTG	CAGTCCAGCA	CCCTCACCAC	ATGTCGGTGC	CCCGCGCACC	GCGTCTGCAG	120
	CACCACCTCG	CGCGTCAGAT	CCTCGTCCGT	CATCCCTCGC	GCTTTGCAGC	GCTCGACGTG	180
	CACGAACCTT	ACAGCCACTA	TCGTCTGCGG	GTCTGCGCGC	AGCGAGGCGG	TTTGTACGAA	240
35	CGCGAACGTG	CCCTGCCCAA	TGCTCTCCCC	GAGCTCTAGT	TCCTTAATCT	CCGGCAGGCA	300
	TTCAGCTTGC	GACGACTCCA	TAGTAGCCCA	AAGTCGTGG	ACGGCCTTCC	AGGTGGCCCTC	360
	TAAGTGCTGG	TGATGGTTGG	TTGAAAAGTG	ATGCCCAAC	AATAGTGTGA	AAAACGGCAA	420
	AGTGGGCCTT	ACGGGGGGAA	CAAAACAAGT	GCTAACTACA	CGGAAGCAGG	AATTAATTTG	480
	GGAAGTGGGC	TTGGAGCACG	GTATAGGAGT	ACCGGAGGTG	GATATGAgTG	TCgAACAGGT	540
40	GTCTGGTGCG	CACGCGTgCg	AAGAACAAGT	GGCACgGTTT	GAACGCAATG	TGGAgGCGCG	600
	GA						

## 1033UP

	GATCCGCGTC	GTCGAAAACA	GGTCCTTGgg	gTGCGATACC	GCCAGCACCT	TGCACGACGT	60
45	CCGCACCAGC	TGGTCGTGCG	TCTCCAGCGC	CGTGATGATG	TCCTCCACCG	AAAACACCTC	120
	CAGCACCGTC	TCAAACGGCG	CAAGCTTCAC	CACTGTGTCC	AGCAGCGACA	GAAGCCCGCT	180
	ATAGTCCAGC	CCACTCATCT	CCCCTGCCGT	GAGCACCTTT	TTCATCGCCG	AGAGTAGTGG	240
	CCGTGCGTCT	GCGTCGAGAC	GCACCATCAC	CCCCAGGTGC	AGCTGCAGCA	TGTCCACCAG	300
	CCCGTTTACC	GACCCACGCG	CGTGCTCCTC	GGGCGCCTCC	AGCACATCCG	CCAGCTGGCT	360
	CATTCCGtCC	TGGATCCTCC	ATTCTTCCAT	CGCGATATCG	ACTCTTCCGA	AGTAGCGTTT	420
50	TGGGGTTTGT	AAAAGTAAAG	GGCACTTTTC	CAGCACTTcG	CCACTTAATG	TCGTGAGGCA	480
	CAGAACCAGG	GCCCTATGTT	GCCGAGTCA	AGGCTTGCTT	CGCTATATTG	CGACTTCAGG	540
	AAGCTGCAAG	AGCTCAATcC	AGATGGGTTT	CAGGCTAACG	tTCTAACATG	GaAAGACCAC	600
	CTGATGAACA	CAGTGTGGCG	GGACgAGCTT	CTGATAGAAg	GGGGCGACAA	GCTGCTGGAg	660
	CGATTGAgCA	CCAAGGAGAC	GGG				

## 1034RP

	GATCATATTG	GTCTTGGCGC	CAGCATCGCC	TCTTCTGGTT	CTGAGCCAGT	AGTATGATAG	60
	CATGCCGCCG	ATGAACCTGG	CAATGGAGAA	ACTAGGTGAG	TTGTACATCC	CGACGCCAAG	120
5	GGCAACGCCCT	GAGGGTAACC	ACTGCGCCCA	TCTGTACTTG	TCCTTATCAA	TACAAATCTT	180
	TACGAGGGAT	ATGACTGCAA	AGATGCTTCC	TAGGATGATC	GAACATTCCA	GTGCGTATGG	240
	TGGGAGTGCC	ATACCCATGA	CCAGACGTGC	GCAGTCTATC	CATACGAACG	CAGTTGGGAT	300
	CCGGAATTGC	TGGCTGGGGA	TTTCGTAGAC	CTTGTTGTAA	AAAATGTACA	TTACGCTAGA	360
	CAACACGATC	GACCAGCTGG	CGCCGATAAT	CTGCGCGGTA	AACTGAGCCC	TAGGAGAAGC	420
	ACCGATTAAA	TGCCCTGTCT	TAAGATCTTG	CATTAAATCG	CCCGCTTGCT	GAGCGCCCGC	480
10	CTCAGCTATA	CTTCCGGCAA	CCAAATTTAT	TAATACAGCG	GCCTTGATGAT	CCCTGGGTAC	540
	ACAAGAGCGA	AAATGATTTG	AGCCAGCTTT	CCGATGCCGC	TGAACGGGTT	GAGATCGGTT	600
	TCCCCAAGAC	CCGGACGCCC	AAAATCGATA	GAAAGATGCT	ATAAGGAGAG	CCA	

## 1034UP

	GATCACGCAC	AGCGGACACC	ACCAAAGCAG	AACCACGGTA	CCATATCTCT	CACACACGGC	60
	TCCCACTAGC	ACAGCGCCTC	CACCTGGCCG	CCCTGGGCTC	GGCCCCCGT	CGGCATAAGC	120
	ACGTCGGGGG	ACCTATTTAG	TTCCAAAAAT	ATTGTTGTAA	CAGTAATAAT	ATCCTCATTG	180
	AGGACATTTT	AGTTGTTACA	CTGAAAAGAA	CAGATACTAC	ACTTGATCTA	AGCCAAAAGG	240
	CAAAGAGATT	TGGTTTCTAA	AAGAAAAGAA	AACATGCCTG	TAAGAGGGAG	GGCCATCGCA	300
20	CATTTTTTCT	CTCCTTATAT	ACCAAGTAAA	ATTTAGAAAA	AGAAACGACG	CGGCTGCTTG	360
	GTCGGCGCCG	TCTGCCTGGG	ACTCCAGAGG	GGCTCACGCA	GGAATCCTGC	ATCCAGGGCG	420
	ATGCGATCAA	GCTCTGAACG	CCCATAGCTG	CCGCCATACA	CGCCGCCATT	CGCGAGCTTT	480
	CGTTGAGTTC	GTAAGCCATG	AAATCACAGT	ATACGATTCT	CGAGCGCAAG	TTAAAGAGAG	540
	CCCACTGGGC	ATACTGCTAG	GGCTACAAC	GCGCACCAGC	TGCGAAAGCG	GAACCTCAAT	600
	AGTTAAGGGC	GGGTGGCAAT	AGTATCTGCT	GCAAGCAGCT	TCTAGAATTT	GGTAGATGAG	660
25	TGCGTTCATG						

## 1035I2

	GATCCTTAAA	AGCTGGCCTC	CGCAGATAGA	CCTTCTGCGC	AGAGGCTGGA	AACCTCAACT	60
30	AGCAAGTCGC	CACCCGAATC	AGATAAGCAC	TAGAGTCGTT	CCAGTAACAG	AGGAAGCGAT	120
	CAAGGAAGAT	AGTAGAAGAG	GACACTGCTG	CCAGGCTTGA	TCGGACAGAG	GGTTTAGCTT	180
	TCTGTGGAAT	TTTCAGAGTT	CGGCGCTTTG	TTTACTTCGC	TTTCATCTTT	CGTGTAAGA	240
	AGCTGTTTTG	AGGATGTCA	CATTTGCCAG	TCGCCAGGTA	GGGTATTGCA	GGGCCGACGG	300
	AGTCGGTGAA	ACAGAGTCAG	GACCCGAGA	GCCGATAGAC	AGGCGTTTGG	TTTGTAAGCG	360
	GTGAGAGCTG	AAGCAGCTCA	AGAGGCCCGC	CTTGGTCAGG	TTGTGCGGTG	GCGGTAGAGC	420
35	ACAGCAGGGC	ATCCCTCGTC	GGTGGAGCGT	NCGGNCAGNA	GCCCAGGCGC	NTCGAACAGG	480
	GGGTGTTTAT	NANGANCNAC	CGACCACAAA	CACGCTNTNA	TTTCGNACCGG	CGGCCAGTTN	540
	CCTCANCNTG	GTTCGCCGNGA	CTTGTTTTNN	GAGCCNATCC	TTGGCNCTCC	GCCNNAGNAA	600
	AAAA						

## 1035I1

	GATCTTTTGT	GGAACCAAGA	TCACCACACA	CGAATATGCG	ACGCCAAGCG	CCGGAACGAG	60
	CCACACATGG	GCCGCGGCGG	TAGCGGTGGG	CCCAAGCAAG	CGTATTTTGA	GGACCTGACG	120
	TGCTGTGGGT	GAGCAATCCA	GGGCATACTA	GGCCCAGGTT	GTCAGCTGAA	AGTGTGTTAC	180
45	CCGGTATCGG	TATTACCCGG	CTCGTATAAA	TGTTACCCGG	ATATGGTGAA	GCCAAAATTT	240
	TCCACGGCGT	AAACAACAGG	AGAGTGTAAG	TGCATATGGC	GGCAGCAGCT	AGTGTAGCCT	300
	AGTGAGAAGA	AGGNCCTGTA	GCTAAGACTA	GCGAGGAGAC	GAGGATTGGG	CACTGATTGC	360
	GCGATGTCGA	TATTTCTTAC	GCCGCTGAAG	AGCAATGTNG	NATATNNGGN	CGCGCTNGTN	420
	GGCAACCNNG	GGNCCNNGG	AGAGNACCGA	GNTTGNNTNA	NGGNGNGGCG	CNCANAACCA	480
	ANNNNTNCCN	CAATCNCTTA	CNATCAANNC	CAANTTNCCN	CNNNCANCCC	CNNNGNNNAT	540
50	NNNNATTNN	NCNNNCNN					

## 1035RP

	GATCTTAAAT	TGTTGCATTG	TGACCTGAAA	GTTGCCCCGT	AGACGCTGCA	TATTCAAGGT	60
	TTCCATTTC	ACGGGACGTA	ACCTAATCCG	CTGCACTTTC	GACAAACGAC	TAATGTATCT	120
5	GTTCCTCGGAC	TCTGGGTCAT	TGCGATCCCC	ACTCCACTGT	ACTTGTCCTG	ACTGTAGTTG	180
	TTGAAGC'TTG	AGGTTATCTG	CCTCGAATGA	CTGCAGTAGT	AGTGATTTTC	GTCTCCCAAT	240
	CGTTTCTATG	GACCGCCTGA	ACACCGAACG	TGCCTCCGCC	TGGAAGGACT	CGAAAAGCCG	300
	CCGCTCCTCT	GCAGAAGGCG	GGAAATAAGA	CATAACTTGC	TCATCGCGTA	GGTAAATCTA	360
	CGTCATTATC	CGCGTCCACC	ATGTTCCGGCT	GGGATAAAAT	GGTGTTCCT	CCAGGGGGCG	420
10	GGGAATACCA	CCCAC'TCTCC	AATCCTGCCC	CCGTTANTGA	ATNGNTTTNT	TNATGGGGNN	480

## 1035UP

	GATCTGGCGT	ACGGTACCGA	TATATTTCAA	CTGAGGTATT	CGTTAGAACA	GCTACCTTCA	60
15	GTGGTTCCAC	GCTATATTGC	GTTGCAAATA	TGTTTGCGTA	CCCTTC'TGGC	TTATCAGTGG	120
	CATTAAAGAG	CGCGCTAATG	GGGACTATCT	CTTTTACTGG	GCCAGTGGTC	TCCAAGAAGG	180
	AAGCATTCTC	AATATATTTT	CCGTGGTTTT	TCAGGATGCC	ATAATCTGGT	ACACTCACAA	240
	ACAATTTATG	TTGCACTGGG	TGAGATGCAG	GGGTATTAGT	ATTTGGAATC	ATGTGGGTGA	300
	TTGTCCCGGA	TGGGGTGCGC	TTCAACAACG	CAGAGGAAAA	AATATCCCCA	GGGGGATATT	360
	ATTNGTCGAA	GCAAGAATCG	CTTCGAGTAG	GGATTGAAGA	TTTCTTCTTG	ATACTTAAAG	420
20	CTGAATTGGT	TCANATGGGG	TCCAACGAAN	GANTAGGNTG	GATGGNCCCT	TNGGGGGGGG	480
	CC						

## 1036RP

	GATCATATTT	CAATGCAAGA	GCTCCATTAA	TAGGTATTGT	CTTGAGACAT	GCGCTCAAGT	60
25	CATTAATGTC	ATGGGAAAAA	TGCACCGTTC	CACCTCCTAT	CTCCAATGTA	TATTTTAGCA	120
	TTTCAAAATC	ATGTTTCTG	TTTACTATAA	AGTGCAACCC	ATTGAGGTCT	GCGGCTTCT	180
	TAGTAAAGCC	TCTAAAGCG	TAATGCTGCT	CTTGATATACT	GCGTAGCTGT	GGGTCAAAAT	240
	CGGTAACAGG	CTGTCGAAGA	AGAGCGGTAA	ATTGTTTCAG	AAATTCGAGA	TGCAATATTG	300
30	GTATGCCTTT	AACAAGTGCA	AAACAAATAC	TTTTTCGAA	TCTTGGTCAT	CTTCATGGGG	360
	TCTTAATAAT	ATGATGTGTA	GTGGGCCCTCC	GAAAAAGAGG	TCACCACTCG	TATTCCTAAC	420
	CCTTAATTAC	CTCAAGCAAA	GCAGGGCTTC	TTGTAACAAA	GTTTCGGGAC	CTGGACTCCC	480
	CATGGGCCCC	TCCAATNTGA	TTGGNCGGAT	NTGNNCCCT	TCCNGATANA	GGNCTGGATG	540
	GCCANCGGAA	NCCNTCCTAG	TGATNTCCCN	CCCC'TTCAGT	GNNNCCNCTN	GAGGTTTGGA	600
35	NGGCNNNTTT	TCCNNTNGCG	GGNNTNTCTG	GNAACCNCCC	CCTNT		

## 1036UP

	GATCCCC'TTT	GGTAACGAGA	GGTGTCGGCT	TGTATTCACC	GCACATCGTG	GGCTATTTGT	60
40	CATTA'CTCTG	GCCCCGTCCC	AGAGACCTAC	AGGTATAAAT	TCCCCATCAA	GTGCCACCAG	120
	AAAGATATGC	TATACTGGTT	TTGAGCTTGA	GCGACTGTTA	ACTGCAACCA	GCGGGACCGA	180
	ACGGGGTAGC	TTTTACTCAT	TTATTGAGGC	TAAATTGGAA	CCAGACATCA	CAATTCTGCT	240
	TCAGTGCGAA	ATGGACGCAT	ACAATCCAAA	ACGCCAGAAG	TATACTGAAA	TAAAATCCTC	300
	TGTGGACTTC	AATGTACGAA	ATGTCCGGCA	CCTGAGCAAA	CTGCTTAAAA	TATGGGAACA	360
	AACAGGGGTG	GTCCCATCCA	CTGATATCTT	GTAGGGGTCA	GAGACCCATC	AACCCATGTG	420
45	TTGAAACAGN	CGGCCCTTAT	GGGTGGTCAA	ATCGNAGGAA	AATCTTTTTA	GGGTGCNCGN	480
	NAGGCANCA	TTNTTTTANT	TATCCGAGTG	CAANATGGAA	ATAANCATCG	TNAATTTGGA	540
	AGGTATTTCC	CGGGGNGAAC	CANCGGN'CN	AANNNTTTTN	NGGGGTNGAA	AGANTCAAAT	600
	TAAATNGGCC	NGT					



## EP 0 866 129 A2

## 1037RP

	GATCATCATT	ATTTCTGCG	TTCGTGCCGA	CGATTGGAAG	GGCGGGGTG	GTTTCTTGAA	60
	GGATTTCAGG	CGTATGAATG	TTGCTCTCAC	CAGAGCAAAG	GCCAGTCTCT	GGATCCTGGG	120
5	TCACCATAAA	TCTTTATACA	AGAACAAGCT	ATGGATGCAT	TTGATTTCAG	ATGCGAAAGG	180
	GCGTGACTGC	CTCCAAATGG	CATGTCCGGG	CTTCCTTGAT	CCACGGAACA	GAGCCGCCCA	240
	GGATGCTCTT	CATAGGTTCA	AAAATCACCA	TAATTATATC	GAGAACGCAG	ATGATTATGG	300
	GCCTGAACCG	GTGATGACTA	AATCAAGAGG	ACGCAATAGA	TCATCCAGAA	AACGCAAACA	360
	TATGGAAGAT	AATCCAGATG	ATAACTACGA	TCCCCTTGCT	GAATTCAAGA	AGGAAAATCA	420
	AAGAGAAAGC	AACACAGGCA	CCGGTGGTTA	CCGTGCGGAT	ACATCTAACC	ACAGATTGGC	480
10	ACCTGCTAGG	AACGATAGCA	AGAAGGCCAA	GACGTGCTCC	AATGCCGCCG	GTATTTCCGA	540
	GGCTACTTCA	NARGATGGTG	ATCGAAGTCA	GAAAGGACAT	GGAACTAAGA	AGARTCTTCC	600
	ATATTC						

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## 1038RP

	GATCAAAAAA	AGAAATTACA	ATTGACTGTT	GCACCCACAC	ATTCAACGGT	TGCACCCACA	60
30	CATTATGAGA	TGCTTGATTT	GGCGCGAACT	GCGCTTTCCA	ACTACAGTCC	CGAGACTTTG	120
	GGTGCCAACC	GAAGCAGACT	TCAACAGTGG	TGATAACCAT	AGTGTCGAAG	TCTAGCGAAT	180
	CTAAGGATAA	TACCAAGAGA	CAAAGCATAA	TCGTATGTGC	ACAGGATGGG	GCGAAGTGTG	240
	GTCTAGAGCT	GTCGGTGCGA	GCAGAATACG	GTGCGGGCAA	TGAGGACGCC	GCAGACGCCG	300
	AGCGTGTGGG	CAGCTCACGA	GGGCCGGAGC	GCTTCCAAGC	GGTCAGACAG	AGTACTAACG	360
	CATTGCAGAC	AAGATGGCTC	ACGAAAACGT	TTGGGGTCTC	CCACCCNNAN	AAACTACGGT	420
35	AAGGGGTCCC	CCAGTGC GCG	TGTGCGCTTC	GNCTCTTGTT	GGTCANAAAG	TACGGGTGGG	480
	ACATCTTCCC	CAATGGTTCA	NAGAGAAGGC	CACGACATTG	GTTCCCAAAT	CCCCTAAGAG	540
	GGGGGGGGCC	CTTCCCCTCT	TNCNAAATCC	GGGGGGGGTT	TGGTTTCNCG	GAGGTTTNT	600
	TATTTTTTNA	NACCCCNNTT	TTTANTTTNA	NNCNCGGTNC	CCAGNNGTTT	GGN	

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## 1038UP

	GATCGGTTCT	CGGGCTTCTT	TAGCTGCCCG	TTATTCAACG	AGTCATCGAC	TGAGAAAGAG	60
	ATAAAAGCGG	TCGATAGCGA	AAATAAGAAA	AATCTCCAAA	ATGATATGTG	GCGCCTTTAC	120
	CAGCTGGGTA	AGTCGCTGAC	CAACCCCAT	CACCCGTACC	ACAAATTCTC	TACTGGAAAC	180
	TTTGAGACTT	TATGGAGCAT	TCCGAGATCG	AAAGGCGTCA	ACGTCCGTGA	TGAGCTGCTG	240
45	AAGTTCTACA	AACGGTCATA	TTCTGCAAAT	CTCATGAAAT	TAGTGATCTT	GGGCCGCGAA	300
	GATCTAGATA	CCTTGGGTCA	GTGGGCATAT	GAGCTGTTCA	AAGACGTCCC	TAACCATGGG	360
	ACCAAAGTGG	CTGAGTATCA	CGGCCAGGGA	TTACCGGCCG	AGACCTGATG	AAGGTAATTA	420
	AAGTGAAGCG	GNTAAAATCT	TAAGAGTGTG	GAATTCATNC	GNGGGGCAGA	TTTGGTTAGN	480
	ATGGAGGCAG	CAGTCGTATG	NGGATTTATC	GCCAGAGGAA	GGTCCCTCCG	NTCTGGAGAA	540
50	AAAGTGAAN	CGNCNNCCGT	NGGNNTCCCC	TTNAAAGGAA	AATNCCCCNC	AANNGGCTTN	600
	ANNAAGGNT						

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## 1039RP

5 GATCATTCTTCT CTTCAATCCC ATTGACGTGA ATGATGAACC GCATTATCTT TTTAACAGCG 60  
 ACAACATGCC ACGGTATATA ATGTCTCTTA CCTCGTGATA TGCAGAACCA GGTGTTTAGA 120  
 CTGGCAATAT CCCTAAACTG GTGTAATATG GTCTTCAAAA GTTTTGTGCT GTCCGAATGA 180  
 GGGCAATTTA GTAAATTAAC CTCGAATTTG TCTAAAGTAT CGCCACCGGC ACATCTTTTA 240  
 AACCGCACCA GCGCGCCGCT TTTTATGCG CATCGGCGCT GTGAATTAGC AAGTTGTAAA 300  
 GGGCTACTGA ATACGACGCC ATGCAGCTCT TCATCGATAT TCACAACCTC GTAATCATCC 360  
 AATTGGTTAG CTTGGATTTT GNGGGCATA TCTCTTATCC CTAAAAAGTG GGTGATGA 420  
 TGGATAAAAC TGATCTTCAT CATATAGAGA AATTTGGGCT CGCCCCAACG CAGACACAGN 480  
 10 CAATGTAGTT TCTTGTGGCA NAGTTNGCTN CGCAGGNATT ACTCGCANCC GGGGAGGTNT 540  
 CACCCCGGAG ACAAATTC CCCCTTTTCT NTGGAAATCG TNGTAGNNCC TANCAAGGAT 600  
 GGGTCAAGGA CCTGGTTGCC ATTCCANTTT ACCATTTTNN CCC

## 1039UP

15 GATCCTTCCA ATAACGGCTA AACATCCATG TGCTGGTTTT AACTATGAGG GAGTTGGAGT 60  
 AATTTTCGCGG TCTCGCAAAG TAAATTGACA GAAAACCCTC AGATCGGTAA CGAAACAGCT 120  
 GAACGACGGA GATTAAGAGG AAGAGGCAAA TAAGCTATAG ATAAGATCGA TAAATATTGA 180  
 GGGGGGGATG GATATATTAG AAACCTAGCTT TAGACTTGAA GATGTGCTTT CACGCTATTA 240  
 20 TAGAGTTGAA AAGGTGGTGC GAGTCAATTA TCAACAGTTC GTACCGAGGA CTCCAGATGA 300  
 TCAATGGTGT ATCCAATCCG AGCTTCTTAA TCCGCAAGAA GGATCCGAAA GCGCTGGTGG 360  
 CGCTTTTTTC GCGGGAACTC TGGTGCTTTT AGCATCAATG ACCAGGACTT ACCCATTTCC 420  
 GGGGTTGGAA GGGATAGGCG AACCCCCCNC CTCGGAGAAG AAGGGCCACT TTACGGCAGG 480  
 GTTTTCCAAG GCNAACCTGC AACGCCNNTG GATCTTTTTA AAGCNTGGGG GGATGNTCAA 540  
 TAANAATTCN GAGGCGNAGA ACCTTTGGCA ATTGGAAAAAN NNNTTTCCCC GNAAGAAAGC 600  
 25 NNAGGGANCC CCCCCGGNCN NATTTTGGGA ATGNC

## 1040RP

30 GATCCAGTGT ACCAGGTAGC GTCAGGCACT TCTAGCGCAA GGGCCGCCGT AAACCTTGGC 60  
 CTCTCACAGC ATTTGGGATG AGTATGGGCC ATCTTTAGGG CACGTGAGTG ATCATGATGG 120  
 GTACAAAAAG AAATGATTTT GCCCAGGATC GAACTGGGGA CGTTCTGCGT GTTAAGCAGA 180  
 TGCCATAACC GACTAGACCA CGAAACCACT TTCTGCAGGC TCTTATTGGA CAGGTGATGT 240  
 TAGCGCAGAA GAACATGAAC GTGATAATAA TTCAGAAACC TCTTATGCTA AAGTGAATTA 300  
 CTATTGCTTA ATAACCTGAA GGGGAATAGGC ATTGCCAGTA TTGAAAATCG GGCTTTGGGT 360  
 TTATTGGCTA ATTATATTAT TNNCANTATA TATATATACC AACAAGGTGA AGAATGGNTG 420  
 35 TCNTGGTTT GGGGGCGATA CCCNAGAACC AAAGTAGAAG TTGACAAGTT GGTGGNAGNG 480  
 GTTCAATTCA GNACTTCATG GCAACNTTTA CNATNNTTTN NTNAGAACCC CCNATTANTC 540  
 TTTNNCTTCG GGGGGTCTCN NCNAACCGGA AACAATNTTN CNGAACTGAG TTNGGGGGAN 600  
 GTTCNTCGGT NTTTTCNCC TTTGGGTCCA AATTGGGCCG GAANCCCT

## 1040UP

40 GATCAGCAAC CTTCTCCGCC GTCTGTGTCC TCGCTTTACC GAGGATACGA AAATAGCCGC 60  
 GGCTCTGTTT CAAATGGCGA TGCTGACGAG CAAACCACGT CTTCTGATGC AAGCAGTACT 120  
 AGTTACATTA TTCTAGAGAT GGAGGCAATG CGGACAGCTC TCGGTCAGTA TTTGAGGGCA 180  
 45 ATCTGCCAAG ATGCAGAGGT ATCCGCCAGT CTGTCCCTAA CGAAATTCCT ATTCAGAGG 240  
 ACGATAGACA AGCGTGCTTT TACGCCAGAA ATCCTGGAAG ATATTGAATC TCGGGAGCTT 300  
 ATGGATGTAT ACAACCTCGA AAATCAAGTT AAATTCAGAA AAATGGCGGT TTGGATAGAA 360  
 CTGTGAAGCT ACAAGTCCTC GCTAAAGTCC CTAAAAGAAA AAATCTTGCA AGATATGACT 420  
 ACATTAAGAG GTTTTCCNCC AATTTAAGGA GAGGAGGATC CCAGNGACNA TTTAGCTCTC 480  
 AGAGATTCTT GGNTGGGGAA AATTTTGTAG GTACCNATNC AGGTTCCCGG AATNAATGTN 540  
 50 NATNTTTTAC ANTCGCGCNG AAATATGCTC ANAGNNNAAG TTTGGGCACC CCCCCCNCC 600  
 ATGANGTTTT GTC

## 1041RP

	GATCCTCCAC	CAGAGCGTCG	GCGTCCCAT	CCTTCTGTTC	ACGCAGTGGC	GCGTTCTTGT	60
	AGAAAACGCC	CAACAGTTGT	TTGTAGGTGA	ACTCGTCCG	GAATTTCTGG	GCGCGAATTC	120
5	GCTCCAGCTC	CTCTTCGGAA	AGCTTTTCAC	GGCGCCACCA	GCTTCTCATC	CGGTTCAACC	180
	AGCGCTTTTC	GTCGAGTGCC	CGCTGTTCCG	CCGCTTCTGC	CGCAGCAATA	TCTCGGCGCA	240
	GATGCCGTAC	GCGCTCCGCC	ACTTCATGAC	GGATGACGCC	CTGCCGCTCT	TCTGTGAAGA	300
	ACTCGTAGTC	CAACCCAGCT	TCGAACAAAC	AACTGCTTCA	CGTATCGCCG	CCATACTTTC	360
	ATCGACGTCT	CGAGATAGTC	GGCCGGAGGA	GGGGCAACAA	ACAACGCGAG	CCGCCGCGGT	420
	TTGGGGCATG	TGTCANGTNG	GCTGCGCCTG	GGCCTTCACC	AACGACGAAT	AATGTTGGAT	480
10	TTNGCCCTNG	TCCCNTGGCG	GNTNCAATCA	GAATGCCGGN	TCAACCNAA	CAAAAGGGAC	540
	AATNNGCCGG	AACCAAGGCG	GTTCANGCC	GAAAGTGTTT	ATTNNCCNAC	TNTTCCGGTA	600
	NAATTTTNT	TTNTCNC	GGNTGTGNNT	NACCNCACC	CCNAAATAA		

## 1041UP

	GATCTGCTTC	CTGAAAAATG	GCGTCTCTGT	CTTACTGGTA	CTCTCAAATA	GCTACGTCTA	60
	GGTACAGGGC	CATTTCCGGA	TCCCAGCCAC	GGGTCCACTG	CAGGAGGTAC	AACAGGATAT	120
	CGCACGCTCT	GCCCTGCGCA	CGTCACTTGG	AGCCTCCCGT	TCTCGTCCGT	ACGTCTCAAT	180
	AAGGTACGCC	GTTTCTCTTC	GCCGATGGAC	TGCGCTAACT	GTATGGCCTG	GCTACAAGTC	240
20	TGTTGGTTTC	GAGCAGCCCA	CTTCTTTATC	CACCCCTCAAG	GTTTACCGCA	ATCCAGCAAT	300
	TTTGGGTCC	GGCACAGCCG	GATATCATGT	GACTTAATTA	CGTCAACGTT	CAAGAGTTGG	360
	GGCGGCGGCG	AGCAAATTTA	ACGGGGGCGN	CGGTCTGTC	CCCCGATCGG	GGGGGGGGGA	420
	GGGNATTANC	ANTCCANTGC	CGGCCAAATC	TTNGTTTACA	NAAAGCAAGC	ANANTCATAG	480
	TGATTTGGGG	GAANANCCCA	AGGTTNNGGC	CNCCANGGNT	CAAANTCNCC	CNTTNTTTTT	540
	TGGGTTC	NCGGAAAANN	CCATTNCNCG	AGGGGCCNAG	GNCCGGGAAT	TTTCCCCNGT	600
25	TNNAGGGGAG	TCNNTTNGGG	GGGGANNNG	CCANAGGAAG	GNGGT		

## 1042RP

	GATCCGTGCT	GCGGACAACC	GCCAGAGCTC	GCCTACAGCC	CGTATATATA	CGCCGGCTGC	60
30	CGGCCTGCCG	CATGCGATTT	GTCCACCTC	GCTCTGCTTC	GTCCCGCCTG	CCGTTGCTCC	120
	ATGGGACCTT	TCATTTAGTG	TCTCGCGAAC	GTTTCGAATG	TACCCTATCG	TGGTACCACG	180
	TTGCCGTGCCG	TGCCGTTACT	ACATCTTCTA	GCGCGGACTG	AGTCACATGT	CTCGCCGCGC	240
	ACTCCTTTTC	TGTAGATAGT	CAGACGACAG	ATAGTCGATA	GTTGGAGATT	TGGGCAACAA	300
	TAGCGGTGGC	CATTACGCC	GCCCATTGTT	CCCATGTCTAT	TGGGAGGCTG	GGNCCCACCC	360
	ACGGGAAC	TTNCCCGTTT	AANCCTNANA	GNCCCNNGGA	ATGNAAAACN	CTTTCTTTNG	420
35	NCNGCNGCAA	ACGGGCCTNN	AGNGATTTT	TTTGNCGATT	NGGGANGCAC	TGAGAAATCCA	480
	AGTNGGAAGG	GGGCTNNAAA	AATNGCTCCG	GGCCANNCC	NCCCAAAGGT	TTNAAAANCN	540
	GCNTAAATNA	GCCNCAGAAG	AACNCGGGA	GGAANCANAC	ANAAANTNGG	CCCCNCCTGA	600
	AGGAAAGGGG	CNGNNNTGGG	GNCGAANCCC	CNGNAACGNT	NTTCTTAAA	GGANAACAAA	660
	NGGTNCAAAA	AAAATGGGGG	NC				

## 1042UP

	GATCGCGTCC	TCGAGCGACT	TGTGAGGGTG	AAGCTCGATA	CGGTGATGGT	GGTGGTGATG	60
	GTGGTGGTGA	TGGTGGTGTG	CTCTGCCCTG	CGGTATGACC	TGGGCTGTTG	GCGTTGGGCT	120
45	GTTGCTGCCG	ACAGCAGCAC	CTGTATCCGC	AATGCCCGAT	ATGCTAGAAT	GGAGCAAATT	180
	AATGGACTGG	TCTGCATTCT	TGCAGAGCGG	AGCCTCGCAC	ATGCTGGATA	TGCTTACGAG	240
	ATCGCCGGAG	GATCTTTATG	TCTGTTTCGC	TATTCAACAC	GTGGTGGTGG	CAGTGCTGTT	300
	GTTTCATGAC	CAGCCCGTAT	CTTCANAGGA	GTCGTAGTTC	ACGCATTGTT	GGGCAAGGCC	360
	AGTCGAAGGA	GGCCATCCTC	CACGGTCGGG	GAGTCCCCGG	GGGACGTTTC	CACAAGCCAA	420
	GGTACCTAGA	AGATGAATCT	TTTTTGANTC	ANCNGTTGGG	CCNCTNGGCA	ATTTNAAGTC	480
50	GNAANTGNTG	AACTTCGGAA	AGTTGGAAAT	TGGNCCNAGG	NCTTCTTCCC	CCNCNCNCT	540
	TNGGNAAGCA	AAAANAAANA	ATTAATTGGN	CCCCCCCCCG	CAAATTTGNG	GTCNGAGAAA	600
	TTTCCAAACC	TTGGGTAAAT	AGTAAGGNCC	CCGNTGNCTG	GGCCCNCCC		

## 1043RP

	GGATCGGCGA	TGGCGATAAA	AGAATTGCTC	CCTGATTGAT	TGTTGTTTGA	AGGAGATGCA	60
	GATGGATTGT	CCAGAAAAAC	CGGTTTTAAG	ACTCGTTCAT	CAAACCTTGT	AAACCATTGC	120
5	CCATCGGCTT	GCAGTATATT	GCCCAAGGTT	TCGCGGATAT	TTCTTCTGTC	TAATGATAAT	180
	CGCCCCACAG	GCTGGTCAGC	GCCTGATGCA	GAGCGCGAAG	AGGGTCGGTC	TATCATAGGA	240
	GGAAAGCTTT	CTTGATCCGG	GGAGCCGGTC	GGGCTGTCCG	TTAAAAATGG	AGGTGCGTCT	300
	AATGAAGACA	TTAGCTGGAC	AGGTCTAGGG	GCTTCAATAT	CAAATTCATC	ATCCGTTTCC	360
	TCCTGTTCTT	CTACGCACCC	TGTCCTTATG	TTTAAGATCT	CAAGCATACC	CGCAGGaGta	420
	CCtCCaAaTa	TgATAACGGT	GaGAACCACA	AcTaCCAGcA	CAGtGGCCAG	AaGAGGGGAA	480
	CTTGGANCTC	GCCCNNNNGA	CCCNtagCCA	GNGNCaCTCC	AAANAGNAACC	CCNAANCCCCG	540
10	NCCNNNNNGG	NAACNNCCTN	NNTTTNGNNT	TGGATNTCCC	CNANNANTNN	AAAACCCCCC	600
	CCCCGGGNTN	TTNNNGGGNC	CCNNNNNCCC	NNNAANGGGN	AAAAANNNC		

## 1043UP

	GATCAGATTG	TCTTGTGATG	GAGAAGCTGG	CGCATCAGTA	GAGTGCAGAG	AAGACCCATG	60
	CGGAACAACT	GTACCACCCA	GGGACTGCCG	TCTTCCCGGA	ATGTTGGGAA	AAACAACAGC	120
	ACGGcCTGAG	TCACTTACAG	TCGAGTGGG	TTGCGAGCGC	GACAGATTAA	AAGAAAAGCG	180
	CTCGGGGTTT	GTGAACAGNT	CAGACCAAAA	CCCAGGTCTT	GGCTCGCGGA	ATTCTTCGCT	240
	TACCTTCACA	TNCAACTTAG	TGTGTTCCGT	GTCCNAAATA	TaCTCCAAAA	TCTTGATCGG	300
20	cGCACCTCTG	TGGTTCATgT	CCTGCACAAG	TTGACCACTG	TATTCCaGTT	TGaCATCAGA	360
	GGGcGAAATC	ATCAgtGTGT	GGCgttCACA	GAGCAAAaTa	aCTCctTtAc	TTCctgcAC	

## 1044I2

	GATCTACAGA	ATGCAGGAGA	CGCTGCTTGA	CACAACACAA	ACGGCTGAGA	CGGCAGGCGC	60
	GGCCGAGCGC	GTGCAGGAGG	CGGACCCGGA	CGGACAGGGG	GCGGGCGTCG	ACTCGGGCGA	120
	GCTGCTGGAG	GTTGTGGAGC	GCCACTACCG	GGCGCGGCGG	TGCGCGCTGG	GGACGATACG	180
	GTACGAGGCC	GCGCGCGCGG	GCCGGCTGAC	GGCGGCGCGG	GGCGCGGCC	TGCCGTTTCC	240
	GTACGAGGTG	GGGCAGCAGA	CCGTGCCCGT	GCCGCTTGCT	GCCGCGCATG	GGCAGGCGAG	300
	CGATCCAACA	GGCTCGTGAC	GGTGGAGCTG	AGCGCGGAGG	ACCTTGAGAG	CGCGCTCGCG	360
30	ACGGGCGAGA	ACGCACGGGT	TGCGCAACCC	GGAGCTTTTG	TGGGTAGNCG	TGTTCAACTN	420
	AGANTCGGGA	CCCNNTTNT	NNTGCTNNNG	NACTNNNGNG	TGNTNNNACGN	NGAGCTGAGN	480
	TGCAGGNCAN	GNNAGNNNNC	CNNNCNNCGN	ACGCCCNCCA	ACCCNNNGAN	CCCNNTTTTT	540
	TAGNNNGNTT	TAANNCCNNC	CCCNNTNTNN	GNGNGGGNNT	CCCCCTTGNT	NTNNNNNNNN	600
	ANTTNTCATT	TTCCCCCCTT	CGNAGGNTTN	NT			

## 1044I1

	GATCTCCGAC	TGCCGCCGTC	TGTACCCGTC	ATCGCCCTCT	GTAGTCGCCG	TCATGCTCAT	60
	CCTACCCAGC	CGCACCAACC	AATGCTCGAT	GCAAGCTCAA	TGCTCGCAGC	CGGCGACTGC	120
40	TGTATACGTG	CTGGCTTAGG	GTGGGGACGT	CCCTTCACGG	CCCGGCCGCC	ATTGGAGTCC	180
	AGCAAGCGGG	GAATGCTGTT	GTGACTGTAA	CACCCATACA	TTGCAGGCCG	TACATTTCAA	240
	CGATGGGACG	CGAGTGCCTG	GGGAGCTGGA	CGGAGACCGA	ACGGGGGGAG	CCAGGCGGGC	300
	GGGCGGCAAT	CCGCAGGCCG	ACCCAGCGGC	CGACCACGCG	GGCGCTAGGC	CGAGGGCAGC	360
	AGGCCAGAGC	CGCGGGCGCG	GTTTTTCATG	AAAAATATAG	TGGCTACAAG	AGGGATAGGT	420
	TGGATATACC	AGAACTCACT	CGTAAGAGAT	AATTAAGCAG	ACGAAATGGT	TGTTTGGAGG	480
45	ACGTTGGTAT	CGCGAATCAC	AATAATTTGA	CAAAAGGTTT	TTGANTCGGG	GAGGTCGNTG	540
	TTGTTGNGGG	NGCNAGACCG	CCNTATTANA	NGAAGNGANG	GNAACNCAAG	ANNGGGGCAN	600
	GGGGTC						

## 1044RP

	GATCGCGTGC	CTAGTGCAGC	CTCATGCACC	GCTTGGAAC	GCCGCCCCAC	CCATGTCAGC	60
	ATCTTTATCT	TGCTCGACCC	TGTGACCGAG	TAAACAAGCA	CCGTTCATCCA	CGTCTCAGCC	120
5	TTCCCACATG	GATGTTCAAA	CAGCCAGGCA	TGGTCAATGC	CTCGTTTGTC	AACTATCTTG	180
	TCGTAATGTT	GTAAGTTGCT	CGAATGAAGT	AGCAGTAAGC	ACTTGGTTCGT	GCGGACGAAT	240
	ATTGTCCGCA	GCCGTTCCGA	GTACAGCAGC	TCTTCTACAC	CATAATTCCGG	GCCAAAGCAAT	300
	TCTGTATATG	TCTGAACTAG	ACGCAGGCCT	CTCTCGTCCA	TACTGGAGTA	CACCAAGGAG	360
	TCCCTATTAT	TTCGGACCAC	CACAAGTTGT	CGAACGGCAT	CAACCACAGG	GACACACTGA	420
	GCACCTTGGG	ACGGAATGGG	ATTTACTAGC	TCAGCCCTAA	GCATCTTATG	ATGAGGGCTG	480
10	CCCTTAGCTT	GCTGAGTGCT	TCGGGCTGCC	TGCTTGTGGT	TGGTGGGTCC	TTTCTTAGAA	540
	CGATTGTTCA	AAACCATGAT	GATGGGGTTT	GGTCCGGCCN	GGTGATTTGA	AGATTTAAAC	600
	CGGTNCCAAG	GAATTGACCN	TGGGGG				

## 1044UP

	GATCTCCTTG	ACCGCGCGTG	GCGCTCTCTT	CTTGAAGGTG	ACACCGTGCA	ACTGCTACTG	60
	TTAGTATCGG	TCCGGTCTGC	GGCTCCGCTC	CACGCAGCAG	GGAGCCCTGC	TCCGCACTCA	120
	ACATACCCTC	TTGTGCAAGT	TAATGGTGTA	CTCGCGAGTA	ACAACGTCCT	TCAAACCAAGC	180
	CATTTCGGCT	GCTTAATTAT	CTCTTACGAG	TGAGTTCTGG	TATATCCAAC	CTATCCCTCT	240
20	TGTAGCCACT	ATATTTTTCA	TGAAAAACCG	CGCCCCGCGC	TCTGGCCTGC	TGCCCTCGGC	300
	CTAGCGCCCG	CGTGGTCCGG	CGCTGGGTCC	GGCTGCGGAT	TGCCCGCCGC	CGCCTGGNTC	360
	CCCCNNCGG	CTCCNNCCAG	NTCCCCACGA	NTCGNGNCCA	TNGNNGAAAT	GTACGGNTTG	420
	AANGNTTGNT	GTNAAAGGCA	NAAAAGAATC	CCCNNTNGGT	GGNTTNNAAN	NNNGGCNNNN	480
	NNNNAGGGAN	GNCCACCNN	ANNNAGAANT	TTAANAAGNG	NNNNTNNANA	TNNNTNGATN	540
	NANAA						

## 1045RP

	GTGGATCCGT	AATGTGGgTT	TGTAGGCCAG	AGGGGATTCG	ACGGTGGCTG	GGGGCCATTC	60
	TGCCCCGTAA	TTAGATGCCA	CCCAATTGTT	TTACATCCC	AGGCGAAGGT	TCGCATACCG	120
30	CCCACATACT	TGGGTAATTG	ATAATGCCGC	CACATGACGG	GATACTAAAC	AAAGCAAAGT	180
	GTCACATtCT	TATTTTCTGT	TGTGGTCAAA	AATCGGGGGG	TAGGCGATCA	ATTTGCATAT	240
	ACAACACGAA	AGGGGATCGG	AGATTTCCTAG	GTCACAGGAC	AGTTTGGGgt	TTtTATTGGG	300
	TGCTTTTGTG	AAACCATAGG	CACTTGACAT	AGGAGCCCTC	TTTAGAGTAC	AATAAGCAAC	360
	TGGCAGCAGC	CCTACAGCTT	GGGcTAAACT	TCTcCaTtAT	GtgAAACGGG	AAAGACGAcA	420
	ATgcCTCTgA	ACGCTTTTCAC	GCCACTTTTG	GtGGcCCAat	tGcATNGNTT	CCGNAANTAN	480
35	NNTTTTNTNN	TNGGGNTTTT	TTGGNNNAAA	AAAACCNNNA	AAAAAGGGGG	GGGGGGNTNA	540
	AAACCANGNA	TNNTTTTPTT	NGGGNNGGGG	GGGGCCCCCT	TTTNTNAAAN	CCNNNCCCCC	600
	CNNNNAAANN	GGNNNTTNNN	GGNNNAAAAA	TTNNNNNTNN	NTTTTtNGGN	NNCCNNNNNT	660
	NCCCCCCNA	NNGNCCNNNC	CCNNNNTTTT	TTTTNTNNNA	NNAAANCNCC	CNNGGGNNGG	720
	CCC						

## 1045UP

	GATCTAATAA	CCACCCGTTG	TATATTTGGG	CGGTAACTA	TATATGGGAA	TCATATAAGT	60
	GCTTAAAAAC	ACCTCACCAG	CAAGGGGGTC	ATCTATAAAC	AAGCCATAGT	GTGtGTATCT	120
	TTGcCTACAT	AGCATCATGA	CTATGTTGCG	CACGCGTCAT	TTGCACTGTT	TTAGCATGTA	180
45	ACTGGCAGAG	CCAGCAACGA	ACAGAGCTAA	TTTTGGAGGC	TTACCATACT	GtTGTCGCTG	240
	GATGTTGAAG	CaCGGCTGTT	GTGGATAAGT	TTAGAACCCG	TCGCCAGCAC	ATTcATACCC	300
	TGAAACTACC	AGTTCCAGGG	GACATGTTCT	TCGtGGCTTT	GACAGAATTA	TTATTGTAGT	360
	CCAGTTAGAT	GtACTACCAT	TGTTGcGCTA	ACATAATCAC	CAtTGTcAtC	TcTGGAAATCA	420
	CGTgTcGCCA	AGCATATTaA	TGTTTGTaCT	TAAACTCGGt	aCTCCCTtta	TCGaaAGGcA	480
50	TCACGGAATC	GcCCTtCACT	aT				

## 1046RP

	GATCGCGCGC	GCAAGCCCGT	GCgCGAGCTC	GAgcaggTTC	TCGAGGTGCG	GGGGCAGCGC	60
	GTCACACGAG	TAgGCGTAGG	GATAGAGGAT	CTCCTCCGAG	TACGAGTGCA	GGTCCAGGTA	120
5	GGCGTAGATG	TCCAGCTCGG	CCTTCGTCTT	GTTACAGTAG	TCGTTCCAGC	TGCGCGCCTC	180
	CACGGCCTCG	AACGGCTGCT	GGCCGCTATA	GTCGCCCAG	CAGGGGTAGG	CGTGCTGGCC	240
	GGTCCAGtGG	TAGTCGAACG	AGTGGTCAAT	GTCGACGCCA	TCGCAGCCGG	GCATGTACGT	300
	GGGCTGCCGG	tTCTTGCGCC	ACAGGCGGTC	GTGCGTCCAC	GTGTACGCGT	AGCCGTCTGG	360
	GtTGAACACA	GGGATCACCA	GGAAGTCGAG	CGCGTCCAGG	tAGCGCGTCT	CCTTGGGCGC	420
	CCGCCCATAC	CGCGAGAGCA	GACGCTCCAC	GACAAAGCAC	GCCGTGctCA	CGCCAATCCA	480
10	CTCGCGAGCA	TGCACGCCgt	CCGTAATTAC	CACCG			

## 1046UP

	GATCCGGGAG	CTCCATcATT	AGAGGGTcTg	gACTTCGGGA	AGACACGCAG	TGGTATGTCT	60
15	GTAACTTTGC	AATTTCAAAT	TAATTCCTCT	TTCATCGTAG	TTCGGGCTGC	TGGGCGATCT	120
	CCGaCACAAA	CGGCTGAGTC	GCTGACACAA	ACAAAACTC	GACTACGGAA	AACGACTAAG	180
	CGTCGCAGAT	GCTATATATA	TACAACTTGG	TTCCTAATTA	GGGTTAGATC	CTTGCGAGAA	240
	ACAGACGTTG	AGCTTGTGCA	CTTCACAATT	TTAGTCCCGT	CTCCGAAGTT	TCCAGGCAAC	300
	ACGAATAACA	ACACATATTG	CCATGGCATC	GGTAACGTTT	AAAGACAATG	CGGAAGTGAT	360
	AATGATAGGT	GAGCAGGATC	GGAGAAGAGA	GCAAGGtATG	GCCAGGCCCT	GGATAACGGG	420
20	ATTTCATCGAC	GCGGATATCA	TGTGGCAAAA	GGACGGtCCG	TAACTCATAG	TAGACATCgC	480
	CAAAGAGAAC	TTCGACAGCT	TATATTGACA	TTCGTCTCTT	TGCTCTACAT	TGTTGAGGCA	540
	AAGATATAaG	AgAGTATGGt	G				

## 1047RP

	GATCGAGTAG	ATGTTCCGCA	GCgCTGGCAT	CTTcagGTCC	CGGTACGTCA	GGATGAACTC	60
	GCCAATGCTG	GTATCCAGCG	TGAACCCGTT	GACGCCCTGC	CCCCTCGTTA	GCATGACGTG	120
	CGTGGACGCG	CCGTACATCG	CGTAACACGC	TGCCACGATC	TCCCGGCCCG	ACCGCAGCAC	180
	ATCCTTGATT	GTCCCGCTCG	AGTCCGGAGT	CAGCTTGAAA	ATCGAAACGA	TCGTGCCAC	240
30	CGACACACCG	GCGTCCAGGT	TCGACGACCC	GTCAATCGGG	TCGCAGCACA	CCGCATACGT	300
	CCCACCGGTC	TCCGGGAACA	CGATCAGGTC	CTCCTGCTCC	TCCGACACCA	GCACCTTGAC	360
	GTTCCCGCTG	GCCTTCATCG	CATTGATGAA	GATCTCATCG	CCCAGCACAT	CCAACTTTTT	420
	CTGCTGGTCC	CCAGTCGCGT	TAGACGCGCC	GGAGAGCCCA	ATCAGGTTCA	CCAGCTCCGC	480
	GCGTCTGATC	GCTGCGGAGA	TGAACCTTGAA	CGCAAACGAC	AGTGAGTTgA	GCAGCAGGTT	540
	GAACTCGCCC	GTCGCGTTTT	TGGCCGAgCT	GCgCTGCGAC	TcCAGGATGA	AACGCgCCAg	600
35	CGTAATGATA	TCCGtGTCgA	tAgCCTCTgC	GGAgTCgCGT	CTCTGTGGGT	TCACGGtAGC	660
	CATTTCTGcT	TGAGTgCGCT	GTGGT				

## 1047UP

	GATCACTCCC	CTCGCTTGAA	ACAATGCCgT	aTAGCGGAAT	CTGGCCGAGC	ACCAAGAAGA	60
40	TCAGCAGCGA	GACGGCTGTC	CAGATCAACT	TCTGGTTGTA	TGGCACTTTG	CGCTCGGGCG	120
	CGATCACCTC	GGGCAAAAAA	GCCTCGAAGG	GTTTGAATAG	ATCCAACAGA	CGCCCACTCA	180
	TTTCAGGCTC	ACAATGTTTG	TAGGTAGCTT	GCTGGGCTTG	GATTGGCTAC	ACAGTTGGAA	240
	CCACACAAAG	TCACTATTGG	GCGAGATGGT	ACTCTAAATG	ACTGCAAGGA	GAAGTGGTTCG	300
	GTTTCGTTTT	CTGAACAGCT	TAATTGGACT	GAGTTGCAGT	AGCTGTACTG	AAAGGAACAC	360
45	GTATCTTGAA	AAAATTATAA	ATCTCAGTAC	CACGTGACCG	GATaCGAGGT	GCTATTCCAT	420
	CTCGCTAGAG	GAGCTATATG	CCTAGTCGGC	GTACCCCTGG	TGAGTAAGAA	TAGCTCTCTT	480
	GGACAATAAT	CCGtGATGAC	CTTATTATGC	TATAAAGCTA	TTTTACATAG	CAATGGATCT	540
	CCGtGtTTAG	ACCTTTGCGC	CGcCAAAAGA	CCAAGTACAT	CAGCACCGAG	AACAGcAGGC	600
	AATCGcCAGG	CGCTTGTGGA	GCTCCAgAAG	ACATgCTgGA	TGCAAACCGG	AAGAACgCCG	660
50	nTcGGAGTaC	AGTTGGCG					

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1048KP

	GATCGTCATA	GTCCGCCTCG	TCGTATTGGT	TCCTTCTGCG	CCGGCGCTGC	ACCGGCATAC	60
	CCATCGCGTC	CACCTGCATC	TTGTTCATCCG	CGTCCATCTC	GTCGTCCAGA	AACACCTGGC	120
5	TATCGTGGAG	CATCCTGTCC	CGCGCATTGA	GCTGCGCGTC	GATCCGTCCG	CGGTCCGCCA	180
	ACGACAGCTC	CTCGTGCTCC	GCGTCGTCCA	CGCCCTCATT	TTCATAGAAG	TCCTTGTTGC	240
	GATTGGCGGT	ATAGTCCGCG	TACATGTCTG	CGCCCACCAG	GTCGACCTCG	TCTATGCGCT	300
	CTTCTGCGTC	ATCCAGGTCT	TCTTGCAAAC	TCGATGCGCT	CGTCGCCGTC	GGTAATCGGG	360
	GTTCCTCGAAG	TCGATCTTCG	TCCCAGGGGAC	CCCAGGGGGG	ATTATTCCCC	CATACGGGAA	420
	GCGGGGCCCG	CTCCCAACTT	GTGGGAAGAT	AGTGGGTGCT	CCGAGGTTCT	TTTGACCTGC	480
10	TGTAATANTC	CNCTGTCTTT	TTCCGGTTCAA	CTNTAGCCCT	CNCGGCCNCG	TTNACCCCCC	540
	ATCCCGTATG	GAAGCANCCA	ATAACAAATG	CCTCCGAAAA	NTTTGTNTTT	TTCCNATTTT	600
	GGAANAAGNA	AGTTC TNANA	ANGAATTTTN	NANTTNNN			

1048UP

15	GATCGCGCTC	CTCAGCCATG	GCTTCCTCTA	ATAGTAACAC	ACGCCCTGCT	TCGTAGTCGT	60
	CGAGGTGCAC	ACCTACCCGC	GCAAATAATG	CCTCATCTGA	CAGCTGCACC	TGGTAGAACT	120
	GTGAGCACCG	GAAGTGCAGC	TTGCTGCAGA	AGCTTGTGAG	ATATTTGTAG	GGGTTGTTCT	180
	GTGTCAGAAA	GTGCTCACC	CGTCGATTCT	CGTAGGGATC	ACGGATACGA	CCTTGGCTCT	240
	GCCCCGACAG	CGGGTACCCG	CATAGCTTGT	TTAGATTGCG	CTCATCTATC	AAGTCTGAAT	300
20	ATGTCGGCTT	GGGGAAAGAA	CCTTCCCACG	TATTTTAGTG	TCTCGGGTGT	GCATTCTTGT	360
	CTTGCGAAGA	GCAGTTCGGA	GCAATTTCGAC	CGTCAGAAGG	TCCCCCTCCT	TTAGTGAAAG	420
	NNGCGATGTT	GGTGATAGGA	ACTTAAAAAC	CGTTTTGGNT	TNTCNCAATA	GNAGCCANNA	480
	CCTTANGTAC	GGTNTNCCGT	TCTTAAACCC	CGCGGGTCCC	NGGGNGGTTT	CAAGTTCTTG	540
	GNGGGANAAG	GTNCCGNTNC	CCGGGGGTNC	GCCTACTTAA	GNGANGCCAN	AAGGNAAAAG	600
25	NCCCCNGAA	AAGTGGNTTT	T				

1049RP

30	GATCTTTCAG	CTTTGGCGTG	CTATGGCAGG	CAGCCTGCGC	CTTTATGGCC	TCAATGCCTC	60
	GCTGACGACT	CTCATGTGCC	TGTGGGCAAT	CTGGTCACGT	GGGTACTATC	CAGCGACGGG	120
	ACTCCCTATG	GCTGTGTCAG	ACAAAGCGAA	ACTCAGCATG	CTCTACGTGC	CCTACTTCCT	180
	GATTCTCTCG	CGCCTCGTCT	TTGTGTGAGG	TCTGGAGCAA	TGCAGAAGTG	CAACACTCTA	240
	TATATAATCA	CCTGACTATG	TACCTATTTT	TGGCATAGCA	CGTTACGTTT	TGTCACGATT	300
	CCAGTCAGTT	AGCTGCCTCG	AGCAACCCGG	GAGCTCCGAA	AAGGGAATTG	GCTACAAGGT	360
	CCTTAGCGCAT	AGNCCTGCAA	CTGGCTTTGG	CTAGGTCAAT	TGGTTTTCTT	GGAACCANTC	420
35	TTGGTATAGA	CTCTTGCGTA	TTGATCGGGC	TGAGGAGTGT	TTTNGNGGNA	GNCAACACC	480

1049UP

40	GATCGTCTCC	TCGGCGACAG	CGCCTTCTAG	ACCCCTCGACG	GGCGACACCT	TGATGCTGCT	60
	CTCGCTCTCA	AACGTACCCA	GACCCTTGTA	GTAGGTGACG	CCGTTTTTCT	TGAAGAGCAT	120
	CTCAATACCG	CCAGTCAATT	GCTTCACAAC	GGTGTCTTGT	GCCTTTTGGA	ACTGGGGCAT	180
	GTTACACAGT	ACCTCGCCCT	TGACGTCTGAT	ACCGCGCTGC	TTGGCATCGA	GTTGCATCTG	240
	GTGCAGCAGG	TGCGAGTTGT	TTAGCAGCGC	CTTGGATGGG	ATACACCCCA	CGTTCAAACA	300
	GGTGTACACT	AGACGGGCGG	GCTTCTCCAC	ACACGCGGGG	TCGAAAACCA	GTTTGTGCA	360
45	GCCTTCGATG	GCCGCCACNN	TTAACCACCG	GGGACCNCCA	CCCATCAACC	ACAACGTCGG	420
	GGTTTTCTTT	TGTTGGGAAT	TCAACCAGGC	CCNCTTTNNT	GGGACGACCN	CTTANNC	

## 1050RP

	NNNTPTTNTGG	TGGGGCGTGT	AGANTAGTGG	TCGGGGNGCC	GCTCCACATT	CTCCATGCTC	60
	ACCACCACGA	CAGACTGGAA	GTACAGGAAA	AGCGACATTG	TCGTGCGAGA	GATGTGCGAC	120
5	GCGGCGTTTCG	AGTTCCCAAA	AGCAGACAGC	GTTGCGGACG	CCAGCAGTCC	AAGCCCCGCA	180
	ATTGTCGCCG	TCGCCCCACTT	CACAGGTGTT	TGGGCCACGG	TGCGGCCGTT	CGTGAAGTGC	240
	GTCTGGATGc	ACGACACCTG	GTCGTTTCGAC	TGGGTTTCGT	GTACCATCAC	CTTGAGGTAG	300
	GCGTCATTGT	CCGGCACCTG	GTACGtCACG	CCGGGAATCT	TNPTTGtGTT	CTCCGcGCTC	360
	ACATACTGcA	CGGcCTGGAT	CTgaaTGTCa	CCGGGtGTCA	CAGGAcAAAA	CTGcTTCtAG	420
	cCGATCCCAT	ACATgTcCTT	CGc				

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## 1050UP

	GATCCTTTTCG	TATGAAGTAT	GCAGCTGTCG	ATATGCTTAG	TTAACTTCTG	CCCAGCTATT	60
	TAAGCTGCAA	TTGAATCGGC	GGTGACTCAG	CTTGCAAAGG	GTAGCAGAGA	GGACGCGATG	120
15	GGTTTATTTCG	GAAAGGATAG	AGGTGAACGG	ATAGCTGAGT	TTCCGTGTTA	CCTGCTAGAG	180
	ACCNGAACGC	ATCTGGTGCC	GNTGNCAGGG	GATTCTATAC	AACCTTGTGA	TCGAGCGGAC	240
	ATATNGCGAG	CGGATACTAG	GGCAGNTCCC	TGGGATAGGT	GAGGCTNTAG	ACGGGGCGCT	300
	GACGGGCGCT	tttGAGGCCg	CAGAGGTACC	CCCGCGGGTt	GCGGAGGTGA	TGAAGGCGTT	360
	CCAGGAGCGG	TACGACTCCC	GGGGACAAAA	ACGCAGGCCC			

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## 1052I2

	GATCTGGGTT	GCGCGTGAAG	ACCACCAATG	CGATGCACAC	GAGTATCATG	ATCAGCAAGA	60
	TTAAAGAAAA	GACAGCGTTC	AAAAATAAAA	ATACCCATGC	CATAATGGAG	CTGACGCTTG	120
5	CAGGCTGTCC	AAAGAGCCCT	GAGAAAAATA	AGAAGAGGAA	CGAATTAACA	AGAGTAACAC	180
	TGGATATCAT	AATGTTTCAGG	ATGTTAGTCG	CGCGGTCGAG	GTACGGCCTG	CATTTAGCCA	240
	GAGCTGCGAG	GTATATTATT	TCAATGACAA	ATAGAGCGAC	GGCCTGGGTT	TTACCGGAAT	300
	TGTGGGCAAA	TGCAATAAAT	ACCGCTTTCA	ACAAAAATATG	CGCGAGGATC	ATGCAGGACC	360
	ACCAGTAGTG	TGTCGCACTG	TACATTGTGT	AGAAGAAGCC	GTATTGTGT	AGCACATTT	420
	CATTGCCGCA	TAGAATGGCA	GCTGGGTTTCG	AGTGACACACC	AATGGAAAGCC	CTTCCACNGT	480
10	AGATAGTGCG	GCAGGCAGCC	CANCCCATAA	TTGACAAGAT	AAANGTNGAG	CTAAGNCTGC	540
	CAGAACGACC	NCCGCCGGGG	ATCANCGTTC	ANTGATTCCC	CACCAGCAGA	GATCGCNAAT	600
	GANTGACCCC	GGCAGTTNTN	CGCAA				

## 1052I1

	GATCTCCGCT	TCAAACCAGC	TAGGGACGAC	CGGAGGTCGT	TCCAGAGAAA	GTCAACAATC	60
	AATATCCTGG	GTAAAGCTAG	CACCGCCGAA	CTACTTGCTC	TTGGCACCAC	CGCAAAGGCA	120
	CACAACGAAA	ACTGGGAAGA	TGAAC TGAAG	AAACAACAAA	CGGTCACCGT	TGATGACCAG	180
	GTTGTTTCGC	CAGAAGATTC	GCCCC TTTGCA	GAGCCAGTGC	AGGAACCAAA	GACCTCAGTG	240
20	TCCGGCTACA	TCAAGAGGAA	ACTATCCCTC	AAGCGTGATA	AATCCACAAG	ATCCAAATCGT	300
	TCGCAATATG	ATAGGTTACA	GGACTAGATA	TGGATGTTAA	GTATAGAAAA	ACTGTATATT	360
	ATTTGACGTG	CTGGGCGTTA	CGGAAACATA	TAAAGATTTA	ATTACTCATG	GGCGGATGGT	420
	ATTTTTCAT	GGGCCCCACT	GGACTCCATT	TGGGCAGTTG	GAGGACGAAG	TAGGAACCCA	480
	ATTGCTGGTT	ACAAGCGCTC	GGTTTCATGT	ACCCTATACA	CAAGTATCCA	TTATTINGGGC	540
	TTATTGATTT	GTGCTCNTGG	GCCGGACTTT	TANCTTTCTC	ACTGGGGGAN	GTCCT	

## 1052RP

	GATCGCGGAC	GCGTGGGCGC	AGAACCTGGC	GTGGAGCATG	GGGCTGATCC	GAGTGGAATT	60
	CATGCAACGC	ATCTTCCGGT	GGTACGTCCA	GGCGAGCGGC	GGCGAGCCGT	CGCTGCATTT	120
30	GACGTCAACG	ACCACGTCTG	TGCTTGCCCA	ACGCTCACTG	GATGCGCTAG	TGGGCGGGCC	180
	CGTGAGCAAG	GCGACACAGT	CGCTATTTGC	CAGCACACAC	ACGATGATCT	TCAGAGGGAT	240
	CCGTAGACTG	GCCTACCGTG	CGAACATAGA	GAGCTCATCG	GTTGTGTGTA	CCGGGCTAAC	300
	GTTCTTCCTT	CTGTTCGGCT	ATTTGGATTG	GCGTGGCGGT	TTACATTTGT	TCAAGCGGGG	360
	CTACTCGGAG	CTGCTTATCC	CGCATGAAGG	TCAATGAACC	CAGGTCCGGG	TCCCTAGACT	420
35	TCCAAGAAAA	ACGTGGGTGA	TTGNGCTCAA	AGGTGTTCTT	TTGGGGTANA	TCCTCCCCCG	480
	NGTTCA						

## 1052UP

	GATCCAGCTC	TTGCGCGGTA	TGAAC TTTCC	CGCCCGCACC	GGCGCCTCGC	ACACCGAAAT	60
40	CGACCGCACC	TCCGTCTGCG	TCTCGTAGTT	CCAAATTTCC	GCGCGCCCCG	AGTACAGCGT	120
	GATCAGCACC	CACGGCTCGC	TCCGGGTGAAA	GTCAATGCCC	TTCACCCCTGT	CTGTCCTCGA	180
	GACAAACGTT	TTCTACTCAC	GTTAGTACTT	GCTCCGCGCC	CTGGATAGCA	TGGTCGAGCT	240
	CTGCGGGTCC	GCCCCCTCCG	TGGGTGGCAA	AGATGGTCTT	CAAACACACC	GTAATAGGCC	300
	GTGCGCGACC	ATGCAGGCC	CATTCTGCTC	CGGACACACA	CATACCTTCG	TTTCCAAACT	360
45	TCATTGGTCC	CCACTTGGGA	TTCTTAGTAG	CTGTTCAACT	CGGCTTTTGT	GGTTCTTGTG	420
	GAAAANTAAT	ATTCCCN TGG	ATTATTTAAA	TAGGGGTCCN	TTTTNTTT		

## 1053RP

5 GATCATAGTG ATTGATATCG GGAGAGGGTT TCgTaTGTA CAGCCTGTAT TCACGTATCT 60  
 GGTCCCTTAC TTCATATATT TCTTGTGGGA GCTGTGAATA TATCTCCATG CGTTCTCTGT 120  
 TCCATTTTTT GTGCATTTTG TGGAAATGCAG CCCACTTCTC GTACGTTGAA GTAGGCTTGG 180  
 GTACTAACGA TCCCTGAACA GGGAGGAGGC ATGTTGCCGAG GGAGAATATT AAGGAATCAT 240  
 ATCTCATTTT TACGTCTGAG ATAAGCTTCA CTCTTATACG ATGTGGAGTT GATTCACTCC 300  
 CGTAGTAATC GTATAGGAGC AAAGCTTCAT CTCTTATACG ATGTGGAGTT GATTCACTCC 360  
 ACTGCAGCCC TTGGTATTTA GCCAGCATTG CATCATATTT GGACTGATAA TATTGGAAGT 420  
 TCTTCCACGC GTCCTTATAC GGATCAATTA CTGATTTTAC AACATCGAGT AATATGGAAA 480  
 10 GATATAACTC TGGATTGCCC TGTATGACTT CCAGCACGCC ATGGAACATA TcCCGAATGC 540  
 CGTCGCGGCA CTGGGAGACT AACTTTGGCG TGTATATCTG CTCTTCGACT GtCCCATGGt 600  
 TGAgGtAGGt ATCTTCAGGT aGAATGAAGT CAATGAGCGA TAAACTGaCT TGCTTGAATC 660  
 gtccCAAAGA GT

## 1053UP

15 GATCTCGGCT CGcTGCTCGC GCTCGAGCCC TACTGGGCAG AGCGCTACCC AATAAACAAC 60  
 GCCCTAATCG GCGGTGCAGA TAAATTGCAC AAGCTCTACT CAACCGATTT TGCGCCCATC 120  
 GTCGCCGCCA GGACTTTCCG CTTGAACCTC GTCGACAAGC TTGGACCGCT GAAAGACCTC 180  
 20 ATAATGGCAA AGGTCAGCGG CCCAAATTAA TAGTCACGTG TACATAAAGG TTTTCTTAAT 240  
 AGCTATACAG CTTGCCCCGG TCCTCAGCTT GCAGCGCGCA ACCGGCGTGC AGCCATGAGC 300  
 GTCCTACTGG AAACCTACCAT TGGCGACCTT GTAGTAGACC TGGACTACAA GACATGCAGC 360  
 GCCGAGAGCT ACAACTTCCT CAAACTCTGC AAAACTCGCT TCTACGACTG TCAGTGCATC 420  
 TAcCGAcCTc CATCCTgAaG GCTCAGCACG CCCTcGGCGA TCCACAGGTG GgCTTTGCAT 480  
 TCCGCACGGA TTTGCCTGTA CACAATACCT CGATCGAaG CCTGCGCGAc ACACGGGCGG 540  
 25 TCACCCCGAA GCTCATTGAA GCCTcCGTTG CCGCTcAACC CGCAGAGCGC TTcGGACAGG 600  
 TCgCCTTTG

## 1054RP

30 GATCCGTCGC CGGTCCGccA ACGACAGCTC CTCGTGCTCC GCGTCGTCCA CGCCCTCATT 60  
 TTCATAGAAG TCCTTGTTCG GATTGGCGGT ATAGTCCGCG TACATGTCGT CGCCACCAG 120  
 GTCGACCTCG TCTATGCGCT CTTCTGCGTC ATCCAGGTG TCTGCAAAC CGATGCGCTC 180  
 GTCGCCGTCG TTATCGGGGT TCTCGAAGTC GATCTCGTCC GGCGACCCCA GCGGCGAATT 240  
 ATTCCCCATA CGCGAGCCGC GCGCGCTCCC AACTTGTGGC GACGATGGTG GGTGCTCGTA 300  
 GCTCTGTGAC CTGCTGTCAC TACTCCGCTG CTCTGTATCG TTTTCATCTC TAGCCCTTCT 360  
 35 GCGCCCGTGT GAACCCCTCCA TTCCGTTATG CGAAGCCATA CCCAAATTAC CAAATTGCCC 420  
 TTCCTGAGAT CTTGAATACT ATCTCCCAGA TGTTTGACAG ACGCGCAGCT TCTcACGATA 480  
 CGAAATATCG TGAtTTTACG TGAcTTTCAA TACCTCATT gGATTGGATT GgtGAAGCAT 540  
 AGATTTTCAG TcaTATTGAA AAATTATTTT CAAACAGGGC AATTGGATGA GCTG

## 1054UP

40 GATCGTCGCG TTgcgCagGG CTGCCCAACG AAGCCTTGAC ATGTCAAACC GCTTGAAAAGA 60  
 AGAGGTGATA TGGGCCACCC ACGAGGCCAA GTGGGAGCAA CTGCTCGCTA CTGGGACCCT 120  
 TCCCCAGAT GGGGCCAAAA GCGACTGGAA GCCTGGCCGA GCATGGCTGG AACCATATGA 180  
 45 GGCCGCGTTT CGGAACCAGC TTGCAAATCG CAAGCGCAG AGCCAGAAGC TCAAGCGCTA 240  
 TAGTGCCCAA ATCAGCAAGG TACACCTCCC GTATTACATT AAGTGCAGTG CTGCTATGCA 300  
 TACCCGTCGC GCCAAACGCT tCGAGTGTt CCAGAAAGAG CTCCACACCG TTAATCCATT 360  
 CGTTCCAGGC AGAGATCTCG GtTCCCTACT CTCCAAGTGG CGAATGGTGA ACCGgAAAAA 420  
 CTACTATCGC TGAATGTATA TAGtTTATAG TCCTATTCCCT TCATcAGGtC TCCCAGCAGA 480  
 50 GCGGCCCGCT CCGTCTcAAC TATGCGCACC TCGTcAGCC ATTCGCTGAg GTCCTTCTGA 540  
 GTTCG

## EP 0 866 129 A2

## 1055RP

	GATCCGTCGC	CGGTCCGcCA	AcGACAGCTC	CTCGTGCTCC	GCGTcgTCCA	CGCCCTCATT	60
	TTCATAGAAG	TCCTTGTTGC	GATTGGCGGT	ATAGTCCGCG	TACATGTCTGT	CGCCACCAG	120
5	GTCGACCTCG	TCTATGCGCT	CTTCTGCGTC	ATCCAGGTCTG	TCTGCAAACT	CGATGCGCTC	180
	GTCGCCGTCG	TTATCGGGGT	TCTCGAAGTC	GATCTCGTCC	GGCGACCCCA	GCGGCGAATT	240
	ATTCCCCATA	CGCGAGCCGC	GCCCGCTCCC	AACTTGTGGC	GACGATGGTG	GGTGCTCGTA	300
	GCTCTGTGAC	CTGCTGTAC	TACTCCGCTG	CTCTGTATCG	tTTTCATCTC	TAGCCCTTCT	360
	GCGCCCGTGT	GAACCCTCCA	TTCCGTTATG	CGAAGCCATA	CCCAAATTAC	CAAATTGCCC	420
	TTCTTGAgAT	CTTGAATACT	ATCTCCCAGA	TGTTTGACAG	ACGCGCAGCT	TCTcACGATA	480
10	CGAAATATCG	tGatTTTACG	TGACTTTcAA	tACCTcAtTT	TGGAtTGGAT	TG	

## 1055UP

	GATCGTCGCG	TTgcGCAGGG	CTGCCCAACG	AAGCCTtGAC	ATGTCAAACC	GCTTGAAAGA	60
15	AGAGGTGATA	TGGGCCACCC	ACGAGGCCAA	GTGGGAGCAA	CTGCTCGCTA	CTGGGACCCT	120
	TCCCCCAGAT	GGGGCCAAAA	GCGACTGGAA	GCCTGGCCGA	GCATGGCTGG	AACCATATGA	180
	GGCCGCGTTT	CGGAACCAGC	TTGCAAAATCG	CAAGCGCACG	AGCCAGAAGC	TCAAGCGCTA	240
	TAGTGCCCAA	ATCAGCAAGG	TACACCTCCC	GTATTACATT	AAGTGCAGTG	CTGCTATGCA	300
	TACCCGTCGC	GCCAAACGCT	TCGAGTGTTT	CCAGAAAGAG	CTCCACACCG	TTAATCCATT	360
	CGTTCCAGGC	AGAGATCTCG	GTTCCCTACT	CTCCAAGTGG	CGAATGGTGA	ACGGTAAAAA	420
20	CTACTATCGC	TGAATGTATA	TAGGTTATAG	tCCTATTCTT	TCATCAGGTC	TcCCAGCAGA	480
	GGCGGCCGCT	CGTTCTCAAC	TATGCGCACC	TcGCTCAGCC	ATTCTGCTGAG	GtCCTTCTGT	540
	AGTTCGTCAC	CCG					

## 1056RP

	GATCATCagC	GCGAGCTTCC	aATTtGTGGG	CTTTCTGTtG	ACATACATCC	TCCaCACCTC	60
	GCATGCGGCG	CGCCAGgGCT	CGCGCTTTTGG	CCTCGGCCTG	ACCTTCACGG	GATACGGGTA	120
	CAGCATGATT	CCTAgCGACg	TgACGAgCAA	GGTCGGcAAG	GACCGCGACa	TCgCgCGCGT	180
30	gGAGCTGGAc	GACCCCAaCG	AATTcGAAGa	TTTCGCACCTG	TACTCgCCGC	TGGCGCAGCC	240
	GGCGCAGGAC	CGCTTCGAAT	CacagCTCTC	gCACGGGCTG	ATGGAAAAAC	GGCGCAGaAT	300
	TCCGGCGCTC	GCGATCGTgC	tagAgATTTT	GGGGCTTgCa	ATTATGTGCa	aAAGCgTGTA	360
	cgACTACAtt	GTGGTcAAGC	GCATgGAGCg	CCGCATctTT	ACTGcGAgCG	ACAGCgAgAg	420
	CCcCGCATAG	ATGTTcATAT	aACTTATATa	TCCCTCATTG	ATCTTCGcTT	GGGCCCCgTC	480
	TAGGGAGCAG	AcCAGcAGTT	TCTTCGTtCG	CCCTNAaGTC	GATgCgCCA	GAGAGACCAG	540
	ACGCCCCAGc	GCGGTa					

## 1056UP

	GATCCAACCC	AGGACTTCTC	GAAAGATAGA	ACTCCGAACA	CAGCCACCGG	CACGAActTC	60
40	TCATCAGCTA	GCAGCAATAC	TAAGCAGACC	TTCAGCGAAA	ATGAAGAAGA	ATCTGATGCT	120
	GAGTTcGAAG	ATGTATAGTT	GTACCCGTAT	ATTGCATTTT	TTTTTTTTTTT	TTTTTTTTTTT	180
	TTTTTTTGGa	gATGTCAAAA	GCTCATCTCA	ACTCCATGAC	CAGCCAGTAG	TGACTAAAAGC	240
	AGTGTGTCTA	GTTCTTCTAA	GTGATTTTAA	GGACTATGAG	CTTTAATGAg	AAGGTGAAGT	300
	GGGTACTAGG	CACTGCTGTT	GCGACTCTAG	TTACGATAAA	GTCTGTGCGAA	GCCGTATATC	360
	GCCTCTATGC	AGCTAAGCAG	AACACTAGCA	GGAGCATTTC	TGGGGAgGAg	AAgGACGTaA	420
45	GACTGGCCAA	ACGGATTCTG	GAGTCTAGGG	CGTaCGATGA	gGAATTATaT	CgGGAGCAGT	480
	TAgCTCGGAa	CTACgCaTTT	TGGGCGAAgA	CGGTaTgGCa	CGACTACaGG	AACAGTACTC	540
	ATATgGTGGG						

## 1057RP

	GATCAGGGCC	AAATCACTGC	TAAGTACAAA	CACAAAGGGC	CAAGTATTAA	GGTGAGAGAG	60
	CGTTACAGGT	GCATTGATAA	TACCGCAGGT	ATATATCAAG	GCGCACAGTG	AACACATTCT	120
5	GCAGACGATA	GATATGTCTG	AGACGAAGTA	GGTTGAGATA	TTTACGCACA	AGCCTCATT	180
	GTAAGATAAA	TGGTCATTAC	TAACGTTTTT	GGGTTTAGCA	GCAGCAGGCG	GAGCAACAAC	240
	GAGGGGCAGG	AGCACGGTGG	TGGTGGACAG	GGTCCAGGAG	TCGAGGATGG	CGGGGAGCCA	300
	CGGGCCAGGG	CGAACACGCG	CAATGTGACT	GTGGCAATCC	AGTACTCGTG	GCTCCACGAC	360
	ATGAGGAATG	TCGGGGGAGA	GGGCGAGGAA	CGGGACAGGG	CCCGGGGGAG	AACGGAGATA	420
	CGTTTCGTGAT	GAGCTTCACG	GACGTGCCGG	ACTCGACGTC	GAACGATCGG	TTTCAGGAAG	480
10	TGATCGGCAT	TGCGGCGCAG	TTTGCAATTGA	GCCGCGTGCG	GCGGCGGATC	AGCCTCCTGC	540
	GGGGGCTCTC	GAAGGAGTCC	TTTGAAAAC	CCCTCTCAGG	AAGCTCAGCG	AGCTGGACAG	600
	CGAGCTGTGC	AGTATATGCT	ACGACGACTT	TGAAGACGAC	ACGTCGATCG	GGT	

## 1057UP

	GATCTAGGGG	TTCTTCTTGC	CGCGCTACGG	GCGCCCCCTCG	CAGCCTCGCG	CTGGCTCCCG	60
	CGCGAGAGGG	GATCGGCAAG	GCTCCTCGCA	GCCGCACACT	GCGTCTATGC	CTGGACCGTC	120
	CGGCGAGCCG	GACAGCCGAG	GAGCAGCCCC	GCGATGTCTG	TCTCCCCGGC	GGCGCTTACT	180
	CTGGGGCTGG	TGTTGAATTT	TCCTAAAAC	GGTGAAATTG	TACGGGCTCG	CTGGAGCCCG	240
20	CGCTGTCCGA	TTGTACACGG	GAATAGCGGA	TCAATTGGAT	GGGGACGCCA	GTGTTACCCC	300
	CGAAACCGTG	CGCAGCGGCT	GGCGGGCCGA	GGGCTGAGGT	GCCGCTGCCG	CGCAAGGCGC	360
	ATTGTCTGTC	GACTGCAGAG	CTGCAGGAGC	TGTTGAAGGC	GCAGGACAAG	TTGCAGCTGT	420
	ACGTGGCGGG	GTTGTGCGAG	AGCGAGGAGA	CGCAGAAGCG	GGTGGAGCAG	CAACGAAAAC	480
	AGCTGGCTGA	AATACGGGAA	ACGTTTGCGG	GGCTGGAAGG	GGAACGACAG	CGCGTGCCAG	540
	AGCGGCTGGA	CGGGTATCAG	AGGCTAATGT	TCCGGTACCA	TGAAGCGTGG	CAGGCGGTAR	600
25	ACGGGCGTGC	CGGGCCCGTT	ACAACGACGG	GTTCTGCCGG	CGCGGCTGCA	CAAGAAATGC	660
	GCGCTGCG						

## 1058I2

	AAGCTTGCAT	GCCTGCAGGT	CGACTCTAGA	GGATCTTGCA	AAGTATGGCT	TGGTAGTGTG	60
30	GTGATGGTTA	TCTGCAGTTT	CAATTGCTTT	GTTAGTTAGT	GTATCACATT	CTTCTGGCTT	120
	TGGCCGATTA	GAGTGCTGGG	CCTCATGGAT	GGGGATCTCC	GGTGTATACA	CGTATATTTA	180
	TTCTCTTCGC	CCAAGTGGCG	GAGTACAATT	TTCTCTAGC	TGGACCTATT	TCGGTTGTAT	240
	TTCAGTAGTG	AAATAAAAC	ATCAATTAA	TACAGCTTCT	GTATGACTCT	GCCACAGGAT	300
	GAGAGCAGAC	ACTCTGCAAA	GTACCGGATT	TCAAATAAAT	GTTTAGGAAT	AAAATCAAAG	360
35	GCGTACAATT	ACATAATTAT	AAAATGCTCT	CGTAGCTATG	TCTTTCCGGT	CTTTTTTTTA	420
	TCTTAAAGTG	AACATCGAGT	CTTGTCCTTC	TAGGTGTTT	AGATGACAAG	CTTACATGCC	480
	TGCNGNNGNN	AAACAGTTNG	TGGAATCCCT	CGGATCCTCN	CCANGTAGNA	AGGNANTACG	540
	NNCAGCAGAG	TCATTACCNC	NACCCACCGG	CTTGCCANCC	NANTTNCCTN	GGNNGNAGNG	600
	GGNNGGNGNT	TGNACCNANN	TTTGNCCNT	NGCC			

## 1058I1

	GATCTTCACA	TTGCGCATGCA	GGTTCTTCTT	GTTTTTAGTA	GCACCCTCCG	GCGCCTTGTT	60
	GGCCTTCAAC	TTGAGTTCAT	CCGCACTTGG	CTTGATAAGA	CCAGCTTTCA	AGTACACCAT	120
45	GATGTCGTG	TCATCACCGT	GCTTAAAGCA	ACAGCGCTTG	CCATAGCGGC	AGTAGCCTGT	180
	CTTACTCCAA	TTGATACATG	GCTTCGTGCG	GAATTTGTCC	GACCGCTCCT	TGAACTTTAA	240
	CTCGTGGAGA	CCATGGGCAA	ATTGGCACCT	GTTATCGTAC	TTGCAAGCCC	CCGTAGTCG	300
	AAATGATTCTG	CATAACTCTG	TCTTGTAAG	CATCTGTGTG	ACCTTCTCCT	GCGATGGCTG	360
	TGGCTGCTGC	TGTGGGGTGG	CGGGGGCGGG	GACTGAACCC	GGCAAAAAGT	CGGCTCCGGC	420
	TGTGCGCCTG	CTCGCCCTGG	GCGCTCGGGT	CCTCCCGACG	GATGCTGCAG	GAGCGCAGGT	480
50	TTTCGGGCGT	CAGGGTAGTA	TCCCATTTGGT	AGGCCGNTAA	TGAGAGTTTA	TCGCCACCTC	540
	NAAGGTAGGT	TCCCCGTTCC	GNAGGGCCAA	GGGNAATCAN	TNGCCGCCCA	AACCGTNAAC	600
	CNCCCCCNCC	CNGC					

## EP 0 866 129 A2

## 1058RP

	GATCATTCTT	GAGAATGCTC	ATAGTTATGG	TTTAACGGTT	CTTCAAACGG	AAGAGTATCT	60
	TCAATTACAG	AGTAGTTTGG	AGAGAGAACA	GGTAACGTCC	TACAACATTG	CCGAGAAAAGC	120
5	AACTACAATT	GGCTACGTTG	CACTTCCAAG	AACCGAGTAC	GATGAACTTG	TAGCTTCGCA	180
	AGCTTCTACG	AAAGAACAGA	ATTTTGAGGT	ATACGCGGCG	GAAAATGGCA	AGGTCATAGT	240
	GGATAAATCT	GAGTATCACG	ATTTGAAGAT	CAAAGCTATC	CCAGTGATTT	CACCATTGCC	300
	TCAAATGAGC	AAAGAGCAGA	TGTTTGAAAA	GGCCAAGGAA	CTTGGAATGG	TAGCTTTGCT	360
	CCATTGACGA	GTATGAGAAG	TTAAAGAGCC	CTATTTCCCG	ATAACGCTTT	GGATTGCAAC	420
	AGCGAAGGAC	CGCGGAAAGG	TTGGTCTCCT	AAAGGAGGAG	TACAACCCCT	TATTG	

## 1058UP

	GATCTGGCGC	CCCAGACGCC	TGCCCAGGTG	CGCCTGCATC	CGCCGCTCCT	GGTCGCGCTC	60
	GTGAGGCCCC	AGCTCCTGCC	GGAAGCTAGC	CCTCCAGCTC	ATGTACGACT	CATGCGTTAC	120
15	CTTCGTTCGG	CGGAATTTCT	TCTGCTCTTC	GAGCTCGCGT	TCGCGTAGCT	GCCGCTCGTG	180
	CTCCTTCTCT	CGGCGCTCAA	GCTCCTTCTG	AAACCACGAC	TCCGCGTCCT	CCTTTATTGA	240
	CGAGATCAGC	GCAAAACACA	TCTGTATTCC	CAGCAGGATG	TCCTCCTCCA	CCTGTCGCAT	300
	GGACTGGCTT	GGAAAGACCG	TCCACCTCGC	CGGTCAAAAT	GAAATGCTTG	TCCGGAATAT	360
	TCTCCAGTTT	CGCAACACAA	GGGTTCCTCC	GTGCTCGTCC	GGACTTCCTN	GTTCTCTCAAT	420
20	CCCNCTCAA	CCTGCTCGGN	TTTCGGCGGG	GAAGGTNCCA	NCGGGCTTAA	TGTCAC	

## 1059RP

	GATCTGTTAC	GCTGCAGCGC	GAAACCTCCA	ATGCTCTGGG	CCAAGGTTGG	CGGCTGGGAT	60
	TCTTGGGCTC	ACTGCATGCT	TCGGTTTTCA	AGGAACGACT	GGAGAATGAA	TACGGCTCGA	120
25	AACTCATTAT	CACACAACCC	ACTGTTCCAT	ATGTCGTGGA	GTACTCCGAT	GGGACCCAGA	180
	TAACAGTAAC	AAATCCAGAT	GACTTTCTCT	ACCTGACACT	TCGGCGAACC	AAGATAAAGA	240
	ATTTCCAGGA	GCCATATGTA	GAAGCTATAA	TGACTCTTCC	ACAGGATTAT	CTCGGAAGGG	300
	TTATCACTCT	CTGCGACGAC	AACCGTGGCA	TACAGAAAGA	GATAACGTAC	ATTAACACCA	360
	CGGGGCAAGT	GATGCTGAAA	TATGATATCC	CATTGGCACA	TCTAGTAGAC	GACTTTTTTG	420
30	GTAAGCTCAA	GTCTGTACAG	CATGGTTATG	CTTCCCTAGA	CTACGANGAT	GCAGGCTATA	480
	AGCCGCTCTGA	CATTGTCAAG	ATGGAGTTGC	TTGTAAATGG	AAAAGGTGTG	GATGCACTTG	540
	CACAAGTGAT	GCATCGCTCC	CAAACCGAAC	GARTGGCCAA	AGAATGGGTT	ANGAAGTTCA	600
	AGCAATATGT	CAAATCCAG	TTATACGAAG	TGGTTATCCA	GGCC		

## 1059UP

	GATCGTGGCG	GACGTGTTTT	TGCGCACCGC	GGACGTGCTG	CTGAAGATGT	CGCGGTACGA	60
	RGAAGCCAAG	GCGGCGGCGG	ARCGCGGCCT	GAGCCTGGAG	CCGGACCACA	TGAAGCTGAA	120
	GGCGCTGCAC	CTGGAGTCTG	TGCGCAAGTT	GGCCGACTAT	AACGGCGACA	TCTAGTCCGC	180
40	GCGCGCGGCC	CGCGCGGGCA	CCACGGGTAT	ATATACACAG	CCGGTCTCCG	CGCGCCATGC	240
	CGCCCGCCGG	GACCGCAGAC	ACAGGCCCCG	ATCTTGCGCG	GCGGCGGGCG	ATGAGCTGGT	300
	GCAACCTCT	TGGCCCGTAC	CCTGCTAAGG	AGGGTAATCT	CCCACCTCAG	TACTATAAAA	360
	AATTTTAAAG	TTAGCCACTT	TCGAGTTACA	ACTCCCCGCC	TGTCGGGTAA	CGGATCTCAA	420
	CTTGTAAGC	CCCTAACGCT	GCTCTACTCC	TTTTGCGCTA	AGGCAATATC	CCGCCATGTC	480
	TTCGTGGGAT	ATCAATGTCA	CGGTTGATTG	GTTTATTGAT	AGGTTGAAGC	GGAAAGCAGAT	540
45	TACTGGCACG	TACAATGTGT	CGCTGGAGAC	GTTACAAATT	CTGATGCGTT	ACGTATCTGC	600
	CATCCGGTGG	TCGACGAAGG	ACGARCTCAT	TGAACAGATC	CGTCTACTC		

## 1060RP

	GATCTGCTCA	TACTGAGCGG	CCAACTGGTC	GTACTCCGTA	TGCAAAACAT	CTGTGGTTTC	60
	CTGGAAGTGC	GCCACCTTGA	GCGATATCTC	ATTAAACTTG	GTAACCAGCT	CTCCCACTG	120
5	ATGATTGACT	GCACTGGTTT	CCGTCAGCAG	GTCTCCAGT	TCGCCAGTTC	TGGTGTCCAC	180
	TTCCGCCACG	TATCCGCTGT	ACAATGTATA	CTCGTCGTTC	GCAGACCCCA	GARCAGAAGC	240
	TCGCCGCCAC	TCTGGCGCCA	GCAGCTCAAT	TACCTGAGGT	TCAATCTCTG	TTTCAACCGT	300
	TGCCAACAGA	GTGTCTACTT	TTTGGCGTAA	CGAACTATCC	CCAAAAAGCG	GAGGCAGCTC	360
	ATCGTGAGAR	GARGCACCGG	GATTTGCCGC	TACATCCTGT	ATGACTGART	TCTTCCGGCT	420
	CCTAAGCATG	GTGCAGTTGC	TGCCTCAACG	GCTTTCCTCC	TGGTGCARGT	CTGCAGTGGT	480
10	TCGTGCTTAT	GCGCAAGCAG	AATACCATGT	TGAGCCGGCG	AAATCTCATC	ACGTGATCAT	540
	CATCTTGCAA	CGGCTCGGAR	GACRCTGATG	CACGTGTCCA	TAGGCTTAGG	GCGCAATTAT	600
	ACGCTAGCTA	GTTATATTGA	TAATATGTAC	ATGATGCCTT	C		

## 1060UP

	GATCTTGCCG	TCCTTCTTGT	CCAGCTGTAG	GTCCGGATGA	GGGTACGCCT	CGCTCAGGTA	60
	CTCCAGCCGC	AGCTCGCCGC	TCTCCATGGA	CGCCTCCAGG	ATCGAAGGCG	CCGGCACAGC	120
	CTCGGAGGGG	AGGGGCGGCT	GCAGGAGGGG	CATCTCCTGT	CGCTCCTGGT	GCATCTGCAG	180
	CGCCCGAGCG	CTCGGCTCCA	GCGCCGGGTC	GAAGTACTTC	ACATTCGTCA	GGCCCCGACTT	240
	GTACAGATTG	AGGATGCAGC	CCTTGAGCTG	CGCACGGTGC	AACCGGTACG	CAGTCGCGAC	300
20	ATACTGGTAC	CCGCTCGTCC	CCCCTCCCGT	GAAGTGCGGC	CGCTCCGATC	CGATCGAAGA	360
	CAGTGACGCT	GTTGGCTGGT	GGCTGTATCG	CCCCTCGCGC	GCCGGCGCTG	CGCCCTGCGC	420
	CTTGTTCAAC	CACCCGAGCC	GAAACACAGT	CCCGTCGTAC	GTCTCCCCGT	TCAGCCCCGCC	480
	TCCACGTGCG	ACCGGCGARC	CCGCCGGCTG	CGARCAAGGC	GACACCTGCT	CCTCGCAGCG	540
	CGCACCCGCC	TTCATGTCTT	CACATGTCAG	CGTCCGCTTG	TGCGCTTGCC	CCGTCNGCAC	600
	CTGTTAACTG	CATCCGCGTC	TGTTGGCTGC	TGCTGCTTGC	TGCTTGCTT		

## 1061RP

	GATCTGCTTT	TGAAAGTaTT	CATCAGCTAA	ATACCGTAAA	GctGGTTTgA	ACGGAGGTCC	60
	TGCCTTGtGC	TCATATATTA	TAGAAGTATC	AATGACGAGG	GGATGCCGCA	TTtTCAAGAC	120
30	GTTCAAGTCG	GCCTGCAATG	AATGGCCGAT	AAGCACATCT	GtTGCGCTTA	TCATCCGCAA	180
	GAGATCCTGT	tGGACGTCTT	GCAAAGtCGT	GGTCACCCCG	ACCAACTTCT	CCTCTGTAAT	240
	ACCGCTGTAC	TtCGTCAAGT	AGtCCACAAT	GGGCTCATCT	GGCTtGACAA	ACTTGTcATA	300
	AACTAAGTTA	CAATCAAAAt	CGACGACGCT	CACACGCGTC	AACACGTATC	CGTTTTTtGa	360
	aaGGcACATC	TCACAGTCGA	TGGcAAACGT	GTGAGAACCG	tCGTGTtGGA	AACTGACAGT	420
	GTCCACCCAC	CCACTGcaCT	TCTCCTtATT	CTGATACTTt	AGcAACAAAG	CCTTtGGGt	480
35	ACTCCTCCgA	TAAGCCAGGT	GTgTTTAGAT	GGaTGGGGTa	CTCATTaTGc	AATAaGTCAA	540
	CAACGGGCAT	AGcAAaTCAA	GcAAGtGATT				

## 1062RP

	GATCTCGGTG	ACGTGGcgct	GGTATGGCTT	CATCCAGTCG	CCGtTCAACA	AGAAGTTTCT	60
	GTTAACGTCG	AAGTTACAGC	TGGTGAAGGA	ATCAACCTCT	GCGCCACGG	CCTTGATCAC	120
5	CTCTGGTGTG	TTCAAATACT	CCTCACTGTA	CTTCATGTCA	TCGTAGCAGA	GCTGGCCCTC	180
	ACACTCCTTG	CGAACGTCGT	AGACGTTCTT	ACCAGtTCTC	TGGAACGGCG	TCAACTGGTT	240
	GCCATTACAG	TACAGAGAGG	CTGGAACACA	CGACCACACG	TTCTGCAGGG	TGTAGCATGT	300
	GCGGATCAAA	CGCAAGCACC	GtGGCAAGGT	CTCGTTCAAT	GCCGAGCATT	GCTCTGGGCC	360
	AAGAATGGCG	GGTTCGCCGc	CACCACCGCA	GGCCATACGC	TCGTAGTAGG	GGTACTGTgT	420
	CAATGGGTCT	gTCAaCCCgt	tCCCAaTTaG	cACAGAGcTC	AACTTaaaCG	AGCGCTCCTc	480
10	GcCTGGGTGc	GAcAAGATCT	CGGCAGcAAT	aGcAGGAaTg	Tg		

## 1062UP

	GATCCTGGTT	GtaTCATAGA	GAATGAACAT	ATTGATAAAA	AAATGCTACT	GTGTACAGTA	60
15	ATGTCTGAAC	ACCAACATGC	TCTTTCTTG	TATTAAATGA	TGGGATAACG	AAGTCTTGGA	120
	AGAATCCTGG	GCGGAAATAG	TAGACATGTT	TAGAGAGATT	TTTGTAATGG	CTAGAGTCGG	180
	TTTTGATGGC	CGAAAAAGAA	GTGCCAACAT	TTAATTTTCA	AGGTTTATCA	GGTAGGTCAG	240
	GGAATATACT	ATCCTCGTAT	AAACCCCTTGA	TTGTACTTGC	AAGGAGCTCC	AAGTCGTCTG	300
	AGTTAGGCGA	TGGTTTCATCT	TTAGTGTGAG	CATCGACGAG	GACCTCACAT	GTGATTCCTG	360
	AGTCAATTGC	ATCTATGACC	TCTCCATTCA	CAATCAAGCC	CATGGGTCCA	ACCTcCTTGA	420
20	GAGCCGCCCTT	GATAAGCTCA	GTACGCAGCT	CGACCGAAGT	ATCCAACGTA	AGTGACTCCT	480
	TTATTTTCGAA	TTGCAGATAT	TCgGGCCGCa	CTGCATGTAT	AGATCCCCCA	TGAATAAAGG	540
	AGAATTGCTG	CACAGTAGTA	AACGCAAATC	CCGCGTAATT	AGTTGGTTGG	CTTCTTAGGA	600
	AGTCAGTGAA	CCGATTATTT	GCGTCCTGat	CCT			

## 1063RP

	GATCGACTTG	ACCGTCACCC	GGTACTGGTC	GTACTTGTCG	ATGAACTGGT	CCTGTAGTTC	60
	CCCCAGTTCC	TAGATGAGCA	CGCCAGTTT	GTCGGTCACG	TCGGACACAT	CGTCGTCGTT	120
	GTCCATGCCC	CACATCGACA	GCTGCGCGCG	AGCGGCGCGC	CGCTCATTTG	CCACCACTTC	180
30	CAGCGCACGT	AGCACCCCTT	TTTCCGTCTT	CACGAACGAA	GACAGCTTCC	GTGCCAACTC	240
	GGGGCCAAAG	TTTCCCGCTG	CATCTTTGCG	GAACGAGGAA	GCAATCCCCG	CACGCCCAAA	300
	GAACTTGGAA	CGTGTGGAAG	AGGGTGGGGG	AGGGGGTGAC	TGGAGGTCTG	ACGCAGTAGG	360
	CGCCTTCTGG	TTTCTCAAAG	AGTATGTTCT	GtGCATATTc	TCGtGCTTAG	ACTGGTCTGG	420
	CAGTCGGtAT	TTGTAGGTCC	GATaAGATTc	TcAGACGACA	GCAAGTAAAG	TACAACGGTG	480
	GTCCGtGCCCC	CTcCAACGTc	TTTTT				

## 1063UP

	GATCTTAATA	GCaATAGTCG	ACTACAGGAA	ACACAAGCTT	TCATAATGTC	GAAATCTTTA	60
	TCATGGGATA	CACTAGACTA	TACTCTACAA	CCATGGATTc	GTACTGCTGT	TGATGCCATG	120
40	GGTTATGAGA	CCATGACACC	TGTACAGGCA	TCGACGATCC	CGCTATTTGC	CAGAAACAAA	180
	GATGTGGTTG	TAGAATCTGT	GACCGGTTCC	GGGAAGACCG	TGGCATTGTG	CATACCTGTA	240
	TTGGAGAGAG	TGATACAGGA	TGATGCCAAT	AGTTCAAAGC	TCAAAAAAGG	CCACTTCCAC	300
	ACCATAATAA	TCTCCCTTAC	GCGGGAGCTT	GCATCACAGA	TACAGGGCGT	GATTGAAGCG	360
	TTTCTGACAT	ACTATCCAGA	TGGAGAATAT	CCTATAAAAT	CACAGTTGCT	TATCGGTAGC	420
	AATACCAGTA	GTGTCAGAGA	TGATGTTGCA	GCGTTTTTGG	AACATAGACC	GCAAATTTTA	480
45	GTGGGTACgC	CTGGAaGGCT	ATTAGACTTT	CTTAAGATGC	CaaACATCAA	GACGTCTTCA	540
	TGTGGCGCag	CTATTCTTGA	TGAgGCCGac	AaGTATTGGA	TATGAATTTG	AGAAGGATGt	600
	CCAGACaATA	CTGGAGATGC	TACCAAGCCA	A			

## 1064RP

	TAGTGGATCC	AGCATCCCCT	CTCGACCAGT	CCTGAGTTCC	GCCGGcTCTA	TCCTAGACCG	60
	CCAAAGCCCA	GcTTGAAGAC	GTACTGGGAG	ATCGTGAAGG	AACCAAACCT	CACTATATGt	120
5	TCCCTGAGcA	CAGCGCTAAT	GTTCGCCACC	TACTATGGGT	TCAGCGTCAC	GTTCGCCCAC	180
	TACTTGAAAC	TTGACTATGG	cTTCAGTAAC	CTTGcGATCG	GCGCGTGCTA	TGCCTGTCCA	240
	GGCGTGGCCC	TAATGATGGG	CTCCCTCTTG	GGcGGtCACA	TPTCCGACCG	CTTCCGCAGG	300
	AAGTGGGTAG	CCAAGAACCC	CGGNAAGACC	TtCCCGAGcT	ACAACCGCCT	CATCTCGCAG	360
	GTGTTtGGcA	TCTGCGTCAG	cATGGCCGGc	TGTaTCGGGT	ACGGcTGGGG	AATTCAATTT	420
	CACTATCACA	TCGcTATCGc	GCTATTCTTt	TCTTTCC'TAA	TGGcGtTGGG	TATGAcCTGG	480
10	tGcTCTaAcT	CCACCATGAC	CTtCCTtAcG	GaGTCCAACC	CAAAAaGAGc	TGcCGGtacc	540
	ATTGCGtaaG	cAAcAGcTT					

## 1064UP

15	GATCTGTTTc	CGCCCGCCTA	TGGGCCCTGC	CTGCGGGCAG	AGGGAGATCG	TCCTGGTCCG	60
	CCTAGGCTAG	GCACCGCCCT	AGGCGGAGCT	TGTCCTGCGG	AGGCGCGGCC	GGCTGAGCCC	120
	CGCTGCGCAG	GCGCGCAGCC	CGTGAGACGG	TAGCGGcCCG	CCTAATGCCT	CCTACGCAGC	180
	GACCGCGCAG	CGGACCTGCA	CGTTAGTAAA	AAATCATTTT	TATCACCAC	CAAGATGCAG	240
	TCTgATTGAA	GTGTAAAGCT	GCAGTAGAAG	AGACAAGTAA	GCCATCATGA	AGGTATtTTA	300
	TAGGTGCTAA	GTTCCCGATA	CAAAGCACAG	GTGGGCATTc	TAGGGCTGCA	GAGACAGGGC	360
20	ATGGGCGTTT	TACGGATAGc	CCgGAGaCTC	CCcATTGGGC	GGGCTTAGCG	GGAGGGTTAG	420
	CGCGGNGTTT	GGAAACGAAT	AATGGGNTGC	CANGACGCGG	GCCACGGNGG	GACTGATGCT	480
	TGTTTTTGT	TGGGAATNAA	TCTTNATACT	AACAATCCCN	GTNGGNNGGA	CAATTCTTAC	540
	CCNGTTAAT	NGGTACGCAA	AAGACCATGN	AGGTGCGNTG	ANGACAACCN	NNTCCCNNT	600
	TTCTTNCGAN	A					

## 1065RP

	GATCTGTAGT	TTGCGAGTCC	CTGATGCGGT	CCGCCAGAGC	AGGCAGCGCG	GGCCAGGGTC	60
	TGCGCAAGGC	AGGCGTTGTG	TCACCGCGGA	GCCACTCTCT	GGGCAGGCAG	TTCCACGCCT	120
30	CCTGAACGAG	CGCGGGCATG	ATGGGGCCCA	GAATGCTGCG	ATAGGCATCC	AGAATGTGGA	180
	ACAGGGTCGT	CTTTATGGCC	AGACGCCTCT	TATTATGTGG	GGGTTCCTATG	TAAAGCGTGT	240
	CCTTCGAAGC	ATCAAAGTAG	AGGGACAGGT	CGTTGCTCAT	GTGGTACAGA	ACAAAGACTG	300
	ATGACATTGG	AGTAGGCTCTG	GGATTCCGCA	CAGACCCTGA	CACTTGGGGG	GCAAAATTCT	360
	TTGTCTTGTC	GAGGGNTTTT	CCCNCTCANT	CCCNGGCAGG	TGGGGGCAGN	CTTCCCCNGG	420
	GCAAAAAGG	CTNTTCCCCA	CCNAGATNAA	CCCCTGGAAG	ANCCGAAGG	TGNCANNAAT	480
35	TNAGNGGAAG	TNNCCTNACC	NCTCCACCNA	ATCGGAAAAA	TTGGGGANNA	ANGCCCCANC	540
	CCAACNCCCA	AANTTTTCTT	GGAAAAAATA	AGGGNGCCCC	CACCCNGGNG	GANTNANTTT	600
	TNTCCCCCCC	NATCC					

## 1065UP

40	GATCTCTTCC	CTTCGATCAT	CCCTCAGTTG	GGTTCTGAGT	CCATCGATGC	GTTGACGCAG	60
	TTGGCCACAC	AGTTGCAGAA	CGCACAGGCT	GCAGCTCCAG	CAACCGAGGG	CCATGAGGCA	120
	GGCGAGAAGA	AGGACAACGA	CATCCCAGAG	TTGATTGAGG	GCCAGTCTTT	CGACGCGGAT	180
	GTTGAATAAG	TGCGCTGTGC	GAGGACTGTG	TTCTCGCCGC	CCATCTCAGA	ATTTGTCTAT	240
45	TTCTGCAGGG	AATATACATA	TATTGAGTGC	ACATATGGAT	ATTATGTATA	TATATGTACA	300
	TACACTATAC	CCGCCCCGTC	TTAGTCGGAC	CACATAAACC	TACGGGTCCG	CGCCCCATA	360
	TCGTTTTTACA	ATAAACGCGC	CGNNCTTGCG	GGNNFNTCTC	GANAACTCTN	TTGGGGGGCC	420
	CNCCNNCCNT	TANNAGGTNC	TTCTNCCGGG	TNGGAAGTNA	AAAAGCNNNN	GTTCTNGTTGN	480
	NAGNGTCCCC	GGGGGAAANC	CNNCCCCGNG	GNNGATTTTC	NCCCAAACCG	NAGAAACNN	540
50	CNTTGCNCCA	AGTTGCCCGT	GGGAGAAAAA	AANCCNATGN	NGAAGNAAAA	TTGCCCCCTG	600
	CCCN						



## 1069RP

	GATCGACCCC	GGTCCCGCTC	GCATCAGCGA	GCTGCCCGTG	CCGATCAGCA	GCCCCGTCCC	60
	TAGCGACCCG	CCGATGGCTA	TCATCGACAC	ATGACGTGCC	TGCAGGTCCT	TCTTGAGCCG	120
5	GATGCCCTCG	TGCTTGCCAT	CGTAGTTCCA	GTCTACGGAC	TGCGCCTCCT	GGTCTGTGCT	180
	GCTGTGGGTA	TGCCGCAGAC	CGCGGCCCTC	ACCAGCGGCG	GCCAGCTTGG	GGCCTTTCAA	240
	CTCGTCCAGC	GTGGACGCCT	CTGATGCCCTG	TGCGAACTTC	TCTTCCGCCA	TAAGTGC GGA	300
	GCTGTTATCT	ATGCTACTCA	AGCTCCCGCC	GTATAGCCTT	GCTATATATA	CTTACGCTGC	360
	GACGCCCTAT	TCCGGACACA	GCTATATATT	GGCCCCCGCT	CTCGCGCGCT	GCTTGGGGAG	420
	CCGACTGACC	CCACCCTGAT	AGTGCCGTTG	CACCTCTGCT	GGGCCGCGCTC	AGCCCCGTTCA	480
10	GCGTCCGACT	GTGACATCGG	GCTGCGCGAG	CGCGATTAA	CACCCGACTG	GGCTGCATGC	540
	CGCACTAAAC	CTCCCTTCGC	GGCGCAGGGC	GCCCTTATCG	CCTCCGTGAT	GACGTACGTA	600
	TGTTTATCAA	AGATCCGGAG	AMCTGTTCCA	GGCTCCTACG	TTGCGATAAG	AGGC	

## 1069UP

15	GATCTTTCTG	CCCTTATCAG	GGATGGCACC	ACCGGTCTTC	ACCTCGTTTG	ACTTGTAGCC	60
	ACAGTGCTCG	CAGACCGTGG	ACATGATGAT	GACCTCTTTG	AAGTGTGGGA	TGTTGACCGG	120
	CTTCATATGC	GTGTACATG	GGTGAACACA	TGATGGGCAC	GTGGCAGTGA	AGGTCTGCAC	180
	CTCGTTGTGG	AAGTTCTCGA	TATCCGTAGC	GTCAGATAAG	AGACCGGCCT	GTGCCGCTTG	240
	CGATTTGTTG	CGCTCGCGCT	GCGACAGCTC	CGCGCGCTTC	TCTTGACGCC	GTGTCTCCAA	300
20	TTGGTCGCGC	GTAATGATGC	CCACCTGGAC	GTTTTGCTCA	TCTGAACGCA	GGTACTCGGT	360
	TTTGGAACAT	TTTGCGCGAG	CTTCGCCTGG	CTTGATTTCG	ATCCAGGAAT	TGCCAGCAGG	420
	GTCGTCCAGC	GTAAGAAGTCA	GCGGTAGAGT	GCCCCGCTCG	CACGACAGCG	CAGCGCGGAC	480
	CTTGCAATG	AACTGCGCAA	TCTGATCGTA	CAGGTTCCTG	TCCACTTCCT	TCCGCGCGCG	540
	CTGGTCGGCG	TCCAAGTCCT	CGATCATCTC	GGTCAGCAGG	CCCTCCACAG	TCGTACGCTG	600
	GCCGCGCTTG	GGAAGAATCT	CCAGGTCCAA	TTCAACGAAG	CGGGAAGCCG	CAGTTTCGGC	660
25	CTTGATGACT	GCCTGTCAAA	ATCGGCCTTC	TCCTCAACCT	TCAGCTGA		

## 1071RP

30	GATCTGNNGG	GGAAACNCAG	CATTACCCGT	TGTGCAAAAA	GATTTGACTG	GTAACATCAC	60
	CAAGCTTCGC	AACAGACAAT	TGTGCGACCC	CGGTGAGTCT	GCAACCCTGC	AGGAGCTTGT	120
	GATTGCAGAG	CGTGCAACAG	GCAGCAAGAC	TGCTTCGGAA	GGGCTGCTGT	GGCTCACCAG	180
	AGGCCTGCAA	TTCACCGCGC	AAGCTCTTAG	AGAAACGCTA	GACCACTCCAG	AGCTCGAATT	240
	GTCTaAGACA	TtCACAGATG	CGTaTtGGAA	GACGTTGACG	AAGCACCATG	GTA TGCTGT	300
	aCGTCCGGTT	TTCAAAGCTG	GCCATGAAAG	CTTGCCCTTA	CAGGAaGGAC	TTTTtTGcAG	360
	AAACTAGGCA	GcGACCAAGA	GAAGGTTGAC	ACGcaACTTT	AAGCAGtGGc	TGGcTGCACT	420
35	TGAAAAGATC	GtaGaGATTc	TgcTTCAaAT	CCCTtGGGGG	AAAcGtGcAA	AGGATTtTaTG	480
	AgTaTTaTTa	TAGAAGCC					

## 1071UP

40	GATCGACAGC	CTCGAAGAAG	TAGCCTCCAC	AGCTTCAAAC	ACAGCGCACA	GGTCTGCATA	60
	CATCACGCTG	GTGCTTGCTG	CAGGCTTAAC	CGGAGAACTT	TGTGCGCGTG	GCACGGCGCT	120
	GGCAGaCTGT	GGCAGCACCC	CCCCCGGCGC	GGGCTTATCT	gCAAGCTCGG	GGAGGATGTT	180
	CTTCACCTCG	GCGTCCTGTT	CATGGgCTGC	CGGTGCGGCT	AGGCACTCGG	gAGACTCTAC	240
	CTTCGATTTC	TTGACCctCG	CTGTTGaCGt	CGcTCCATCT	TGAGGcCTCT	TCAGCGCAGc	300
45	GAAGAATCGG	ACCAATGTGG	CCTGCTTCTT	TGGaGtLAGAC	ATTGGcCTGA	AGTaAaACCC	360
	TACTGACCTG	CCAaATAGcT	cCACTTTGGT	CTCGCGACAG	GAGCTTCCNA	AGANTGACAT	420
	TNNNTGTNGN	NAAGGCCNNN	NNNTNNCAAA	GACGAANCTN	NTATCAAGGN	CCNNNTNCC	480
	CCAGNCNNNA	NAAGNAANAA	NNNNATNNNN	GGNATNNNNN	AAATTANGGT	TNNNNNATNN	540
	NCTTNGNAAA	TTNNNTNNGNN	TTNNNTNATTC	CCNNNGGNTT	TcNNNTTNCC	NCNCNCCTNN	600
50	GGNTTTTTTN	NANNNTNAAN	NNNCC				

55

## 1073RP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
5	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAAAATA	TTCTTTAATTA	TTAAATTATA	TAATAAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACTAAT	AAAAATAATT	420
	AATTAAATAA	ATAAATAATT	AATTAAATTT	AAAATGTTTA	AAAAAAGAAA	TAAATAATAT	480
10	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCATT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACCTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCCT	ATTATTATCT	T		

## 1073UP

	GATCTTAATT	TAAAATTTTA	ATTAACCTATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTCTATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
20	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATFAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTAA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCCCTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCN	TTTTTTATTA	TTATTTAAAT	600
25	TATTATTAAT	TAGTAAATTA	TATTTATTTA	TTTTATTAAC	ATAATTTTTT	GNATAATAAT	660
	AT						

## 1074RP

	GATCTAAATA	TATATAATTT	AATTTATAAA	GATTAATATA	AACTTTTTTTA	TTATAATATT	60
30	TAAGTATTAA	ATTATTTTAA	CTATTATTAT	CATTATTTAA	TAAATTAATT	ATTTGATTAT	120
	TAATACTTAT	TATATAATTA	TTATATAATT	TACTTAATTC	ATCATTATTA	ATATTTATAT	180
	AATTATAAAA	ATAATATTTA	ATATGAATAC	TATTTAGTCT	ATGTTCAAAT	TTTAAATTAG	240
	TTATTAAAAAT	ATTATTAGAT	ATTATTATTT	TCTTTAATAA	ATTATTAAAT	AGATTATCAA	300
	TAATTAATAT	ATTATTTTAT	AATTGTTTTAT	TAAAATAATA	TATTTTATTA	TTATAAAGAT	360
	TTAATTTTAT	TAAATATTGT	AAATTATTAT	TTTTATTATA	ATATCTATTT	TTATAAATAT	420
35	TATGTTGATT	TATATTATTT	AACTTTTTTAT	AAGAATTATT	ATTAAAATTA	ATTTTAACCT	480
	TAATTTCTTA	TTATTAAATTT	TTATATTATT	TAATAAATTA	TATTCATTTT	ATTTATTTAT	540
	TTATTTAATT	AAATTAATTA	TTTAATTAAT	ATTTTATCAT	TATTTAATTA	ATTAATAAAA	600
	TATTATAAAG	AATGT					

## 1074UP

	GATCTTGATA	CTAGAGCTTA	TTTTACTTCA	GCTACTATAA	TTATTCCTTAT	TCCTACTAGT	60
	ATTAAAGTAT	TTAGTTGATT	ACTAACTATT	TATGGTGGTT	CATTAAGATT	ACTAACACCA	120
	ATATTATATC	TATTATCATT	TTTATTTTTA	TTTACTGTAG	GTGGTTTAAC	TGGTGTAGTA	180
45	TTAGCTAATC	TATCATTAGA	TGTAGCATTC	CATGATACCT	ATTATGTAGT	ACTACATTTT	240
	CATTATGTAT	TAAGTTTAGG	TGCTGTATTC	TCTATGTTTG	CTGGTTATTA	TTATTGAAGT	300
	CCTCTTGTTT	TAGGTTTAAA	TTATAATGAA	AAATTATCAC	AAATTCATTT	CTGATTAAAT	360
	TTCTTAGGTC	TTAATATTAT	TTTCTTCCCT	ATGCATTTCT	TAGGTATTAA	TGGTATACCA	420
	AGAAGAATTC	CTGATTATCC	TGATCTATTC	CTAGGTTGAA	ATTTAGTATC	TTCAATTTGGT	480
	TCTATAATAA	CTATTATATC	ATTAATGTTA	TTCTTTTATA	TTATTTATGA	TCAATTAATA	540
50	AATGGTTTAA	CTAATAAAGT	TAATAATAAA	TCTATTAAAT	ATATAAAACT	ACCTGATTTT	600
	ATTGAATCAA	ATAATATTTT	CTTAATGAAT	ACTACTAAAT	CATCATCTAT	TGAGTTTATA	660
	TTA						

## 1075RP

	GATCTATCTA	ATTACAGTAA	AGCTGCAAAG	GGTCTTTTCG	TCTTCTACA	AATACTTAGC	60
	ATCTTCACTA	AGATTTCAAT	TTCACCTAGA	TTAAAGGAGA	GACAGTTGTT	GTATCATTAC	120
5	GTCAATTCATG	CAGGACCATA	ATTAGTGGAC	AATGAATTTT	GCTACATTAT	AACCCCTCATA	180
	ATAAGGCTGC	TATTTAATAA	AATTTATTAT	TATTATCTTT	ATTAATAATAT	TAATTTTTTAT	240
	ATTTTATCAT	GGAGCAGAGT	TCACACTTTA	TACTTTAACT	TACGTTTCTG	CAAAGTGTTG	300
	TGTTTTTAGT	AAACAGTTGT	ACAACTTTGT	TCTTATTATT	AATTATTATT	TTAATTAATA	360
	TCTCTTTATT	GACTAACGTC	AGAGCTATTT	TTGCCGAGTT	CCTTTCCTTT	AATTATCTAA	420
	TTACACCTTCA	TATACTCTAC	TAACATACCT	GAGTCGGTCT	ACATTACGGT	ATTTTATACA	480
10	TAAATATTTT	TTGAACCTAA	TAAATTTATA	AAGACATTAT	TTAAGTTAAT	TTATATATTA	540
	GATTATTTCT	ATCATATTAT	ATTTTTTAAT	ATATTACTTA	AGAACCGCTT	TTATTGTTAA	600
	ACCTTATGCT	TTAGGTGATA	AGGATTATAC	CTTATTTTC			

## 1075UP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAAT	ATTTGGTTAA	60
	CAATAAAAT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAATTTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAANGGGGGT	TAGCGTTAAT	CGTAATGGCT	TANAGGGTTC	240
20	GTAGAATGAT	TATTTAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTTATT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
	AATTAAAGTA	TTCCGCCCTGA	TGACTACGTT	AGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTACAGACTT	AAGCAGTGGA	ACATGTTATT	TAATTCCGAT	AATCCTCCGA	TAAATCTTAC	600
25	CATTTTTTGA	ATATTTAATT	ATAATAATTT	ATAATTAATT	ACAGGCGTTA	CATAGTTGTC	660
	TTC						

## 1076RP

30	GATCTTAAAA	TAAGATAGAA	TGTAATAAAA	TATCATTCAG	GTACAATAGA	TGCTGGTGTT	60
	ACTAAAGGAT	TACCTGGAAT	ATAATTATCA	GGATGTCCTA	AAGTATTAGG	TGAAAAGAAT	120
	ACAAATAATG	AAAAGAAAAT	TATAAATACA	AATACTGTTA	CTAAATCTTT	AAAAATAAAA	180
	TAACCATGCA	TTGGTAATCT	ATCTAAATTA	CCTGTAATAC	CTAATGGATT	TGATGAACCA	240
	TGTACATGTA	ATAGCATTAA	ATGCAATAAT	ACTATTGCTG	CAATAATAAA	TGGTACTAAA	300
	TAATGAAATA	GAAAGAATCT	TATAATAGTA	GGATTACTAA	CACATAATGA	TCCTCATAAT	360
35	CATAGTACAA	TATCATTTCC	AATAAATGGA	ATAGCACTAA	ATAAATTAGT	AATAACAGTA	420
	GCACCTCAAT	GTGACATTTG	TCCATATACT	AAACAATAAC	CTAAGAAAGC	TGCTGCTATA	480
	GTTAAAATAA	AGATAATAAC	ACCAACTGTT	CATACAATAA	CTCTAGGTGA	TTTATAAGAA	540
	CCATAATATA	AACCTTTACC	AATATGAATA	TACATACCAA	TAAAGAAGAA	TGAAGCACCA	600
	TTAAGATGCA	TATATCTAAT	TAATCAACCT	AGTTGTTTCAT	CTCTCATAAT		

## 1076UP

	GATCTAGAAT	TATTAAGTCA	ACTATTAACT	AATATCTATA	ATAATAATGG	TTTATCATTA	60
	AAATCATTA	AGATAATTAT	TAATAAATTA	CCATTTAATA	ATGATATATT	ATTATCAAAA	120
45	AATTATGTTA	ATAAAATAAA	TAAATATAAT	TTACTAATTA	ATAATAATTT	AAATAATAAT	180
	AAAAAGATT	TAATTAATTT	ATATACTTTA	GATAATAAAT	TATTAGATTT	AAGTATTCTT	240
	AATAATATAT	TATTAGGTAA	ATATTTAGTA	GGTAGTAATA	TCCAATTARR	GGGTAGACTA	300
	TTAAATAGAA	ATATTACTAG	ACTAATAAAA	ATAAATATTA	TGAAAGGTAC	ATTTAATAAT	360
	TATATATATC	AATGAAGTAA	ATTAAATAAT	TTATATAAAT	TAAATTTATAT	ATCACTTAAT	420
	ATTAATAAAC	TTAATAATCT	ATTTATTAAAT	AAAAATGGTA	TATTTAATAT	TAAAATTTAA	480
	TTAAATATACT	TTTAAATAAT	ATTTCTAAG	TAATTTCTTA	TTTATTTTAT	AACATTTTAA	540
50	AATGTTTTAT	GTAAATAGAA	TAATAATCAA	TTAAATAATA	AAAATTAAGA	TGCCACAAAT	600
	AATCCATTTT	CCTTTATGAA	TCAATTAACCT	TATGGTTTTC	TATTTATTTT	ACTAATTTTA	660
	TCT						

## 1077RP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAT	ATTTGGTTAA	60
	CAATAAAATT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
5	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAATTTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAAAGGGGGT	TAGCGTTAAT	CGTAATGGCT	TAAAGGGTTC	240
	GTAGAATGAT	TATTTAAAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTTATT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
10	AATTAAAGTA	TTCCGCCTGA	TGACTACGTT	AGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTACAGACTT	AAGCAGTGGG	ACATGTTATT	TAATTCGATA	ATCCTCGATA	AATCTTACCA	600
	TTTTTTGAAT	ATTTAATTAT	AATAATTTAT	AATTAATTAC	AG		

## 1077UP

	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTCAATAAA	GAATGATTAT	TATCAAAAACC	120
	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTAC	TTAATTAAGA	ATTAGGAACT	180
	TTATCTATTA	GTCTGGGCTG	TTTCCCTTTT	GATTATTAAC	CTTATCGCTA	ATAATCTGAA	240
20	ATATTTAATT	TTAGATTAAT	AATATATTCT	GAGATTTAAT	ATTTTTAATA	AAATAAATAA	300
	TTATPCCCTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTCGTAGAAA	ACCAGCTATT	TGCAAAATCAG	ATTTGACTTT	CTCTACTTAC	420
	CATTATTCAAT	CAGATAATAT	TGCTACATTA	ACCTGTTCAA	TCGTTTPTAT	ATTTTATTAT	480
	ATTTTAAATA	TAATAAATAT	ATATTTTAAT	CATTTGATAA	TAGTAAGATC	ATCTGCTTTC	540
	GGGTTAATTA	ATATTAACTA	AATTTAATTT	ATTTTAATTA	ATTTTAACAT	TGTTAAATAT	600
25	TTATATTATT	TTTAATATCA	TTTTTTATTT	TAATATTATG	CTAATATTAA	TTACTTGC	

## 1078RP

	GATCAGGATG	GCGATGAGAT	ACTACCTTGA	AGCAGCAGCC	TTGACCTCAG	CTAACTCCGC	60
	AAATTCCCTT	CATTTTTTCGA	AAGCAGATTA	TAATTGCTTC	TAAGCCATTC	AATTGCTTTA	120
30	CTTTTCCGTT	AATCAATGCT	CTATTTTACC	ATCATTCGAA	GTAAGAGTAT	GTCGATATGT	180
	CTGACCTAAG	CTACAGATTA	TCTAATCACA	TAGTTATGTA	CGAACCAATA	AGATTATCGA	240
	ATTTCTGTTG	AAAACCTCAGG	CGAACGGCAC	AGCGTTGCTT	GCGCCTATTA	GATGCTTTTG	300
	CCATAGCATA	TCACGAAGTG	ACCTCACAGT	TTTTAAGTAA	CCGGAATAGT	CTGTAGATAT	360
	GGTATTGTGA	AAAGTTTATT	NGCTGGTTTT	ACCCCTGGG	AATCTNGGNG	CTGGNCTGGG	420
35	TTCTTAGGTG	GGGAATCCGG	NCCCCCNNT	C			

## 1078UP

	GATCTCCTTC	CTTCTGGTG	TCTTGCCAAG	CCCTTATTTG	TTGACCAAAG	TATTCTTCAC	60
40	CGTTGCCCTG	TACTCTGTTC	TCATAAATTT	CCGCGGTAGG	ACACCTCTGG	GCTTTCTCTT	120
	GGCGATCTAT	GAGGGCTTTG	CAATCATCTT	CACCGCCGCT	AAAGTTTTCA	CACCATTTTT	180
	GTATGAGCAG	CTACTTCAGT	AAGCCCCCGT	ATTAGGATTG	TTAAAAGAAG	TAGGATCGAT	240
	ACCCTTCAAT	TCCAGATGAT	CGTTGCGGTG	GGCTATTAAT	TTGTTAGCCA	CCTAATACTG	300
	AAATTTACAT	ATTATTGCAC	TAGTTAATTA	ATATTTATGA	TGCAATGGGA	ATCTATATCG	360
	GTCTCTCGTT	CCATCTTCTC	GTAATTAGAT	CACGTCGGAT	ATNGTNGCCC	CGTACCGAGG	420
45	AGGGACCCGA	TTGGGNTTAT	CTTTATGGTC	CCGAGAANTN	ATAGAGNGCC	NNAANATAGA	480

PAG1078i1

1 GATCTAGTTC GTTAACTTCC GCAAAACACC TGTCAAGCGC TTCAACAAAC  
 5 51 GTCTGGATCA GATCCAAGAT GGCCAGTTCT GACTCCTGGT CGTCGACAAT  
 101 GAAAGTAAAA TAGAGTGTTG CATAGTTCTT GTAGATTATT TGGATATCTT  
 10 151 CGTTAATGGT TCACTACCA CTCGATAGTA GCGAGGGCGG CGTAATTAAG  
 201 AATGAAGACT GAATTGAACT GTTGCGCTGG CTGATCAGCT CGTAAACCTG  
 15 251 CTCCAGTAGT AGCTTCTGCT TCGGGAGATC GACAGGAGTA TAGTACTTTA  
 301 CAAGCCTAGG TTGGCACTTC TTGTAACTT CATGTGTTAG TAGGATAATT  
 20 351 TAAGTACTGC GGCTGCGCGG TGGCAAAGGG GTTCACCCAT ATCAGGACGG  
 401 CGNCGNNTCA TCCNCNGTCC CCACCACGGN TACNCGCCNC NCGCA

Pag1078i2.

1 GATCTAATAT TCAATTGGCA AACTCTTGAG AGTGTCTTGG AGGAAATTAT  
 25 51 TCAAGGGGGT ATGGTAATTG AAACGAACGT GAAGAAAATT GTGGAGACCG  
 30 101 TCGACGAGCT CAATAGAACT TCTAACCAGG AAGCCAGGTT TGGGAATGGA  
 151 CTAGGAAACG CTTTTCAGGC CATCACCATG GGTGGCTTTT CAAATTGGGG  
 35 201 TCGCGCGGCAG TGAATATTAG CACACACTGT CTTGAAACCC CATAATAAAT  
 251 GAAATAAATA CTCCTTGCTA GTGTCTAAGT ACGAAACAAC GCCAAGGCTT  
 40 301 TTGGATCATC TATGTACGCA TTCAGTTCGG CAGCACTCAC CATGGGCACC  
 351 AACTCTTCTT ACTTGCTATT TCCTGTGTCT TCATTGCGC TTCGGCTGCC  
 45 401 TGATGGTCTC AAAGCTCCTC CCTAATCCTC TGTAATTCTC CTG

## 1079/RP

1	GATCGCTCAT	TATTTTTGGT	CGGAGCCTGG	GCCCTCTTCT	GCTTCTTCTC
51	AAATACCTTC	AAATTTTCGT	CTATATAGGT	CTGCAGCTCT	TCCTTCTTCG
101	AACATTCCGC	CTTGTGAAGC	TGGTTGAAAT	ACTGCAGGGC	CTCTGCACTC
151	ATGCGATTCA	CCATTGAATT	GCGCTCTTGT	ATCTCTTGCT	GGAAGTGTTC
201	TTGTTTGCGA	ATGGCGTTTT	GCCGCAGTTG	AGCTTGCAAA	CTGGTTGTAT
251	CAGACTCGTC	CACTTCATCT	TCCACGTCCA	GTGGATCCAT	CCCTGCAGCT
301	AGTCTAGGTG	GAGTGGTCTA	TGTACAGTGC	TGCTGTGCGT	GTTAGCGCGC
351	TCACCTTCTG	CGACTGTTCA	AAGATGTGCG	TTTCCAGCAA	GAAAAGAGAC
401	AACCGGAAGT	ATAAGTACAG	CACGCGAGCC	TAATTTTGTC	AGCTTGCCGA
451	TTTAGCTCAG	TTGGGAGAGC	GCCAGACTGA	AGAGAAACTT	CGGTCAATCG
501	TAATCTGGAA	GTCTGTGTT	CGATCCACAG	AATTCGCATA	TTTTTTGCTC
551	ACGTACCCCA	CCGGGTANGA	ACTGGCATTG	CCTACCTAAT	GGCCAGCAGT
601	GGAAAGCGCT	CTTGTGATAT	ATATATATCA	AGTAACACAT	CTATGTAAAC
651	TTTTGACACA	GTCCCAAGGT	GAATCTTGCC	TCGGATCTGC	CTCATCTGAR
701	TCC				

## 1079/UP

1	GATCAGCGAG	CTAGGTACCC	GGACGAACAT	GCCGTTGCGC	AGCTTCCCAT
51	ACTTCAGCGA	CCGTGTGTGT	AGCGCAGAGC	TTCCGTCTTG	GAATAGCGAC
101	TGCACCTCTG	CGTTCAGCAG	ATCGCCCTCT	TTCAGAAAGC	TGCGCATCTG
151	CAGCTCATCG	CTCTCAGACT	TCCGCCGCAG	CACGCCGCCG	GGCAGGTTCA
201	CAGAACCCAG	CATGAGCACT	GCGTGCTGCT	TTCCGCCAAT	ATCCACCTTC
251	CATCGTTTGT	TGCCGACCTC	CACGATCCTG	CCGACAATGT	GGTCGCCCGT
301	CTCTGGCGTG	TACCGCCCCG	GCCAAGGAAT	CACCGACAGG	AGTCGGTTCA
351	CCCTGGAAC	GGTGCCCGCC	ACCGACGAGT	ACGTTTTGTT	CTCCAGGAAG
401	TATGTGCCGT	GGCCTCGCAT	CCACACAGGA	TCATCTGTAA	TCAGCTCTCC
451	TGGCGTCATA	ATCACCGACG	AATCCGCTCC	TTCCATCTCC	ACGTCCAAAT
501	CAAACCTCTC	TTCTTCATCG	TCCAGGTACT	GGCTCCGATG	GAAGTGAAC
551	CCACGCCGCT	TGCGGATCGT	TATTACCTCG	CTCATTACTG	CTGAGACGAC
601	ACGTTTCARA	ACTTCAGAGG	CTCGCTAGGC	CAGGCGAAAC	AGTGTTGARG
651	ATACGCTTTG	TTACTTCTTG	AAG		

## 1080UP

	GATCCGGCCA	CGCATGTATT	CCACTATGTA	CGCTATATCG	CGGCCTCGCC	TCCGTGCGGG	60
5	GCACCGCCTT	ACACCTCAAA	GCCGCAGCCT	TTTCATGCAGC	CCTTGTAATT	TTGCACCAGT	120
	TCCTGGCACT	TGACCGCATC	CACGCCGTTG	AACAGCAGAC	AGCTGTCTCT	CGCTTCCTTC	180
	TCGGGCTTGC	ACACACAGCA	TGGCTTTGGC	TTGTCCGTAC	TACTACCTTG	TGAAACACCT	240
	GGCACAGAAG	AGGATTCAGG	CATGATTAAT	GCTACAGTTC	TTGGAGATCT	TCCAACACCG	300
	CCCGCTCCTT	GGGGTTTTTC	TCACTTTATT	TTTGCTTCAA	CGCGCAAAA	TTGTTGTCTGA	360
	ATTACAATAT	ACAGAGGCGC	AGTAACCCCT	TTAGTGGCTT	TTTGGCTTCT	TGGGCTGGAA	420
10	ANTTNGACCC	CCCAACNTNC	C				

## 1081RP

	GATCTTTTCGC	AGTGACTAGT	GCATGCGGCT	ATTTAAAAAG	TATCGAGTTA	CCCTTGGAAG	60
15	TTTCAGCATT	TATAGTACTG	ACGGAGCCGC	TACAAAGCCA	AGGCTTTGAA	GGTACTAGGA	120
	GACATATTCA	GGCGCATAAA	TCACCGCAAG	CTGGATTGAG	CGATGTTTTG	GGTTGTGTTT	180
	ACAGGAGCCA	GCGCGGTGGC	ATGCGTTTTT	GCGTATGGGA	TGGTGGACCG	ATATCTCTCC	240
	TTCAAGCTGC	ACAGGCATAC	GCACCCGTTT	GTGTTGGTAA	CACTTTTTCGC	AAATATGACA	300
	CTGTTGCTCT	CGATCACATA	CCTGCTTCCA	CTCGATGTGT	TTTACTCAAA	CCAGACAAGC	360
	GGGCGGGAAG	ACGAGCGGCC	AGAGCTGCCG	AACCTCGCGT	TGTTCTGGGC	GGTGATCTAC	420
20	TGGGCGGAGT	TTGTGATATG	CTGGTTGGTG	TTCCCGGTGC	TGATTTCTGA	CGTGGATCTC	480
	AAGTACTTGT	ATCCGCGCGA	GCCACAGGAG	CCGGGGCGGC	GCAGCGTGCT	TCGGCGACTG	540
	CGANGCGCCG	TTATATGCAA	TCTCAAGTTC	TATGGTCTTT	GTCTACTGGG	GGTGATCTGC	600
	NGGCTGGTAT	ATCTCAAGAC	GACGACCGAT	CGCGGGCGTC	AGAC		

## 1081UP

	GATCCAAGAC	GAGCTGCGCC	AGGGGAGAAA	ACCCCCCAC	ATATGTCCAG	CGATACGCTC	60
	AGCATGGAAA	ACCCAACCGT	GGACTTGCGC	TCGTAGTTGT	GCTTGGCCTG	TGCGATATAC	120
30	TTTCAGCACAG	ACATGATGAT	TTTTATAAAG	TACAGCACAT	GGCAGTAGAA	CAGTGTCCGAC	180
	TGATTGTTCA	ACCCTGTTTG	CGTAATGCTA	ACCACATATT	GCACTGTGCC	AATGCAAAAA	240
	AGCCCGATGA	ACAACATGCAT	CATCTTCCGG	TGCGCTGTGC	TCATCCTATT	CGCCGGCTCT	300
	CCGGTGAAGC	CCCATAGTCT	GGTGCCCCAT	AGCACCTGCG	ACGCCAGCAG	TCCGTTAAGA	360
	AGCCAGCTAT	GCATGGCATA	CCAGTAGTCC	GACCAACCTA	CCGACGGCCT	CACCGCGCTG	420
	GACGTGTCTG	CTTCATTCTG	CCAGAGCACG	TCTGCACAAC	CAGCGAGAGT	ACTAGCGCTG	480
	TATACCCGAT	GCAATTAAAC	ACCACGTAGC	CTTTCGACAA	TGCTCTTGCG	CTCTGCCGCT	540
35	TCCAGTTGAT	CCATAGTGCC	GGATACATCG	ACACCGACCA	ACATGTCCGG	TACAAGTATC	600
	CGAGCAACTG	TCTCTTCCTC	ATTCCAGCCT	CGTTCCAAGT	GCTTCTACGC	CGGTCTTCTG	660
	GCGTCAGAT						

## 1082RP

	GATCCACGAG	CAAACCTATTA	TTAGGCGCCC	CCCACCCAG	TCTGCAGCAT	TCGAAAGCCT	60
	TCCTAGCCTT	TGTGCGATGT	CCCAAGGTAC	AATTTTCTCG	CAGCTGAAAA	TACGAAAGAA	120
5	GCGCCAAGAA	GTGGCCTTCT	TTGAATCCAA	CGCCGACGCC	AATGATGTCT	AGGCGGGCGA	180
	ACATTTTATA	ACAGAGCTCG	ATAAGGGCGA	TAAGCGGCTC	GGCCTGTTTT	CTTCGATCGG	240
	CTTGATATGC	AATANAATGC	TCGGGACAGG	TATCTTTGTC	GTTCCCGCGA	ANATCTTCCA	300
	GTTGACTGGC	TCAGTATACT	TTGCGCTAGG	GTTATGGGTA	CTAGGAGCTT	TAATTGCTCT	360
	AGCAGGTCTT	TATGTTTACA	TGGAATTTGG	AACTGCAATA	CCGCGGAACG	GTGGCGAGAA	420
	GAACCTACCT	GAGTTCATCT	TCAAGAAACC	GAAATTCTTC	ATTACGTCAA	TGTACTCAGC	480
10	ATATGTCATC	TTTTTAGGCT	GGGCCGCGAG	TAACCTCTGT	ATGGCAGCTG	CAATGTTCCCT	540
	TGATGCTGGA	AAGGTCTGAG	CAACACGTTG	GCGTTGAACG	CCGTCTTGGA	GTTGCGGTCA	600
	TTTTCTTCTG	CTTCCTTGTC	AACTCTCTCA	GTGTCAAAGC	TGGGTTGTTA	CTTC	

## 1082UP

	GATCCGACGC	TTCCGCAAGC	GCCGCTTCTC	CTCCGTGTAC	TCCTCGTCGT	CGTCGTAATC	60
	CGGCACCATC	GACGCCTCCG	GCTCCTCCTC	ATCCGCCGTC	GCGTCCCTCT	CCTCGTCCAC	120
	CGTCTCCGCG	AGCAGCGAGT	CGTCTCTCGC	CCCCGTCTCG	TCGTCTGTCG	GCTCCAGCAG	180
	TGCGCCCGGA	AGCGGCTGCT	CGTCCGGGAG	CGGCCCGAGG	TACGGGTACT	TCACCGGCCC	240
20	CATCTCCCGC	TCAATCCGCG	GGATCACCAC	CTCCCGCACG	TACCGGTCCA	TGATCTGCGC	300
	ATAGTGGTAG	ATTTCCGACT	CCTTCGTGTT	GTACATCCGC	GCGTTCACAG	TGATCCGCAC	360
	CAAGTCGTTT	ACGAATCCTT	GGGCCCGCTT	GTAGTGGTTG	AGCTTCTTTT	TCACCGTCGC	420
	GAGGCTGAGC	GGCTTCTTGA	TGATCCGGTA	GTAGTCGGGA	TAATCCTTCC	TCAGCGGCAA	480
	AGTGTAGAAA	ATCGGCAAAA	TCTCAATACC	ATTTTCCTCC	TTTAAGTCAA	ACACGCCATC	540
	CAACAAAAC	TTGAGCTGGT	CCCGTAGCAA	CATCGTTAGC	CCTCGCCACC	TGAAAAGCTG	600
25	AAGACTTTGG	TAGTGTACTA	TGTGTTCGGA	AACAACATCC	CACGCGTCGT	TTCTGCCCGT	660
	TCACAGCCTT	GCTTCAAGTT					

## 1083RP

	GATCATCAAT	TTCTTTTTTG	CTGTTTTCTT	ATTTACAGCC	TCTATTTCTG	AGCGAACATG	60
30	CGACGCCACA	GCAGTCCTAA	TGAGCTCATC	TGTTAGTTCT	GTTGCAACCG	CGTTACGCAG	120
	TTCAATCCCT	TCTATTGCTT	TGGAGCCAGA	ATCTCTAGCT	TCATCTTGAG	CGCTAGCTTC	180
	AGTTTGGGCT	CCCAGTTTTA	AAGCTGTTTT	GTTAAATAGA	AAAGTATTTT	CCTCTTTTAG	240
	CTGGGAATTG	CCAGCAAAATG	GTTTTCTGTG	CGATGACTCA	AACGGTACAT	CTTTTTTAGT	300
	TTTTGTTTCC	TCTAAATAT	GCGGTGAGGT	TGTAGAGCCG	ACACTAGACA	TAAATGGTGC	360
35	CGTAAACTGT	TTGCTGGACT	GCAGATCAGA	CTGTTGCTGT	GGCTTGAAC	GCATGTAGA	420
	TTTCACTTCA	CTTCCAGCGC	GGGATTGGGT	AGTGGGTTCT	GATGCTTTAT	AATCTCCACT	480
	ATCGAAGTTG	AAAGTTTATG	ATATATCCTG	GTGTTCTCCG	TGCAAGGAAG	AcCCCTGCTC	540
	AATGATGCTT	TCCGAATATG	TGGGTAGATT	TGAATCATTT	CTCCCTAGNA	GCAGCATCAT	600
	CCTCCGAAAG	AGA					

## 1083UP

	GATCCTGAGC	GGTGCGGACG	AGGAGGAGCG	CGAGGAGGAG	CCGGAGGCGG	TTGTGGGGGA	60
	AACCGTGAGC	CGCAGCGCGA	CGGGCGGGAC	GAAGCGGCGC	TTTGCGGATG	AGGAGGCGGA	120
45	GAAGGCGGAA	GAGGCGGCGA	CGGCCGCCCT	GGACGACGAG	GAGGCGCCCA	AGAAAGCGCG	180
	GAAGTAGCGT	AGATAGAAGG	ATATAACTGT	ACAGTACCAT	GCAAGACGAA	TCTGAGGCCG	240
	GCGGACGCGC	GCTGGCGCGG	CGCCGCGGTA	GCTGCGGAGG	GCAGAAAAAA	TCGCCGTCGA	300
	CAATCTCTGC	GTCATCATCC	CGGCCAGAGG	ACAAGATGGC	TGGCAAGAAAG	ATTGCGGGTG	360
	TGCTAGGCGC	GACGGGCTCC	GTGGGGCAGC	GGTTTATCCT	GCTGTTGGCG	GACCACCCTG	420
	ACTTTGAGCT	GAAGGTGCTT	GGGGCATCGC	CGCGATCCGC	TGGCAAGCGG	TATGCGGACG	480
50	CGGTGAATTG	GAAGCAGACC	GAGCTGATGC	CGGCGTTTGC	CQAAGACATC	GTGGTGAGCG	540
	AGTGCAAGGC	TGAAGCATTG	TGCGGCTGCG	ACGTTGTGTT	CTCTGGGCTC	GATGCGGACT	600
	ACGCAGGCCC	CATCCAAGCG	GGAATTTGCC	GACGCCSGAC	TGGCTGTTGT	CTCGAA	



## 1201RP

	GATCTTTCGAG	ATGAACCCAA	TATGGAACAC	GGGCTTCGCC	AGCTCGATGT	GCCCGAAGTG	60
	GCCCGGGCAG	TCGTTTCATGC	CCTCGCCACA	CGTCTGACAC	TTGAAGTTCC	GGTCGATGGA	120
5	GCCCGAGCCGG	GGGTTCGTTCA	GCCCTCCCAC	CTTTGCGCGC	ATCTGCGTCT	CGTCCATCGT	180
	CTCTGGAAAC	TCAATCTTGG	CCACCGAAAT	CGCCCGCACC	TCCTCGGGCG	AGAACAGCCC	240
	AAACTGCACC	TCCTTGATGG	TCCGCAGAGG	CGCGCTCGAA	TACGGAAAGT	CCACCATCGC	300
	TGTGTCTGAT	TACCGCTCCC	GGAGATACAC	CCGTTTGCAA	GTTCGTGTGT	GCACCTGACG	360
	CCCAGCCGCC	ACTCGCAATC	CTCGTTTACG	CCGACCGCTT	TGTTTCGCTC	CCTTGCCGCA	420
	ACAACGAAGC	TCTGTTATAT	GTGCCCCGTC	GAGACCCTAA	GCCTGCTCCT	GTGGAACACA	480
10	CGCTCACGCC	CAGAAACTCG	TGTCTTTACC	TTGCAGCTCT	GGAATTGGTN	CGCGCCAAAC	540
	CNGCTTATTG	CTTGGGCGAA	CNCCTATGCT	CCGTGTNATC	TCAGCTGGAA	TNCACCANAA	600
	ACNGACCCCC	CACCTACCCC	NCAACTCTGG	TTATTGGATT	TTGCCGGGAA	TAAACNCANT	660
	GTTNCCAATC	CTTNACCCCC	CAACTGTTGT	NTCCNCTGTT	CNGTNCNCTN	TTACTCNTNA	720
	CCCTCCNACN	CCAATTTTTT	TTNCCCGTTG	CCCT			

## 1201UP

	GATCCTCCGA	TTAGCCTCGT	CTTAAAACTC	AACCAAGCTG	CTCTGAAACA	AACAACACGT	60
	ACCACTTCTG	TGTTGTTTCT	CTGCGCTTGT	TGACCGTCCC	GCAACTACTA	TGTCGTTACG	120
20	TGTGTTTTTT	CGGGAAACTT	GCCACCGTCT	CAGAATCAGA	GGCTGTGAGA	TTCTTCTGTC	180
	GAATATCGCT	CTGGACGTTT	GCTTACGTGC	GCCCGGCCAG	TGCTCTTAAC	CGGCGCCGTA	240
	GCCCCCGGCC	CTGGCCGGTA	CCAACAAGCA	TGGCAGGAGA	CACAGAGTAC	TACAAGCAGG	300
	CGGTGGAGGA	GTACGCGGCG	CTCAAGCAGG	ACACGGACCC	GGAGGAGTGG	GACAGGCGGA	360
	TCGCGCAGAC	GGGCTGCTAA	GTCGAGAATA	TGGCGCTGCA	GCTGTGCCAC	GCGGAGACCG	420
	GGGACTGGCG	GGCGTGCGCG	GCGGACATGG	CGCGGTTCAA	GGCGTGCTGG	GCGGCGCAGG	480
25	CAACCGCGAG	CGCGTGACGC	ACCGTGAGCG	GTGAGCTGCG	GGCTGTAAAT	AGGTGTATCT	540
	GGAGGCGTGT	CACGTTGACA	CTGGACACGT	TACGAANCAT	TNTCNGGNTN	GGCCNCCGGA	600
	ATGGCCANCC	CCNATCTNAN	NACCCAAACN	GGGGTATGAT	NTN		

## 1202RP

	GATCGAAAAC	GCTGCCACCG	AAAGCTTGAC	ACTGAAGGGA	TTTGAGTATT	CTCTTGCAAT	60
	TTCCAAGGCG	AATACCAGCT	TGTCCCAGGC	TGCCGATCCA	ACCTTCCCCT	CCTTCAGGGC	120
	CTGCTTGATC	CTGTGCTCTA	TCTGCAGCTG	AGGTAGCAGC	TCTGTGATCA	GCATGACGAC	180
	GGCCAGCGCA	GAGGTAAAAC	CTTTTCAGAAA	GGCCTTTGAG	ATTGCATTGT	CGATGAAACC	240
35	GAGCCTGAAG	ATGCCCCATGG	CGAACACCAG	GACCCCTGAT	ATGCATCCGA	TAACCCGAAC	300
	GGTCATCAAC	GGTTCAAGCG	ACTTGTGCGC	CCATGCATCG	CAGCTCTGGC	CCACCACAAG	360
	GGACGCAACC	GTCTGCGGCC	CTACAACCAT	CGTCGGGACG	CTGCCGAAGA	CTGCATATAT	420
	CAGTGGGGGG	ATCACCAGTG	CGTACAGCCC	TGCGTATGGT	GACACATGTG	CCATAGTGGT	480
	CAGCGAAATG	GCCAGCGGTA	TCTGGAATGA	CGTCAGCGTC	AGCCCAGCAA	GCATGTCTCT	540
	CGCATTTCCC	CAGAATACTC	TGGCAGCCAG	CGTATAATGG	GCCGTAGTAA	GACNCATAAA	600
40	ATTTNTTTCC	TNCCATACCGT	TGTCNNTTTA	TNGNCTGTAC	CCCNATACGAC	TTGTCANAAG	660
	CAGNTNCCCC	CCGCCCGGAG	ACTTCCANCC	CNTCCCTACT	CCCAATTTGG	ACCANGACCC	720
	GGTTCTCTGGT	GCTTN					

## 1202UP

	GATCGCCGCC	GCGCCCCAGG	ACTACGTGCA	CTTTCTCTCG	CTCACACACG	TACTGGACGA	60
	CCCGCAGCAG	CCCGAAGCGG	ACTGCGTCTGA	GCACAGCTAC	ACGCCCCGATC	CGCTGCAGCT	120
	CGCCGTCTAC	GCGCACGCCC	AATGAGAGCT	CATCGCTCCC	GCGCAGTGCG	ATTTTTTTGC	180
	CGGCCGCCCG	CAGCGCTCCG	CCTGGCCGTC	ACCGAAGCCC	CAGCGATGAC	AGCCAGCGTC	240
50	CAGGATATCG	TGGTGGCCAC	CGCCGGCGAC	AGCGCCGGCG	GGCGCGACGG	GCGCCCCAAC	300
	CAGGCGGTCA	CCCTCCCCGT	CGCGCTCGAG	AGCGCGACCG	GCGAGGTGCT	CGTGCGCAAG	360
	GCCACCGGCA	AGACCCGCGT	GCGCAAGGGC	CAGACAGAAG	AGCAGTACTG	CGAGCAGCTG	420
	CAGCAGTACT	TCGAGCGTGA	CGGCGGTCCC	GAGTGCACGG	ACGAGGGCTG	GCTCGACCGC	480
	GCGGCGCCCC	CGGCCGCGCG	GCGCACCAAG	CAGGAGCGCC	AGCGCCTCGC	CCGCCGTCTA	540
	CCAACGCCTC	TACTTCTCTG	GCCGCGGTG	CGAANCCGCC	GCNNTCGCCC	GCCACTGTCTG	600
55	TATACGTTCC	CNGNTCNGGG	CNCCTNCCNA	TTNGCGCCCC	AANTNCTCNA	NCTCNNTNCT	660
	NNTNCTNCCN	GACCCNNTNN	CCCTTAATTT	TTNNTTNNTN	NNNTTNNTCTT	TTCCCCCTCC	720

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NCTGTTACCC TCNCTNCNTC CNTGGTNNTT CCNTTTGGTG NGCTNTCTTC CNTNCTC

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## 1203RP

	GATCAAAACAG	CTGCAGTTGT	TGAAAAGGTT	GCTTGAATCC	AAACCAAGGA	AGGACGTATT	60
	TTCGTTTCTA	GGCCTGGATA	ACTAATCTCT	TCTCCACTCT	AGCTGGGGAT	AACACCTGCA	120
5	GGACGTGAAC	TAACAAGTTG	ACTACTATAC	AGCAAAATAA	CTCGAACAAG	TTATACAGAA	180
	TTTTGTAAAT	ATATTATAGC	AGCCCTATTA	CTATAATTCC	ATCATTGTGT	AACGCTTTAG	240
	CCTTCGTTCT	CAGACTCGTC	GTCATTTTCT	TCATGATAGT	TGATATTTTT	GCGTTGCCTT	300
	GAGCTTTTCC	TTACTGGGCC	TGCATTGAGG	CTCCTACTCT	TTGGCCTGTA	GTCACCTGCA	360
	GAGCTTGGTG	TATCTTCGTC	CTCGCTTCCC	TCATCGACAA	CTTTGCGCTT	CTTCTTAGTT	420
	TTAGATGAGG	CTGATGATGG	CCGTTGCGCT	TCTTGAATTC	TCTTCCTCTG	CCCTTGGCGA	480
10	TGTTGAATTG	GCGCGATTAG	AGAAGCGCGA	TACTTTGGCC	CTTATATTTA	CTGTCAGTGT	540
	TTCAACATGC	TGGTCTGATA	TATAGCTCAT	GAACGCGTTT	CTTTGCGCCT	CTTCCCATAT	600
	TGGGGAATGG	CTGATAAAGT	TCAGAAGGCA	GATTAGCTCC	CAGGTAGACT	GGTAGATTCC	660
	ACCCCGTTG	GTTTTAGCTC	AAANATNATC	AATTGGCAAC	CNGCTAGANA	TAATNTNTGA	720
	ACATATGCTC	CGTGTNGGAT	CCGNTGCGAT	CTCCCC			

## 1203UP

	GATCATTGGC	TCGCTGCTCG	GGGAGACCAT	CTCGGAATGC	GACACTGTGT	CGATGTCTGT	60
	GCTGCGGAAG	ATCTTCAACA	AGTTTCTGAC	ACACGATTTT	GGCCCCGCTG	GCTCCCTGCA	120
20	GGCCTCCGCG	CGCGACCCGG	CCTTTGATTT	TTCTCTGACG	ATCTGCCAGT	CGTACAGTAA	180
	CCGACTCGGG	CGGCAATTCA	CGAAGTTCTA	CTCCGAGATC	CTGTACGGGA	TTACGAACCC	240
	TGGCTCGGCC	GGCTCAGGCG	AGACCGCGGG	CCTGCAGTCG	ACACTTGAAT	CGGAGTTCAA	300
	GACTCTTCTG	AAACTGCATA	AACTTACGGC	CAACATATGG	GAGCATGTGC	CGGAACCTGT	360
	GGGCTCCGTC	GTCGGATTTG	TGCATCAGGA	GTTATGCTCA	GACAATGTGC	CGCTGCGAAT	420
	TGGGGCTACG	CGACTTGTAG	GTGATTTGTT	AGCCGCACCC	TCCGCTGCCA	ACTTCGTCAC	480
25	GATGCATACG	GACACATATA	ATGCCTGGAT	GTCGAAGATA	GCGGACATAG	ACGCCACGGT	540
	GAGGCGCGAA	TGGGTGAAAG	CCATACCTAA	GATACTGGAT	AACAGTCTGA	TTTGGCAACA	600
	GATATCTGCA	AAGGCTCAAC	AAGACACTAA	TGGATACCGA	CGATGTGGTT	AGACTATGCA	660
	GCTTAGAAGC	GCCTGAAAGA	ACTACAGTCC	CCACGATTCT	GGGANATCTC	AAAATTCCAC	720
	TTNTTCCNAA	TTGTTGCGCC	TACCCAAANA	AAACNAANCT	TAGGAACTTT	TCATTTGTAC	780
	C						

## 1204RP

	GATCCGCTTG	GCTAGGTCCT	CAGCCGGCAT	GTCGTCACGG	TATAGGGCCT	CGGAGCCAAC	60
	TAGGAAGCCG	CGCACCCTGT	CCGACTTGAT	CCATGGCAAG	TAGGTCCTGA	GCGCATCCCT	120
35	CTCCATCGAA	AAGTGAGCGT	CGTCGTCTGG	CCAGACACCG	ACCCATAGCT	TGAAGCCAGC	180
	ACGGTCCGCA	GCAGGACCCA	AGAAGTGCAA	CGTGTTCGAG	TCAGAGGTAG	AGTAGACTTT	240
	GACCGTGTCC	GTGTAGGGGC	GCAAGGCCCT	GAAGTCGTCG	AGGTAGTCCT	GAGTGTACTT	300
	GCAGGTACCG	TCGTGCTTCT	TCACACCTAG	GTTGAAGGCC	AAATCGCCCA	TAGCGTGTAC	360
	AGACGAGGCA	CCAAGCAGAG	CTGCGGAAAC	AGTGGCAGAG	AAACGCATAG	CTAACGAATT	420
	GATGGTGAGT	TAGTCTGGCT	AAAGTGCGCT	GTACTGGAGA	AACGACAGAG	AGGGACAAAT	480
40	ATATGTTAAT	ACCAGGTCAG	CGCCATCTGC	CGGAGGAAAA	AGAAATGTGC	CGCGTGTTC	540
	CGGCACCTTC	CTTAATTTAG	AAGCATATAT	TATCACGTGA	ATATCACGTG	AAACACGTTA	600
	AGCCTACAGA	GAGCTATTGA	CGGTGGCTCG	GAACACGTTA	GCACTGAGTT	ATGTACTAAG	660
	GTGGCCACGC	ACCATGCAGC	TGTCCCTCGAT	GCAATATAAC	CCCCCGGGCC	CCGGCAGTCA	720
	ACCGCCATCA	AAAGTNCTGN	CCCCGAGNNC	CCTCAAATGT	CCNTG		

## 1204UP

	GATCAGGAAG	CAATAGGTAC	TCAATTGCGG	AAGATTTCAGA	GACAGCAAAG	GTCAAGTGCA	60
	GTTCAGCAAC	ATCGAATCCA	CACAAGTTAT	GTCGTACAGA	GGCCATAACT	ACAACGCAAT	120
50	GGCACCCGGG	GGGCAGACGT	TCTCCAACAG	TCCATATACG	AGCAATATGG	GGTCCACGGG	180
	GGCTCGCGGG	CGCAGCTCAG	AGCTGTTCCT	GAAGTTCGAG	CGATTTGCGA	AGCGCATAGA	240
	GGACGTGACG	GACCACCCGC	TGGTGCAGCG	GTTTCGTGCCG	TACACACCGC	TGATTGCGCG	300
	GTTTTTTTATT	GTGGCCACGT	TCTACGAAGA	CTCGATCCGG	ATTCTGTGCG	AATGGCCGGA	360
	GCAGGTGTCT	TTTCTATCCT	ACTACCGGCG	CTACCCCGCA	GTTTTTCGTAG	TGCTGTTTTT	420
	GATGGTGGTC	GCGGTGCTGA	TGATGGTGGG	GGCCACGATG	ATCCTGCTGC	GCAAGCAGCA	480
55	GCTGTATGCG	ACTGCGATCC	TATGCGCGTG	TATCATCTCC	CAGGATTTGT	GTACGGGCTG	540

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TTCTCCGGCA	CTCCTTCGTG	TTTGCGGAAT	TTCAGCGTAA	TCGGCGGTTG	CTGATTACTT	600
CCGTGACTCC	ATCCGTGCAG	AAGCGCATCA	CATTCCGGCAT	GCTGCCGGAG	CTAACAGCAG	660
GAAGGCGCAC	CAAGGCTACA	TCCTGCTTGC	GGCCGCATAT	CATAGTCTTA	GTTTGTGACT	720
TTACCTCCGC	AAACTGGTGA	CGNTTCCTCN	CCTCGCGNAC	GGTNCTCCCC	TCGGTN	

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## 1205RP

	GATCGCACTT	CAACCCATTC	AAGAAGACGC	ACGGCAGTCC	GGAGGACGAG	AACCGTCACG	60
	TGGGCGACAT	GGGCAACGTG	CTCGCGGACG	CAAACGGCGT	GGCCGTAGGA	TCGGCGAAGG	120
5	ACCCTCTAAT	CAAGATTTT	GGTCTTACGT	CGATTCTGGG	CCGTACGGTC	GTGTGCCACG	180
	CCGGCAAGGA	CGACTTAGGC	CGCGGCGGCA	ACGAGGAGTC	GCTAAAGACG	GGCAATGCGG	240
	GCCCCAGACC	TGCTTGCGGC	GTGATTGGCA	TTGCCAACTG	AGCTGGCTGC	TGCCGCGTGC	300
	CGGAAGCTCT	GGAAGGTTGC	CAACTAGAAG	CTCTGATGAC	TATGTTAGCA	GAATAAACGT	360
	TTTATGGTTC	GCTGTGTTGG	CGCTGTATGT	TACAATTGCA	GCAATTAGAA	GTCTGCTCTC	420
	GCGCCCGACG	GCACGCTCGG	CAGCGAGTAG	CTTGGTAGGA	TGTTTGCGGC	CGCCAGCAAC	480
10	AAGCCGAGGA	AGGGCTGCGA	AGGGTTCTAG	CACCTTGGAC	ATGTTACTCT	GGTTGGTACT	540
	GCGTGCGGAC	GTTAGTAGGG	TTGGTTCGACG	AGCTCGAGAA	TCTCGCACCG	GTGCCGTCTC	600
	GTCTCTGCCC	CCNAATTACG	CCAGCNCCCG	ATTTCTGCNC	ACTTTGGTTG	ATCCCNATCN	660
	ATGAAATNTT	CCNCCCAAAG	AGCCTGCCGT	TATTTCTNAN	ATGACATCGG	TTCCCCCGAA	720
	AAGTGTCTAA	ACATCCCTGT	CCCCCN				

## 1205UP

	GATCTTCAGG	TTCCGCGACA	TGATTATCAG	CGAGATGGGG	TGGCTGCGCC	GGCGCCCCGG	60
	CTCCTGCACA	CGCTGCGTGA	ACTGCTCCCG	CTCCGGCAGG	TCCTCGGGCA	GCACCGCAGA	120
20	GATCATCTTG	TCCAGCAGGA	TGTCAATGAA	GTGCTCCTGC	TCCTGTACCT	GAGACACCGC	180
	GCGCAACTTG	GCCGCGCGCT	GCTCCTCCGT	ATCCTCCTCG	TCCGACATAC	CGGCGCCATT	240
	GTGCTGGTTC	TCCTCCTGCC	AGAAGCTGTC	CGCGCTGCTC	TCCAGCTCGT	GCCGCAACGC	300
	GAACTCGTCG	AAGTCTGCTG	CGATTGTTTT	GCGCTGCTGG	TCTTTGCCCG	TCCGCGAGCG	360
	CTCCCATGTC	GCGTCGAACA	GTGAGCACGC	GATGTTGGTC	ACCAGCTCCC	GGTTCGTGAC	420
	GCACGCGCCG	GCCTTTTCAT	CGTCTGCCAC	CCTCTCCTCT	GCCTCCATGA	TGCGTTCATA	480
25	CTTGCGCGCC	AGGAATPCCC	CCAGCAGGCA	ACGCGGCTTC	TTGCTGCCAA	TTGCAACGCT	540
	CTCAAGCGCC	TTGGTCTATC	GTCTCTCTTC	ATCGGTCTCT	CGCCCCCAGG	TCATATAGAT	600
	TGCGGCTCGC	GGTAGCACAC	TGGCGAAGGC	TGCCTTGGTT	ATATGCCGCT	AGAAGCAGTC	660
	TCGGCGGTCA	GTTAGTCTTT	TCGTGATGAT	GACGTGTTCA	CGATGACTCG	GATATAGAAC	720
	AGTCATCTAT	CGATTGAGAA	CATAGCTATA	TAGAAATGAT	TTACTGTAAT	ATATCGA	

## 1206RP

	GATCGCGTCC	GTCGTCTGTCG	GCTCCTCGTC	CTCGTTGAAC	TCCGTCCACA	GCTTGAACGG	60
	CCGCGCCGAC	AGGTCCACCT	TCGCCACCGT	CTCCGTCACC	ACCTCGGTTT	CGAACTTCAC	120
35	GGACTGCGCC	TTTATCCGCT	CCATGAGGTC	GCTGCCCGTT	AGCCCGTCCG	GGAACCCCGG	180
	GAAGTPTCTA	ATCTCCGTCG	TTGTCTGTCAG	TTGCCCGCCT	GCAGCCACTC	CGTTCGCGAA	240
	CATGCCCTCG	TACAGCGTCG	GCTTGATCTC	CGCGCGCGCT	AGGTAAATGG	CCGCAGTGTG	300
	TGCGCGAGGG	CCGGAGCCAA	TGATCGTAAC	TTTGTGATGC	ACCATTCTGT	TCTGCAAAAGC	360
	TTGTCCCAAC	CGGTATCTTG	TTGCTGCTGC	TAGCATCAAC	TGTGCACCGC	TAAGTTTTCG	420
	TCGCGCTTGC	TGGTPTTATA	CCTCTGGGCT	TCACCATCGG	TGAACCTTGA	TCGCCGTTAC	480
	TATTTCCGAC	GCTTATGTCC	GCACCTGACA	AATTCCGGCT	CGCGGGTGG	CGACTGCGGT	540
40	CAGTGGGGGG	TGCAGTACAA	GATACGCACC	GCGGGCCTNT	NGNNNTCNC	GGCCCTCTCN	600
	GNGGCCCCGC	GNCCCTTCNC	AGGATCNTTN	CCTCANCTAN	AACNNGGCC	GGNGNNNTCT	660
	TTTTTTTGTN	CNGCNAACGA	AGGCAATMNA	ATNTTTNNTN	GGNCNTNNGT	TNGAANTGTC	720
	CNNCNGTGGG	CATCGCNGCT	TATNAACACN	C			

## 1206UP

	GATCCGCTGC	TCGTGCACCA	CCTGCTGCAG	GTAGGTTGCT	ACTCCACGCG	CGAGATATGG	60
	GTCTTGGTCA	ACATCTTACA	GCTGACCTGC	TTTAACGAGA	CAACCAAGGA	CAAGTACGAC	120
	CGCCGCATCA	TCAGTTTCGG	CGGAACGGTT	TCGACGGCCC	TGTCTGCAGA	TAAGACCTTC	180
50	GCTCAGGAGT	TTAACTCCAA	ATGTCTCAAC	TTTACGACCT	GGTGGCACCT	CATGGCCCGC	240
	CTAGACCACG	CTGTTTTTCAT	GTGGTGTCTA	GACATTATCG	TGGCCGAGAA	CTCACAACCC	300
	TTCAAAAGCA	ACCCCATCAT	CCGCGATAAG	CTCAACGGCA	AGGACTGGGA	CTACTACCGT	360
	GATCTACACG	TTGTTGTTCAN	CTATAGGATT	ATCTGCGCCC	TGACTCTTAC	AGTGCTTCTC	420
	AGCTATCATT	TTGGCTTCAA	TAATCTCTAC	GACCTCTCTT	TTGTGACCCC	AGCCTTCCAG	480
	ATAATAGGGG	CCGAACAAGC	GACTTGGGGG	ACGTGCATGC	AACCTTTATC	AAGAAATGGC	540
55	ATCACAACTA	TAAAAAGTTC	TAGTTGCTCG	ACTTGTAATC	TCATCTCTAA	ACATAATATT	600

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CTTTTATATG	CTTGTATTAC	TTANCCTCAA	CATGATNACN	TATGCCTGGA	AGATTTCCNC
GNIGGCCGTN	AGAACNGATT	TGTGTCAACT	TNTATAAAAC	TGACCCCGTC	GCCCCCTCCG
TAACCCGANA	TTTCCTGATN	CNTGATCCTA	TGANGATGCC	GGCNCATTNN	CANTATTC

660  
720

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## 1207RP

	GATCTGTTTC	AAAAATTGGA	AACGCTTACC	ACCTCACCAA	CACACCAGGA	CTTTATTTTCG	60
	TAGAAACAGG	CGATCGGCCT	GAACAACAGT	CACTAGAAAC	GGTGCACCAA	GGCAGCTTGG	120
5	CAACGAGGAG	GCACCCTAGG	GCTCAATGCG	TTGATAGTAA	AGCATGTACA	CGAGCTTTGT	180
	CTCCGAGAGA	AGGAACGACG	TCTTGCACTC	CGACACGTAC	GAGTCTGAGA	TACACCACCA	240
	CGGGTGCGTA	GTGGTGCGAC	GTAAGCCTT	CAGTTTGCGG	GGACGGCCCT	GGGGACGGGG	300
	GAGTACCTTC	GTGGCAGCCG	AAGATACGCC	CGATGAGCTC	GCAGAGCTGG	CTCCGGAGCT	360
	GTCTGTCTCG	GCTGACGCGT	CGGGCTTGGA	GACGGGTTCT	TCCGTTAGTA	GTGACTGTTG	420
	ATGGAAGCTC	CCCAGTAACG	GTCTTGAGCA	AGCGGCCATC	GGCCCAGGCG	GAAGGCTTCC	480
10	AGCTGGCGTA	GGGCACAGGC	ATTCGAGGGG	CTGGCTGCGG	GACGGCGTCC	GACGAGATCA	540
	CATCTGAGCG	AATGATATCT	CGCCCGTCC	TGGTCCCTCC	TAAGTCAGTT	TGTTGGCGAA	600
	CATGCGTTAT	GCCCTGAGAA	TGGTTGCCAT	GTGCTTGATT	CATGCGCCAA	CAGCTTATAG	660
	CGAATGCCAA	ACCCCCACCA	TTGTTNTCCC	CNACACTGCT	CNTGAGACAC	CCCCCCCCGA	720
	AANTNAATGC	GGTTTNTTTG	TTAAACCCN	TNAAAA			

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## 1207UP

	GATCTAATGA	GCGATAAGTC	ACCGGTTATA	GAAAGTTTCG	CGAATCCTAC	AACTGACTCC	60
	AACTCGCCAC	AGGAGATATC	TCTATTAGAA	AAGAATATCA	AGGATGTCAT	GCGTTCACTA	120
20	AAGGGCGTTG	ACACGCACCT	ATGTGAACAG	ATCATTAACG	AAATTCCTGT	GGTTGATTAC	180
	GATGTTTCGAT	GGGAAGATAT	AGCTGGTCTT	ACAATAGCAA	AGAAGTGTTT	GAAGGAAACA	240
	GTTGTTTACC	CATTTTTGCG	GCCAGACCTT	TTTCGGGGTC	TCCGGGAACC	TATCTCCGGG	300
	ATGTTGTTAT	TTGGACCTCC	AGGAACAGGT	AAAACGATGA	TTGCCAGGGC	CGTTGCGACT	360
	GAATCGAATT	CAACTTTCCT	TTGCATCAGT	GCTTCCTCTT	TGTTATCGAA	ATACTTGGGT	420
	GAGTCGGAAA	AACCTGTCAA	GGCCTTATTT	TACCTAGCCA	AACGGCTTTC	CCCCCAATT	480
25	ATATTCAATTG	ACGAAATCGA	CTCTCTACTA	ACTACCGTTC	AGATAATGAG	AACGAATCAT	540
	CCAGAAGATT	AGACGAGCTC	TTGGTCCAAT	GTCCCTCCCTA	ACGAGCGCCA	CGGCTAGGAA	600
	CAGAGAGGCG	AAGAGGCCAG	ACGCGTACTG	TCTTGCGCCG	AACCACTTAC	CGTGGGCAAN	660
	AANGANGCTG	CNATAAACTT	TTTCACGGGT	CTATNATCCC	TTGCCGGAAT	ACAACNAAAT	720
	GTTCTTTGAA	AACTTNTTGG	CTCCAAAAAG	AATTTTCGAAC	TNATTCNNCN	T	

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## 1208RP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCAATCAT	TTAATACTCC	TCTAATTCAA	180
35	TCTTAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TTGGTACCAC	AAGAAATGCTG	AAAGCATTAG	360
	GGGTGTGTAC	CTTAGCTCTC	CTAATTAAAG	TTTATAAAAT	TATCCTTAAC	TAATAAAAT	420
	AATTAATTAA	ATAAATAAAT	AATTAATTAA	ATTTAAATG	TTTTAAAAAA	AGAAATAAAT	480
	AATATGTTTA	TATTTAAATA	GATTCAAATT	TCCAACAATT	CCCATTCAAT	TAGTACTACC	540
40	ATCACCATGA	ACAATTGTTA	CATCATTAGT	TTATAGTTTA	CTATACTTAG	CTACTAACA	600
	TGGTATATGG	TATAATANCC	CTAATAAACC	TTATANANTT	TTTACCNAAC	TTNGATTAAA	660
	AAAAGGGCGA	NCNNCTTTGG	NGGACCCCTA	CCCNTAAAG	GNGTAATGGT	TCCCCAATTG	720
	GTGGCCGAAA	TAANTTGGCC					

## 1208UP

	GATCTTAATT	TAAAATTTTA	ATTAACCTATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAATA	120
	AATAGAAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
50	ATTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCCCCTGATA	TATATAATTA	TTAAATGTTT	420
	CTTTCATAAT	ATTATTTTTT	ATTAGCTTAG	TAATATTTCT	ATTTAATAGT	CTACCCCTTT	480
	AATTGGATAT	TACTACCTAC	TAAATATTTA	CCCTAATAAT	ATATTATTAA	GAATACTTAA	540
55	TCCTAATAAT	TTATTATCTT	AAGTTATATA	AATTAATTAA	TCCTTTTTAT	TATTATTTAA	600

ATTATTATTA	ATTAGTAATT	ATATTTATTA	TTTTATTAAC	ATAATTTTGT	ATAATATATA	660
TCCATATAAT	GGTATTTATT	ATATACCNTN	ATGAATTAAT	GANAACCCCTA	TATATGANAT	720
TAGTTATAGT	GACTTAATCC	CNATCTCAAT	ATATATAATT	ATTATAGAAN	ANATACTTTT	780
TC						

## 1209RP

GATCAGCCTA	TGTAGCAACT	GATCGGCGCT	GGTCCGTGTC	AAACGCCGAA	AACACCCAC	60
CAGATTACGC	AGACACTCCC	ATATTTTGAC	CGACTGGAAC	TTTGTGTACA	CAAAGCTATT	120
CAGCTTGTC	CTGGCCACCG	TCAGCGGCAT	GTTGTTTCAGC	CGAGTCGCTA	GCGCCGCACT	180
GCTGTTGCCC	TGCGCCAGCG	ATGGCTCCTT	AAGATCCTGC	GTTTCGCATAT	ATTGCGCAAA	240
CTTCGATAGG	TCTCGACTGA	GCGAATTACC	GACATGGTCC	AGTAATAACA	ACACCCACAGG	300
GCAGCCCCC	CAGCTGTAAT	TCACCGTTTT	GACCAGCAGA	AAGTGCAATT	GTAAAAGAAT	360
GTACCAGTAA	TGCCAGTAAA	ATGTGGAAAA	GACCTGGTCC	TTCTGAAGAT	ACGAAATCAT	420
CACCTGAAGA	TTCTTCAGTC	TTCTCCGTCC	CGAACATCTT	GGAAAAATCT	GCNGNTCGTC	480
GCTTCTCTTC	CACTCGAACC	GCAGGGCTTC	CAAGGACACT	CCTTGCAATT	GAA	

## 1210RP

GATCTAAATT	TATCAGCCCA	TGGACGGATG	GATTTACGGC	AGCGTGTGCG	CGCAGCACGG	60
GGCACGCCAG	ACTGCGAGGT	GGCAAATAAT	TCACATAGCA	ACCTGCATTA	TAAACATCCC	120
AAGTCATTAA	ACTTACTAAA	TATTGTTGCG	TAACCAAAAAG	CACCGTGTAT	CATCATCTTC	180
ATAGTCTTAG	CTGAACCTAC	TGTCGCACCA	GCCCTTTACT	ACGTATTGTA	TCTCCCTTTT	240
ACAAATGCTTG	CCCACTGCCA	GTTTTCCGCA	CGGGCGTTAG	CATGAAGTCT	TTGCCCGCCTT	300
TGTACCACGG	CTTGACGTCT	GACTCTACGC	GGACCAACGA	GGTTAGACGG	AGTGCACCCG	360
GGACCGAGTC	ATCCTCGCTC	GCGTGTTCCT	AGAGACAATT	TGAGGTTCCA	CGGAGCATCC	420
ACGCCCATGC	AATCCTGCCC	GTAAAAGTTT	GCACANTTCA	TCCACACTT	GGGGGGTTNT	480
TATCACNCCA	NCCTGATCTG	GTACGNAAAA	NTTTTCNTN	TTTGGTGAGG	AAATCAGGTT	540
CCCAATA						

## 1210UP

GATCGAGAAG	ATGCGGCGCC	GCAACGAGGC	CGCCACGCCC	GAGGCGGGCG	GCNACGAGCT	60
CCTGACGCCG	GCGGAGCGCT	ACGCGCTGGA	GCAGGGGCGAG	GGCTTCCTGG	CGCCTGTGCT	120
CCCTGTGCGN	GAGCCGGCNC	GGCCCCCTGGC	CGTGCCCTGC	AACGAGCTTC	CCGATGAATA	180
CTGCATCACC	AAGACTGACT	TCGACCGGCT	CGCTAGCCAC	GGCATCCCGG	TCGAGGACGT	240
CCACGAGGAC	AGCAAGGACT	GGTACTTCCA	GTGCCCTGT	GGAGTAGAGG	AGGTTAGCCC	300
GGGCCTAGAG	AGCCCCGCGC	TGCAGCAGGC	CCTGGTCTGC	TGCGACCAAT	GCCTCCGCGT	360
GGCAGCAGCT	GGGACTGCCA	GCACCCCGCA	GCGATTGAGC	TTGCTGGCCN	GCGGGCAAGA	420
CTCCTCACTA	TTTTTGCCCTC	CNTGCCCTC	TGGCCTGCCC	CACGCGCCCG	CGCCCTCAGC	480
GGCGGNGNCG	GGCGCNAAAC	CCCTACCAGA	ACCAAANNAA	CNACGCCNCC	GCCGCCCNTC	540
GGTGAAGCGA	ACCCTTTTTN	NCTCCTGTCT	TCCCNCCCTG	AAAGACCTAN	TTCTCCTTCA	600



## 1211RP

	GATCTCCTCC	AGTAATGGCG	TCAGAGCACA	CTGGTAGCGG	ACCCCTGCCA	GGTAGCTCAT	60
	CGGCAAAAAG	ATAGCACGCG	TATGTACCCA	CCAGCGAGCC	GGGTGATAAG	GAAACTGGTA	120
5	CGGCAGCAGC	CATAGCTCTG	GTGGCGCTGG	GTTACAGCCC	TCCCAC TTGT	ATAAATTGAG	180
	CACGGAAGC	CACACTTTAC	CCCAGTACGG	CGAGCCAATA	GCACCCCCCA	TGCGCAGCAG	240
	GGTCTTCCGC	GCCCCGTGCA	TCACGATGTG	TTCGCGCTCC	ATCCCTAAGA	GCCGCAGCAG	300
	AACGTAGTTC	AGCGCGGTGC	CCATCGACAG	TCGACTTGTC	CTCCGAATGC	AATCCCCACC	360
	CGCCGTCGAC	AGGTGTGCCG	TGTTCAACAC	GTTAGCGCAC	TAGCTCCCGC	CGCTGAGGCT	420
	CAGGAATACC	ACCCCGCCCA	CATGCATCGC	CACCACATAC	CCATATCATN	ACATCNGGCC	480
10	CCCTGTTACA	ACAGGAAANT	GCCCNAACTT	CCTCCTGCAG	ANGGCCCAA	CCGCCCCCG	

## 1211UP

	GATCTACATC	ATGGGAGGCT	AGGAAGAGCA	AGGCACCGCG	TGCATTTGTA	GA CTACACGC	60
15	TATAATATGC	AAATGGCCAA	TACCTTTGCC	CCGGATCCAA	AGAAGGGCAC	TGTCAAGCAT	120
	ATGGTTATCG	AGACGAGCTT	CAACCACTTG	GCTCTAGGCA	TGGTCAGCCA	GATATTTCCG	180
	CACTAAACAA	CGTCTAGAAA	ATGACTTGAC	CTATGACGTG	CCGGGCTTGA	CTCATCTTAC	240
	TATCCTCAGG	CCCGGCCCTC	TTCTTGCGCA	GCATGGCTCT	AAACCCGTAA	TAAGCCCTAC	300
	CAACCTGAT	ACAGGAAACA	TGCTTACGCG	CTGTTACACT	TATAAGAAGA	ATGTTATGCG	360
	CACGCAATTT	AATTGGCTTG	CGCCAGTTTA	AGAAGTTGGG	CCAACACTAA	GTCACCCGAA	420
20	CTATCCGCGA	AGGCTACCTA	TCATTTACCC	TGGAAGTGGG	TTGTTTGGCT	ACTCANTCCC	480
	CAGCNTGAAA	ATTGCCCCNA	ATTGCCGCTC	CAGAANCCTG	ATCCAACGGA	ACTACTCGAC	540
	CAATCTAAT	TTCCCTTATA	ATGTGAATTA	CACTGTNAAT	TCAGAANTGA	ACN	

## 1212RP

	GAGATCTCCC	AGTACGTCTT	CAAGCTGGGC	TTTGGCGGTC	TAGGATAGAG	CCGGCGGAAC	60
	TCAGGACTGG	TCGAGACGGG	ATGCTGGATC	CCGAAGCTCT	TCATAAGCAA	CAACCGCGGT	120
	TGCCGCGTGT	AGTCATCGAA	CCGTCCCTCA	GCGAATCCTG	CGAGTCTCCA	CCTGACATCA	180
	CCATTGCCCA	CGATGCACCG	AAGCGTTTCT	GGAAGGAACA	CGCAAACTAG	CAAGAAGCCG	240
30	ATGCCGGCCA	TGATGCTAGT	GAAACCAAA	AACCATCTCC	AACGGTCATT	ATCGAATAGG	300
	ATCAAGCCAG	CAATAATGGG	CGCCCAAAAT	CGGGCCACN	TTTAGGGCCC	CAACATNAAT	360
	TACGCAATTG	CCTTGCCGGG	GTPTTTCGGN	GGTGTGATT	TCNCTTACCG	TACGGGCCCC	420
	TGAGAAAACG	AGAACTCNGA	GGAAATGCTG	CNCCCTNTT	AAAAAAATAC	NCCCATCGNG	480
	CAGGNTGAAA	GCANTTACNC	TTGACTATAA	ATCANCCCCC	GANAAANTTA	NACTCG	

## 1212UP

	GATCAGCAGT	GTCTTCCGGG	ACGTCAACGG	CTTGACGGTC	TTGCGTACCG	TGGCCAGCGT	60
	CCGCACGCCA	TGAAATGCCT	GCACTGCCTG	CCGCAGTCCA	CAGTTGCGCA	GCGATGCCAG	120
	ACACGAAAAC	ATCCTCGTTA	ATGCAGCTTG	GGTCTTCCG	TGCTCACTGT	GCGTCTCGAT	180
40	TAAGCCCAGG	TTATCAGTAA	CATCAAAAT	TTACATAACT	GCCACGTGAT	ATACACGTGA	240
	TAAAGATCTA	CACCCATGCC	CCCTGATTGT	GTAAAAAAGC	AACTTTTGAA	AAATTTTCTA	300
	CGGTTCCATC	CGATGAGATG	AGCTTAGCCT	AGTGCGAGTC	CAATATCAGT	GCACTAAGTT	360
	TATCCAGTGA	TACTTGTTCT	CGAGCTTTCA	GCAACAGCAT	CAGTTTACAA	ATCGCACCAG	420
	CAGTTATCCC	TGGAAAGAAA	TCCTACGGTC	CGAACTCCCA	TGATAGTTTG	ATACGGCCCT	480
	TACAGACGCC	AGCGAAAATC	CCACATCTCC	NGGNGGCTTC	AAATNNNCTT	CCGNGGTTCT	540
45	AAAGCTTAGG	GGNATTCCCA	TGCANGGGTT	TATNAAATTT	GANAAAT		

## 1213RP

	GATCTTTTTT	AGAGAGTTCA	GTGTGCGGAC	CAACACGGTC	GGAGGCCCTT	CAGCTACTTC	60
	CAGAAGGTCG	TAAAGAGTCT	CCAGTAGCCC	CAGGGTGCGC	TCGTGGTCAT	AACAGTCCAT	120
5	CTGAGGTAGC	GTGTTAATAA	CCGCTTTCAG	CATGCTCGTA	GAGGACTTCT	TTACTAGGGC	180
	AGAACTTATA	AACTTAAATG	TCTCGTCTAT	GCATTTCAGG	GTACGAAGAG	CTGCCAGTGT	240
	CCGAATGTCA	TCAGCCGATC	TGCTCGTTTT	ACTTTGCTCA	GAATCGCGCC	ATAGTTTAAC	300
	TNCNGTTCCC	AAATTAACCC	GGTTTCCCN	GACCCTTTTN	AACAAAAAGG	AAAAAAAATT	360
	CCGTTTCCCC	CCCNCNCCCC	NNNNTGGGCN	AAAAATTTTT	TNCCNCGG	AAAATTTTANC	420
	CCCCCNCTT	AAGNCCCATT	AAAAAAAAN	NNNNNTTTT	TTTTTTTTNT	NGGNGCCCN	480
10	NAAAAANNTN	CCCCNNTTTN	NAAAAANNNG	NGGNTTNNG	NNNNANANN	NANN	

## 1213UP

	GATCGCCAC	TTCACGAACT	CCAGCTCCGC	AGGCCGAAAC	GTCGTGCGCA	GCTCCGCCTC	60
15	GCGCGACGCC	CCCACGTTCA	CATACACGTA	GAAGCGCCCG	CCCTCCGCGC	CTGCCCTGTC	120
	CCCCCGGTAC	CGCCGCCCA	GCGCGTGAGT	CACCCGCTTC	ACCTGGTACC	CCAGCCCCCG	180
	CAACCGCAGC	TTCATCTCCG	TTACGTATGT	CCCCAGCTCT	CCCCCGTCGC	CGCCAGCGC	240
	GCCCAGGCAC	TGTGCCAGCA	CTTGCTCGTG	CACCGCCCC	CGCGCCCGCA	GGATGCACTG	300
	CAGCAGCAGC	CGCCGTCTAT	CGTCGCGCGT	CGTCTCCGTC	ATTGCTCTCC	TGCGCCCCCG	360
	ATGCACGCAA	ATCCGCTCTC	GAATGCCTTT	GGCTGCCCC	GGCTTGCGGT	GTCTGGGGTT	420
20	GATTGCCACG	AATGCTGAAC	CAAACTGACA	CATTTTGCCA	AAAGAAACGC	CAATGTCTCT	480
	CGAACGAATT	TCNCGNTCTC	GTTGAACTAA	CCGCCGCGCC	CAGTTGGGTG	AAGCCGCTGC	540
	TGTTCCACC	TATCCGCTAG	GGTTCAGCCT	TCCTGTGNTT	CCACTANTGG	NAAACNCCTG	600
	CTT						

## 1214RP

	GATCGTTCAC	GTCAGCCAAT	TCTGTGTGCT	AGCCCACTAC	ATTGTAGAGC	TTATAGATTA	60
	AACCTCGAAT	GCAATCATTG	GGGTAAGCCA	CAGCTTCTGT	AGTCTGCCTA	TAGCAGAACT	120
	TTTCATCTTC	AAGGGTATGT	CTTGAAGGCG	GCTTTAAGGA	ACCCTTCATC	GAAGTACTGG	180
30	GTCTTTCTAC	CCCTCCGCGG	GAGCAGGATG	TTAGCCGGAG	CTTCTGAATC	AAACTCTTGC	240
	ACTTCAAAC	CTTGTCTGTT	ACCGAACGCA	ACTTTAGCTG	CGCCTTCAGG	TTTTGTTTTCT	300
	TTACTGCCAG	AACCTGTGGG	CGGTGATGGT	AGGAATTTTC	TCCCATCTGG	GTTAAGTTCC	360
	TTCCATATCN	ATTGACACTG	CACGCCCAAA	CATTCAATTT	TCCANANCCC	CTACCCCCC	420
	NANATGTTAA	TTTTTTCNGGT	TTAAAGGACT	TATCNNCCCT	NTCAATTTTTT	CTTNAATNAA	480
	CTCCATTTGT	CCCNAACNAA	CAATTNAATT	CCCCGTGTTCC	TTCCCA		

## 1214UP

	GATCAAGACC	TGACGGCTTC	CTAAAATCGC	TAAGTTTAGT	ACATAAATTG	CGGCAAGAAT	60
	TACCCAAATC	ACCTGCTGTG	GAGATACGAG	GCAAGCTGAG	CGGGTGGATG	TGCCCCATTCC	120
40	ACACCAAGTAA	CTCTTTGGTG	TGTGGCTGTC	ATGGTACTGC	TCGCTACCGC	CGTGTTCACG	180
	GCCTTGCTTA	ACGGGAAGCG	ATGCCGGTAA	AGCCAAATCA	TGTAACACCC	AGCGATAAGT	240
	CCACGAGCAG	ATGCTGAGAG	GCTCGACCAG	AACGACGTCG	CATGGGTGAT	GCTACAGATG	300
	CCTATGCGTG	TGACAGGTG	AAGCAACTGT	GTTCTGCTTC	AAGTAATAGC	CAAACCTGGC	360
	GCGGTAGAGA	ATGACACTGC	GGTGTCTGTG	CATATGTTGG	CACTATGCAA	GGTTACAGAT	420
	TCGCAAGCTG	CCCGAATGTT	GGCCCAAAAT	CGAACCAACCA	GCCAGCTATT	GGTATGGAAT	480
45	TATATACAAC	TTGGTNGGGG	AGGAATTCCG	GTGAAAAACG	GCGCACCAGG	NAACCTTACT	540
	GGAACGGGAA	NCGGGNAATT	TCCCCCCCNC	CCCGGGTTTT	TGGAACCGGC	CCCNNTG	

## 1215RP

	GATCAGAGCA	AAGTGATTCA	AAGCGATTTT	GGACGACGCG	TAAGCTGCCA	GCGCAGGATG	60
	GCCCATCTGA	CTGAGCCCCG	AGGTTACGGC	AATGAAAGCG	CCCTGCGACT	TACGTAGCAG	120
5	TGGAAGCGCC	TTGCTGGCCA	GATTACAGAC	GCTAAACAGA	TTAATCTCGA	ATAGGCGTCT	180
	CCATTCCCTTG	ATGTCCGCCT	CCGCGATGCG	TTGTTGGTAC	GAGACACCCG	CGTTCGCTAC	240
	GACAGCGTCT	AGCCGCCCAT	ACTCCGAGGA	CACCTTATCG	ATCACGGCCT	GCACCACACG	300
	CTCGTCAGTG	ACGTCTCCGA	CAACATAGTC	GAATTTCTTG	CCATGTCTCG	CCTTCAGCTC	360
	CTGCAATTTG	TTTCCGCCC	GTGCAACCCC	TACTACAACC	ACGTCGGGGG	TTGAGCACAA	420
	TCTGTCAACG	GTTGCCGCGC	CAATGCCACG	CGATGCACCT	GTCACAATTA	TAACCTTCAT	480
10	TCTTGCTTGG	TACTTTATCT	TCAATGGGCC	ACGAACGCTC	CCGCTGTTAG	TTTATATATG	540
	ACTTCAGGGG	CTGTTGGCAC	AGCTCACTAG	CACACTACCC	TTACATGTTC	ACACCAGTTC	600
	GAGAATGAAT	GGCACAGTTC	CATTTGTAAT	CATGATTATC	AATACAATAT	GTGTTGTAAT	660
	TATTGATTTG	TAATATGCAT	AATATAGATG	GTTATGATTT	GTAATACAGT	AAATATACGG	720
	TAAATATAAA	GTATTTTAAG	GAATATTTAT	AATT			

15

## 1215UP

	GATCGCCCCG	GGCCTACGTC	ACTGCAGATT	GGCGCAAGCC	AGGAACAAGA	CGGACACTAA	60
	GTCAATCTGT	TTATGTAGAT	TGGGTGCGCA	GCAGCGCACG	CGGCGCCGCT	GATCTAGCCG	120
20	TACCGCACCA	ACGGCGGGAC	GCATGCGGGC	CCGGCGCGCT	AAACCACGAC	CGTCGTGCCC	180
	GGTGCCAATG	GACCGCGCGG	TCATCCACCC	CGCTCAGCCG	GAATGTAGAC	CAAAAAAAGA	240
	GTGTGGTTCC	AGCTCTCAAA	TTGGGCTGGT	CTCAAGGGGT	CGCGGCCCCG	CAATCGCCTA	300
	TATAAACGGA	CAGCGGAGAC	AGTCCGTGCA	CTGTGAGGA	CAGGCACACC	GATGGTGAGG	360
	GTTATCATTG	TGACAGGCGC	GTCGCGCGGC	ATCGGTGAGG	CAACCGTTGA	AAAGTTGTGC	420
	ACAGCCCCCG	ACGTTGTGGT	GGTGGGAGTT	GCGCGGGCGG	AAAAGACTTG	AAGGTGCTGA	480
	AAGAGAGATA	TGGCAGTAAA	TTGCACTACG	TTGCTGGAGA	CGTCACCGAT	GAAAGCGTGG	540
25	TGCAGGCGGT	GCTCGACAAG	GTGTCTCTCG	ATTATGGGCG	GCTAGACGCC	ATCATAGCGA	600
	ACGCAGGCGT	CTCGCGCTTC	GAACGCATCG	CCGAGGCAGA	CATCCAGCAG	TGGAAGCGCA	660
	CGTTTGAGAT	CAATTGTTTA	GCGCGGTAAG	CCTGGTGAGC	AAGGCGCTCC	GATGCTAANG	720
	AATCCCAGGG	TTACGGTGAN	TGTGGTTACC	TCNNGANTCA	ACNAGGTAGN	TANCCG	

30

## 1216RP

	GATCAAGTCT	TTTATCACTA	CAAATGAGCA	GCGCTTAAAT	TTCCAGAATC	GTTTACAGCT	60
	GGGTACGCTT	GCAAGCAAAAT	TTGGCCTTTT	TGAGCTAGCG	GAGGAACAGT	TCGCTCACGC	120
	CAAGCGCCTC	ATGCGCGCTA	CAGAGCGCCG	CGAGCTTTAC	ATGTATTACA	AATCTCTCAG	180
35	CGCGTTCTAT	TCCTTAGCCA	AAATGCCGAC	CTGCTTAATA	GATACTCTGC	GTGCCTTTAA	240
	TAACGAGCCG	CACCTCGTCC	TCCGTAACAC	ACTACTGGCT	GCGCTCTATC	CGAACACATA	300
	TCCACTGGCT	CCGCCGCAAT	AATGCAGAAG	AAGAGGTCCA	TAGATGAGCT	GAACCAGCCA	360
	GCGCCANCAG	AATGTACTCC	CACTTATGCG	AACTCCNANA	NTGGAAGGCC	CTGCATACAT	420
	TTCCGGTCCC	ACCNACTTCT	GCGTTCTTGT	GCTTACCAC	CTTGTGAACC	GAATNGTGCG	480
	GCATGCCTTG	CCCCAAAACC	CCTGGAATC	CATAAATACC	TCNCGGGGGT	TANCTGCGCT	540
	CCCCCG						

40

## 1216UP

	GATCTGTGAA	TATATGCTTG	GGGTGCGATTG	GTTTGCCAGT	GCTATAGAGA	GCGGTCACCG	60
45	GCGTACGCAC	GGCAACTCTT	CGAGTTGTCA	GCCCAAGTAG	CCTGATCATA	TACAGGTGAT	120
	GGATGGCTCC	TGTATACCTT	CCCACACTGC	AAGCCCCCTGA	GTTGCTCAGG	TGTTACTGCG	180
	GCAGATGGTC	ACATCGCTTC	GGAGTATATA	GTCTGCGCTT	TGAGCCACTT	AAAAGGGGCT	240
	CGCCGGCTAG	CCCGCGCGCG	TGGTCACGTG	ATTGCCATCT	GCCCCGAACG	GAAACGTAAC	300
	AGGCGGTTGT	AACGTGGTGC	TCATCCGTCA	GCAGGCCGGT	CTCCCAATGT	ACTTCGCATA	360
	TGTTATTTTA	CGTTTATGTT	ACCTATCGAG	GGTCGCTCAG	GGTTATGCCC	GCGGTGCTGC	420
	CCTGCCACGG	AACCCGCAGC	CTGCAANCC	CCCTAATTGC	CCATGGTGAA	TTGAACTCNC	480
50	AAGCTTATAT	CTCCTTGCC	GATCCCCAT	NATGCATTG	AAGTTCNCCA	NAGGACAAGA	540
	AACANACNCA	AAAAACNAAA	TGGTTAAGTA	AAATTGATTT	GGTGTTCCT	CCT	

55

## 1218RP

	GATCTTTGTG	GGCCACGACG	ACCACCGGAG	TACCGCCCGT	GGCTTGGACG	TACCACTGAA	60
5	AAATGTTCTG	CATGAATCCC	ACCTTGATAA	TACCCATGGA	CCACTGGAAG	TTCTGCGACC	120
	ACGCAGCAGC	GATGGGTGGC	ACACGAGCCA	CTCCCATCAT	AGACGTGATC	GCCAAATTTT	180
	GGAAGTACGA	GAAAAAGAGAG	ATCGAGTTCTG	AAGCGATGTG	CGCGGCAGTG	GTTGAGTGCC	240
	CGATCACAGA	CACAAACCCG	GAAGTCCAGG	ACACCCACAC	CAGCTATCGC	GGCGAATCGG	300
	CCACGAATGC	ATACTTCGTC	TGCACCGTCT	TGCCGTGCCG	ACAGCACCCG	CCCTGCAACA	360
	CAGGCCCATTT	GGATGCTCCG	TACTGGTGTG	TCAGCTTTCC	GCNAAGGCCT	TTACACCATC	420
10	CGTGCTTCCC	AGTTCCCNCG	AAAATATACC	CCNCCTTGGT	ATCTTCCCNT	GAAAAATCAC	480
	CGCCGAAATTT	TCCCAGTTGA	ANCCTCTTTG	ATTCACCCCT	CNTGCCCTCC	CCCAGNNCGG	540
	GANATTCACA	ACNAATNC					

## 1218UP

	GATCCACAGT	TTCCGCACTG	AACTTACTAT	CCCTCAGCAA	CCGCAGGTCA	TCGTCAAGCG	60
15	TTGTGACATC	AGGCTTCACC	CCGTAGCTCA	TAATGCCGTG	GACGGATGCC	TTGGTAGAGT	120
	AACAACCAAA	AAGGCATGTT	GGATCAGCTG	CATAAGCTAG	TAAAAAAGAG	CAGACGCCGC	180
	CTGAGCCACT	AAAGGCAACG	ACCCGCCAAT	ATATGATAAA	TAGAGAATAT	AGAATGTTGC	240
	CAC TAGGCCA	AGATGACCTG	CATTGAGATC	CAGCGACAAA	GTGCCAGGAA	TTAAGGGATC	300
20	TTCAACATTC	CTGATCATAT	GAGAAGAGCA	ATACAGGGTT	AAAACGGCGG	CGTTTAAAT	360
	TTACAGACT	CAATCAAATG	TTTCACAATA	CCTGGTTTGG	ACAAGTCCGA	GACATCCCCC	420
	TAAGTATCT	GCCTCCCCCA	GCCAAGGATT	TTGCGCCATA	TACGGGCCAT	ATTTTGCCTG	480
	ACGATTCTTT	TGCATTCCCT	CCCGAACCAC	AAANACCTTA	GGGGCACNAA	CGGCCCATTT	540
	CCCNANNGAA	AAAAAAATA	GGTGCTTTGN	ATNNCCCGNA	CCCCCCCCC	CCCCTNTTTC	600
	CCNG						

## 1219RP

	GATCCTGATA	TTGTACCGGC	TCATAAATAC	TTTGGATATC	TTCCGACAAT	GTATCGTACC	60
30	CGATACCTTT	CAGCACATGG	ATCAGTATAT	CATGCTTCTT	CCTAAATGCA	GCAACAGTAT	120
	TGAGGACTTC	CTTCAGACTG	TCCGTCTGAG	TATCTATCTT	CATAAAGATG	AACCTTTTCGG	180
	ACCTCTTCCT	CATCAGCTCT	CTGATGAGTG	ACGTTGAATT	CTTTTAATAG	CGCTTCCCAC	240
	TGGTTTGATA	ATCTTGATAC	AGTGGTCCAT	AGTCCTCCCT	GGAAAGAAAT	GAAGTCGGAA	300
	GAAATCAGTT	TTGGCAGCAC	TCTCTCAGTT	TCTGATTCAA	CTCCCGTTAG	ATATTTCCCTC	360
	CCACAAATGT	TTACGGCCCT	ACAGTTGGTT	TCTTTTGAN	CCTTCACTTC	CNTCCNAAGC	420
	CATGAAAATG	ANTCCATCNC	CNCCCCC	CTTTGTNAAA	NTTCCCATTC	GCAAATTCNC	480
35	CAGTTGAATT	CCCCCANCCG	GGTGTTCCCC	GCGTTCCCCC	NAAAAANAC	NGAGGGGGGT	540
	TTTAAAAAAN						

## 1219UP

	GATCGCGGCG	CTGCCGCCGG	CGTCGGAGTG	GCGCCACGTG	GGCCGGCCCT	TTTGGCCAAA	60
	TCCCAGCGGT	GGGCGGGTTT	CGAGCTGCTT	GACCTTCCGC	GGCATGTCAA	AGTGCGGCGT	120
5	TAGTTTGGTC	CTGTAGGCGA	ACTGTAGCGG	CGATGCGACC	GTCTCGCCGA	CGGTGGGGAG	180
	CAGGCCCTCG	GCCAGCAGCT	GGGGAGCAAA	GAACCTGAAC	GCATTTGACA	CGGTTCGCTG	240
	TTTGAGCTGC	AGCTGTCTGG	CATACGTCAG	GAACGTATAC	TGGCAACCGG	AGCACTTCCC	300
	GAAGTACTTG	CAGTTGATGA	GGTCGTCGTG	GCGCATTTCA	GCAGAGGTCT	GCACCTCCAG	360
	CAGAGACGCT	TCCGCGTAGT	GCGGTGTGTC	TTGTGCACTT	GGATGGTGAC	CACGTCGCCC	420
	TGGCCAGCCC	AAATTTGGCAC	CCAGCACTAC	TGTTTCCCTG	TTTGCTATCC	TCCCGGGCTG	480
10	TCCAACAANA	CCCATCCCTC	CCCATCCACT	TTACNTCCAC	ACATCACTTT	CATCAGCNCC	540
	GGTTGTTCTT	CTGCTGCATC	GCCCCCGAA	TTTNTTCAGA	ATGATTACTC	CTCCNCNG	

## 1220RP

15	GATCGCGCAG	TTGTGCGCCT	CAGCCAGCCG	CTTTTGGGCG	ACGCGCGGGA	GCGTGTCCAT	60
	GTACCCGTCG	GGCACGCCCC	CGTCGCCCTC	GCCGATCAGC	TGCAAGTGCT	GCTGTAGCTC	120
	CTCCGGGCATC	AGTCTCACGA	TCACATTTAG	TAGCGCGGTG	CTGTGCGCAT	CTGCCCTCCTG	180
	GAACATGTCA	GCCAGCTGCC	TCCGAAGTTC	GGACCGTGTC	CCCTGGTCTG	CTGTGAGAGT	240
	TAGTATTCCT	GGCCGCAATC	GGTCGCACAT	TGGCATCACT	TACTATTGTC	GCTGGGCATT	300
	CACCTCCCTG	GATCACTGGT	GCTCCCGGTG	GCGGTAAGGG	GCAACAGACA	GGCTTTTTTTT	360
20	ATTTTCCCTCT	ATAATACGCT	GCTCTATGTA	GCGTATACTA	TACAAGTCTT	AACTAAGGTG	420
	AAGTGAGAAG	TCATTATTTA	GCTGCGTTTC	GGCCGGTTCAT	GCAGCCGGCT	ACCATATTAG	480
	CATGCCCGCTG	GCCTTGACGG	CTTTGGACGT	GGGGGAATTG	TTGATGCCCA	AGGACCTTAT	540
	GGAGTTCAAC	CTCACGGAGA	GGTTTCCGAG	ATCGAAAATG	TCACTTTCGG	CAAATTGCGA	600
	CACACCGTAA	TACTCGGCAA	ACGAGTTCTC	GACACCGCTG	AGCTCGTCGT	CGACGTCGTC	660
	GACATAGGAC	AGAAGAGGCT	TCGTTCCGGC	TGGCGGGCGC	GCGCGCGCAA	CCGGAAGNGC	720
25	CCCCCANAG	CTGGCGCCNG	GCCGCC				

## 1220UP

30	GATCCAGAAT	ACTCGTCGCA	CCACTTCTTG	AACCGCGGGT	ACAGCGCGGG	GTCCGTGCGG	60
	TCCAGCGCGG	CCTTGTGCGC	CGCGTGGAAC	AGCCGCGCGT	CCTCCTCGTA	CAGGTAGCTT	120
	GGCGTCAGGT	CCGAGCCGCC	GCCGAACCAC	CACGTCTGCG	GCTTGCCCGC	CGCGTCCCAC	180
	GTCTCAAAGT	AGCGGTAGTT	GAGGTGCACG	GTCGGCGCGT	GGGGGTTCAC	GGGGTGCATC	240
	ACCAGAGAAA	TGCCGCAGGC	GAAGAAGCGC	ACGCGGGCCG	CCGGCTGCCC	GGTCACGGGG	300
	TCCGTGGGGA	GGTGCAGGTT	TTTGTCGTCG	GCCCCGATGG	CACTGACGGC	TGCCGGCGAC	360
	AGCTCGCCGT	GGACTACCGA	GACGTAAACG	CCGGCCTTTT	CGAACGTGGT	GCCGTGCTGC	420
35	AGCACGCACG	ACGTGCCGCC	GCCACCCCTC	TTGCGCTCCC	AGGAGTCGGC	CTTGAACCTG	480
	ACCGTGTGCA	TCCGCTCGAA	CGCGGCTGTA	ATCTCGCGCT	GCTTGCGGCG	CACGAGCTCT	540
	TCCATGCGCT	CGCGCATGTG	GGGGGTGTGG	GCGGATGCCA	TTGCTGGGGC	GCCGCAAGAG	600
	GCGAAATNAN	CNGTGCGCC	GGCGGCTTAT	ATAAAAAGCGT	GGCACGGGTG	TTTGGCCAC	660
	GNCACCANGG	GCTGCNAACG	TCCGCGCCAA	NANANCCAGG	GTCCCGGCCA	NAACACNTCG	720
	GCGGGCGGCC	NAACGCCGCC	NCNCACAATC	ACNCCGACAA	TCGCGCNCNG	GGATTCC	

## 1221RP

45	GATCTCTGCT	GTTTGGGCTT	GCAAGCATCT	TCCTCGCTAA	CTCGTTCGGC	GTTTACGTTT	60
	GAGGTTCGGG	GGACGTATGC	TANACCAGAG	GCATTGCGGG	GTTGAGGGGA	AGAGGTGAG	120
	ATTATGAATG	ATATATACTG	TTATACCGGC	TGCGGGTGGC	TGTGCGCGTC	ATCACGAGGG	180
	ACTTACAAGT	TCAAAAGGTC	TTCATCGATA	TTTACCAACT	TGTAATAACG	CTCTGTGAG	240
	TCTGAGTTGG	AGGAGCCGGG	CTGGTCGCCA	TACTCCATCA	ACGTGTTTAC	CATTGCGCGT	300
	GTATAGCTGA	TCAGGTTTTT	GAGGGATGAC	TCGCTCTCCT	CCTTTAGGAA	CATCAAAATG	360
	GTGGTGTTC	ACAANCNGGA	AAACCTATCC	TGTTAGTNNA	GAAGGGTTGA	GAACACCGCT	420
	AATCCCTTAG	GCACTCCACC	ATGGTTTTAT	CCGTACCCCA	TTACCCAAAT	TTCCCCCAAG	480
50	TGCCCTTNA	CTTTGNCGAA	CCCCCGCNAA	ATNCCCGTTT	TTAAAACCCN	AAAAANG	

## 1221UP

	GATCGACCCT	ATCAACGCCT	TGCAGGCTGC	TATGGAGGGC	TATCAGGTCA	CCACTATGGA	60
	CCAGTGCGCC	AGCTACGGCC	AGGTTTTTGT	CACCACCACC	GGCTGCAGAN	ACATCATCAA	120
5	GAAGGAGCAC	TTCTTGGCCA	TGCCTGAGGA	CGCCATTGTG	TGCAACATCG	GCCACTTCGA	180
	CATCGAGATC	GACGTGCGCT	GGCTAAAGGC	CAACGCCGTC	GANGCCGTCA	ACATTAAGCC	240
	ACAAGTCGAC	CGCTACTTGC	TTTCCTCCGG	CAGACACGTC	ATCCTGCTTG	CCGATGGTTA	300
	GACTAGTCAA	CCTAAGCTGT	GCCACTGGCC	ACTCCTCCGT	TTGTCTATGT	TTGCTCTTTC	360
	TCCAACCAGT	CTTTGGCACA	GATGGTCTCN	TTCAAGGGCA	ATNAAAAGGC	CTTCAAANAA	420
	ATTNNTTNNT	TTCCCAAAAA	ACGGCCNTCA	AANCGGGNTT	CATTCTNNC	CNAAAATTGN	480
10	AAAGGCGCNC	CCATTTCCCC	CTAAATTGGG	GTTTTNTTTT	AAAAACATTCC	CCCCCCCCCA	540
	TTTCCGGGTT	CCCAAAAGGG	TNTTTNGGGG	NCCCTTAAAT	NTTA		

## 1222RP

15	GATCGAATAA	TAAAAGTGGC	TAATACTTGG	TAATAATATA	ATAGAAAGGG	AAATAGAAGA	60
	GAAGTCAAAT	GGGAAATAGT	CAACGGCGTA	CTAGGTGAGT	GTTCAGTTGC	ATGGAATCGT	120
	AGTCAGAGAG	GTTTATCAAA	AACGGCAGTC	GTCTGATGAT	AGCAGTATCA	CGAAGTGCTC	180
	ATGCGCCCTG	CATACAATGG	CAGGCTCAGC	GCAGGATCAA	ATGGATAGCA	GCGGGCGTAC	240
	CCGCGAACGG	ACTCAGTGGG	TGGAGTGGCC	CCGGTGGTAC	TTGAGGCCGT	TGAGGTTCTT	300
	GTAACGTTTT	CCACAGACCT	CGCACC GGTA	AGGCTTGTC	TTCTCGAACC	CATGCCCGTC	360
20	TGGATAGGGC	TCGTTGGACT	CCGGGTCCAT	GATGCTAAAA	GTGCCCCGTC	GGGTTTTTCAT	420
	GAAGCTTTTT	ATTCTGGTGG	CCGTGGTTTT	ATGGTACTTG	AGTCCCCTTT	GATCCTGGTT	480
	AGTCTTATCG	CAGCCCATGA	GGGACNNTTG	AAGGCTTNTC	CCNCCTTGT	CCNCN	

## 1222UP

25	GATCTCGCTC	AGACCGTCAC	CCACGTTGTC	TGCAAGGGCC	TCCGCCGCTT	TANCTGCCTG	60
	CCACGGCTTG	GAGCACGCTA	GCTGCACGCC	AAACCCGGGC	AGCTCCGAGC	AGTGCGCCTT	120
	GGGCAGCGCC	CACTCCGAGT	TGGTGCCCTG	GATCAGCGGC	ACAGCGAGCG	CCATCTCACT	180
	GTACGTCACG	TCGGCGCCCA	ATTGGCGCAT	CAGGCGCCGG	AACGGCAGGT	TCCCAGCGGT	240
30	GGTCAGCGGA	GAAACGATCT	TCTTGATGAT	CAGGTCCAGC	GGCTTCTTCT	CCTGTGCAAA	300
	GTAGCGTGTC	TCGTGATACT	GGGCGTACAG	CTCGCGCTGC	CGGGCGCGCT	TGTTGCTCAA	360
	TTGCTCCTCC	CGCTGCTGCA	CCTGCGGCAC	CTCTGCGACC	GCGCCTCCGG	GGCCGCCGCG	420
	GCCCCCTGCA	TCTCGTCGCC	GGAACCTCTG	CTGGATGGCG	TCAAAAATCC	ACNATTTCTC	480
	CCTGCNCNGG	AAGGGCCCCA	NTTTTCCCCA	ATNANCNCCA	ATGAACCATT	GNTNCCCCCN	540
	TGGTTNCAAA	ACNAATTTTG	CCCCCCCCCG	AGATTNTCCC	A		

## 1223RP

40	GATCGGTTTT	CACCTCAATT	CGTTTCTGGT	CGCGCAGTTG	GTGATGCTGC	TGATGCTGAA	60
	GCTGTAATTG	CTGTTTCTGC	TGAGCAAAC	GCTGCTGCTG	TTTCATCCAG	GGATTCTCCG	120
	GAGGAGCTGA	GTCCGGTTTG	CGCCGTCTCT	GCTTGTCGTT	CAACAAGTTG	TTATATAGCT	180
	GGTTCATACC	TTGGGAGGTC	AGGAACTGAC	TGACATTGCG	GTGCCCCGTC	GGGTGGTCTA	240
	GCAAACGGAG	CATGGCCTCT	CTCTCCTGTA	GAGTTTTCTT	TGCCGCCATC	TCAAACCTCC	300
	TAGATTCCAT	TATCAGCGCT	TCTTCTCAG	CAATCTCAGC	CGCCGACCTC	GAAAGCAGCC	360
	TCCGTCAAAT	ACTTCTTCCG	CTGTATTTCC	CTGGTCTTTG	GAATACGCTA	GGATGGTAGT	420
	AGCGGTTTCC	CCGGGTCTTT	CGCCCTGAAA	TTATTTTTTG	CATACGNGGT	TAAAAATCTC	480
45	CCCGTANTTC	CTCCAACGGT	CCTNNANNCG	NCNTAAANAN	ACNGGTCNGT	AAATNATAGC	540
	NNCC						

## 1223UP

	GATCGCGCGC	TTGAACATGG	ACGTGGACAC	GGCGAAGTGG	CGCTGGAGCG	CGCGCACCGC	60
	TGCGTCCCTGG	AGCTCTGTGT	GTGCCATGGT	GCGCTCTGTC	TTGAGCTGGC	GCACAACCGC	120
5	GGCGGATATG	GCCTGGACCC	TACTGGCGGC	GAGGACATCT	GGTAGCGCGG	CCGCCTGCTC	180
	GGACTTGACC	ACGACAGTGG	CGACGCGGAC	CTTGGTGGTC	GGCGCCGTGA	ACGCCGTGTT	240
	GACTGCAAAG	TGGTCCGAGG	GCGCGATGGT	GCCGGGAGGG	AGGGGTTTTG	GTGAGGATGC	300
	GTGTGCGCGG	CGCGACGGCG	AGCGAGATGA	GCTGGCGCTG	CAGCTCGGCA	TCTGGATTGC	360
	GGTCAGGTCC	TGAATCTGCT	CGGTGGTCAG	TTCTGCGTAG	TCTCCGAAA	AACAGGAAAA	420
	ATGGTTGGCG	GCATNGTTCA	ACATCCTTGG	CNCCCTGGGT	TAAAAATGGC	CGAACTGGNN	480
10	GCCGATTTCC	CCGAGAACCC	ATTTGTATAT	CCCCCTTCCT	TCTGCNTNCC	GATTTTTTTT	540
	CAAAANTNAA	AACCCCCCCT	AAGAAGANNN	CGGGGNNGCC	CNCGGCGGN	TTTTTTTTTC	600
	CNCCCCCA						

## 1224RP

	GATCAGTAAC	AACCATAGCA	GCCGCACCTA	CGAAAGCATT	CGATACATTT	TTAATAAATT	60
	CGACAGCAGG	TAGTAGTCTT	CTTCCGATT	GCTTTACAGG	CTCGCTAAAG	ATGTGTTTCGT	120
	AGCTCTTCCA	AAGAGAAATT	TGTGTAACCT	CAGAGTCAGC	AGCGGACTCA	AAACAGCACC	180
	TCAACCAAGC	GGTTGACCGC	ATAGGTTTCA	TCAAGCCCAA	TAGTTTTTGG	AATAGATCAG	240
	GGGGAAGAGT	TGGAACATGC	GTAGGGGGTC	TCGGTTTTAC	TCGCCTAAC	AGTTTTATCT	300
20	CTACTTTTGA	AAGTATGTCG	TAGTCCGGA	GCTCAACATT	GTAAGTCAAC	AAGCTAGTCA	360
	AAACTGTAGT	CAAGATTGAG	TTCCGCTCAG	GGTTTTTGACA	ACAGAGTAGT	TATTCTCTCA	420
	CTCCCCAGGC	AAGATGTACT	GGTATAGAAA	ATCCAGTTGA	AGCCATAACC	AGCTCGTTGT	480
	CACAGTCCAC	CAGAAGATAG	GANACATCAG	GTTGAAGAAT	TCCTCATCTA	GGTTATCTGC	540
	TGCCTTTTCT	GTTCTGCTTT	GGACCAACCC	ACAACCCNAA	AACCAACGCN	AAATCAAANA	600
	CCNGGTTTCT	TCCTTGNTCC	CCCNAAATGA	AANAGGTTTT	GAAANGGTTN	TCCCTCTTGC	660
25	CGGGCCAANT	AAAAAAAAGG	CCCNACAGNT	CNACNATATT	ANCANTCCCC	NAAAAAGGCC	720
	TTCTGNTCTA	A					

## 1224UP

	GATCGGGTGC	GGCACATGCC	TCATCGGGCA	GGTGGGGTGG	CGGAGGCATA	AACCCACCCC	60
	TGGTTGTTGC	AGTGAATAGG	TATGGGTACA	GCTTGGCGG	CCACGAATGT	GCGGAGACGT	120
	TTCAGCTGCC	AGAGGGACCC	GACCGCACCG	GTGGACTGTT	GGCTTGGTTG	GACGCTCCAG	180
	GGTTACGAGC	CGGCGCCCTG	CGGAGCACAT	GATGTCGAGC	TGTGCATTGG	TCCAGGTGCG	240
	CACTAACCAT	GCCAAGGGCA	TCCGGCCAAG	GCGGATGGGG	CTGGACGGCG	CCAGGGCGGG	300
	ACGACTATCA	CTAAGAAATC	ATCGATTAAA	ATATAAACTA	CATAAAGTAA	AGGGCGGACT	360
35	GAGTGCACCT	TCAGCGCACT	AGCAGCGAGT	AGCCGTAGTT	GAACCACTTG	CNTGCGATCC	420
	GTGGCACGAA	GCGGAAGTAA	CCGGAACCTC	GATAGTTTCA	AACGAAGAAC	CGAAAAAGCC	480
	TTAAAAATGG	TTACNCCCTA	GGTCCCCCAA	CNGGTCCCTC	TGTTTTGGAAT	TAGGGTGGGC	540
	GGAAACCCAA	ATGCCCCANT	TGTTNTCCAA	TTCCCCGGNG	GCCCCAATTT	NAATTTCCAA	600
	ACCNATCNEN	ATCTCGGCTG	NATCCCCCCC	NTTGCCCCCC	TCAATGGCCC	CGAACCTTTT	660
40	NTGNCCCCCC	CCCAAGGGCC	CTTGNGNATT	TTTTTTCCNG	CCCNCCCGNT	TNTCTTAAAA	720
	NAAAGCNGCA	TTTTTCAATT	CCCCNGGAAC	NCTTTTTTGT	TT		

## 1225RP

	GATCCTTTTC	TTTCTTCTTC	CCTCCTCCGA	GGATTCCCTT	TTTGAGCTTG	CCCCTGCGC	60
	CCAACCCACC	GCCTATGACA	CTAGTACCGG	CGGACAGACC	AGCGGATAAG	CCCTTATTGG	120
	CAAAATCGCC	AACCTTTGTC	TCCACCTTGG	TAACAGAGAC	AGTGTAACCTA	GGAGAAAAAT	180
	TGAAGTTCAA	GTAAAGAATA	CCACCGTCCT	CGCCGTTAGG	ACCAGTTAGC	TGGACTTCCA	240
	TTGGGGTTTC	ACTGTCTGGG	TCCACCTCAG	CTAGAGCGAT	GGTTGCGGTG	CCAATGAGAT	300
	CGTCACTGTT	TCCGGCATCC	CAGTCCATGA	CCTTGATGCG	CAGGTAGTTG	TTAATCCGGT	360
50	TATTCAACTG	CAGGGATGTG	TTCTCGTTCC	AAACAGGTTT	AAGCGTCTTC	TTCTGGGTTT	420
	TGGTCTTGT	ATATTACCTC	ATCTGAATTG	TCGAGGTTAG	AATTTGACAT	AAGGTCCGGC	480
	TTGCCGTTCC	GGTCAGCAGG	TAGAGCCTGA	CTGCATTTAG	AACCTCCAGT	GTTAGGTCCG	540
	AGTGTTGTA	TCAGTTTGCT	TGTNGCATCT	CNAACCCAAA	AAGGAACCAC	AACCGTTANN	600
	TCCTTTTNG	ACCCAACCTT	NTTTACAANN	AGGTTTAAAT	TACANTTTCN	ATTTNTTTGN	660
	TGGAANGAAC	CCCNAAAGNT	CCNCCTGTTT	TACTGANCNT	NPTCCCNAAAT		

## 1225UP

	GATCCTACTG	GAACCACCCA	CTCAGGAGCA	GGTTAAAAAA	CCAGCCAAAG	TAAAGACAGA	60
	GACAAACGTA	AGCATCCCAA	AGCAGACCCC	TACTCCAAAG	TCTAAGTCGG	CTTCAGCTTC	120
5	GTCTTCTAAA	GTGCCTACAC	CCCTGTCAAA	GCAGGAGCCC	GAAGCGCCGT	CTACCATTMT	180
	TGACGCTCCT	TCTTCTTCCT	CCTCCACTCC	GGTGCCTGGG	CACCTGGGATA	TCTTTAGCAA	240
	ATTTAGGAAA	GCATCCAGTG	ACTTTGACAA	GCCCTTTGTG	GCCGAGTCGA	ATGAAGTTGC	300
	CGAGAAGCCG	TCCGGGAAGG	CCAAACGGCA	AACTACTCCC	GCTGCCAGCA	AATTAAGGCC	360
	CGCTGCAAAG	AAAATAAAGA	CGCCCGCGCT	CGATGAAAGC	GAATCTGATT	TTGACCTTGA	420
	CCTCAGCGAC	TCCCAGCCCC	CCATCGCCCC	TAGAAGTAGA	GCCTCGCGAG	CTGTGCGCAA	480
10	AAAGCCAACC	TACGTAGTTG	ACCTTTCCGA	TGACAGTTTT	GTTGATGGAG	ACGCCCAGAG	540
	ATGTTGAGGA	ACCGATACTG	ACGAATCCTT	CCAGCTCTGA	CTAGCACTCT	AGCTCGCGCA	600
	TTGACAGTNC	NCTACCTTAT	GGAGGNTTCC	GAAATCCNTT	GAATACCCCC	CGTTTTTTTAC	660
	TAAAACCCCC	NCTTTCTTTT	TCACCCCCCA	ACCCCCAGGG	GACGAATACT	TTTTTCTTTA	720
	CTTTCTATCA	NGGGGTTTCGT	CNCCNCCCN				

## 1226RP

	GATCGTCCTC	GCATGGGAGC	ATCAGATGTC	ATATCGGCGA	AGCCTTTCCA	TATGGCGGCT	60
	ACGAACGATA	CGAGTTCGCG	TCCTGCTTGC	GCTGTTGGGG	TCTGTGAGCG	TGCTGCTATT	120
20	GCTGTGCGTG	ACGCCACACA	TGTGGCCTGG	ATGGCCATCT	CCGGCAGCAC	GGGAGGTCCC	180
	GGCTTCACCA	GAGTCACAGG	CCCCGGCTTC	ACCAGAGTTA	CAGGCCCCGG	CTTCAACACA	240
	GCCACAGTCC	CCAGCAGGGT	CTAAGACGCT	ACTGCAAGAC	TTACTGCTAG	ATAGCAAAAA	300
	ACCGGAGGGG	GCCTCTACGC	CACAGATGCA	GTGCAAGCGC	TACTTTGAGG	GCACATATCT	360
	CCGGGAGCCT	TCCTGGGGCA	ATAGCGTGTT	GCGCATGGCA	GACGACTTTC	TTACGGCTAC	420
	GCAATACACA	GCGAGGCTGT	TGGAGCGGTG	GCGCATATTT	GCTGATTGTT	TCGTTATTCA	480
	GATTTCCGAT	TTTCAAATAC	NCTATCCAAA	CAAAAAAATC	TGCCCAANTT	CCATCAGCGA	540
25	ANTTCCCTTT	TCNTNGGCAA	AAAAAATAAN	NGAGGANATT	TTGCCNTTCC	CCNGAATTTT	600
	NCCCGGGAAA	ATTTTTTAAGG	NGGNTTTTTT	GNAANGGGC	CCCACCAAAA	NANAAAAGGN	660
	GCCTTTTTTG	GAAAACGGGC	CCTTTTCCCC	GGNGNGAACA	AATTNNTNNN	GGGGACGCC	720
	NGAATTTTTC						

## 1226UP

	GATCGCTTCA	AATTTCCAGC	CGTTGATATT	CAAAGAGTGG	TCACGTTCCG	AAAGATGGTC	60
	CTTCTGTTTC	TCTGTACGTT	TGGAGGGCCG	GCCTACCGGG	GCGTTCGGCG	TTGTCTCCAC	120
	GGTGCGGTGC	TGTCTATGSG	GGACATCCTG	GATGTGTGTC	TGCAACGCAT	TAGCAAATGA	180
35	GTTTTGTAG	TGGTACTTAG	GAAGTTTATA	ATTTAGGCTC	AGTTCTATAC	TGCCGCTAAT	240
	ACTTTGACCT	GGAACAATCA	TCGTTATGTG	CTCACCTCTG	GCGTGTCTCT	TAGCGTATTC	300
	CCGCCGTGCT	TCAGCATTTG	GTTGTTCCCTG	GATCGTTGGG	TATGGATCCT	CCCACCTCTG	360
	TAGCCAGTTG	GTATCCAGCT	TCTCACCTTG	CTGATGCGAT	TCTGGACGCG	GGGGTTTCAG	420
	CAGGCGTTAG	CAATGAAGTT	GGCGTTGCCG	GTTCAAAAAA	AAANACCGGN	GGGGGCTTGG	480
	TAANCCCGNC	CCTTTAAGGG	CGGCCCCATA	TTNCNCNATNA	CCNNNACCGC	NCCCCCATN	540
40	ACGCCCCCAA	AANATNTTTG	AAAAAATTGC	CNTACCTTTT	TGNGGGAGCC	CACNCNCTTA	600
	NATAACCCAT	TTTTTGAAAN	ANGCCNNTCT	TTTNTTTAAC	NCCNCGGTTT	NCNANTATGC	660
	NGGGGCAAAA	TTAAACCNC	CCCCCNAAAT	GNAATCNNTT	TCCCCCNAA	NACAAAAAAT	720
	ATTTTNTNTT	NGGGCNGGGA	AT				

## 1227RP

	GATCGATGAA	CAGACTGGAG	AACAGAGAAA	GGTGGTGCCC	CTCGAACTCG	AACGGTTTTT	60
	CCCCTCGAT	TTTGATGAGA	TATTACTCCG	GGATACGATG	CAGAGGAACG	CAGCTATGGA	120
	AGAGGAGGAC	TACAGGGAGC	TGGGGAAAAG	AGATATTGAG	GTGGCGTTCC	AGAACACCGG	180
	CGTGACGCTG	GATGACAGGC	TCCAGTCGTT	GCCGGCCATA	TCGCTCTTCG	GGAGGTATGT	240
50	ACGGGATATC	GACGGGATGT	CGGAAGCGCT	TGCGGACGGG	GACAGGCACA	TCATGGTGT	300
	TGCGCCGACA	AATGACGCCA	TTACGGCGAT	GCCCAAGAAG	CCGTGGGAGT	ATCCACGGAA	360
	CATCGACAAG	TTGGAGCAGG	CAGGCGCGTC	TGCGAGCGAA	ATCCACGACG	CCATCCAGGC	420
	GAATGTGAGA	CGCTTTGTGC	TAACCCACGT	GGTTTCCGAC	ATCGACCTCT	CTAAGGTGGT	480
	TCGGGAAGAT	TGCTCCAGCC	GTGTTTGACA	AGCGACTTCA	TCCCAAGAGC	ATGCAGGGGA	540
	TATTCTTTTG	CGCCAGGAT	GGCAANGGTT	TTACAGTNTC	NTCCAANANN	GGGCGGACCT	600



TGCCGTTNAG	ANGTTACCCC	CCGCTCTAAC	GGTTTATTTT	GGTINTCACN	CCCCCTTGGN	660
TGCGAATTNG	AAAACCCCTCC	NCCTGNCCCN	NCCCAATNAN	TCNCTTGAAT	CCCNTTTNG	720
GAACCNNCNN	TTNCCCCCAN	CNCC				

## 1227UP

GATCATTGTC	CGGACCAAGA	AATATTTTCA	CTCCTCGAAG	AGCTGGCCAC	TAAACTTCGT	60
GTCTGGTTAG	GTTCCTCTCC	AGCTGATGTG	CTAGATATCG	AGGTGAGAGG	TAAGCTTATT	120
GAATACTGCA	TGAATACTGC	ACTTTATTGC	GGTGGGAAAA	TAGAACATCC	TACATCGACG	180
ACTTTGATGA	CTGACCATGA	TGAAGACGAA	TCTGAAAGCT	CTGATTCCGA	ATAGTCCAGG	240
CAAGTTAATA	CCCAATGCTC	GGCTTTAGCC	TCAAGGGAGA	TATCGGTAAC	AGCTCTATCT	300
ATGCTGCCAG	CACGTACGAG	TTTTTACTAA	ATTTGGCATA	CAGTTTCATG	TATTTGACAT	360
AAGCTTAATG	TTTCATTTCG	AACACAAGGC	TTGCCGATGT	GTAAAGTGCG	CCGCGTCTCT	420
GCATTCAAGA	CAGCATACAT	GAACCTTCAG	TTTTTATACG	CGATCATGTT	GATTTCCTAAT	480
AGGGCTAGTC	CATGGCCCCCT	ACCTATAATA	TACTACCATC	CAGCCCNCCG	AACCGNAACN	540
NNATTTTTTA	TTTTAATNAA	ATTTTGGGGG	NATNCCACAC	NNNCCCTANC	NNGGANTTCC	600
AATGTTTTATT	TAANTNAAAA	ANCAGTTTGA	AGGGTATTCC	NNCNCNCCNC	CCCACNGNT	660
TCAAAACCAA	ACNANACCGT	GAAGCNGNTN	NTCCCCCNCA	AGGAGNGCCC	CCCCGCTTCN	720
AAAAACGGTN	NCCTTTNCCN	CCCTTGCNCA	ANATTCCCCC	CGCTGCCC		

## 1228RP

GATCCATTGG	GCCCAACGAT	GCTAATGAAG	TTCTTGCCCTC	CAAAACCCAC	ATTGTGCACA	60
CCCTTGATCG	ACTTGAAGTT	CTTCACCTCT	AAGCCAATCA	GCCTCCCCAT	CTTTTTGAGA	120
CACCTGAAGCT	CAGTCTAACT	GCTCTCGATG	TTGTTAGTGC	GCTGTTAATA	TGTCCAAACA	180
AACGCGATCA	TGGTTGTGAA	GAACGCGCG	TTCCGCATACA	CGCTCAGCAC	GTAGCCCAGC	240
GGCCCCGCGG	GCCCGAAGAT	CACTGAGATC	GGCAGGAACA	GCGGCGTCCA	CAACAGCACC	300
AGAAATACCA	AAATCGCCGC	AAACGTTATG	ATGTACAGGA	TCACCAGAGT	CACCGCCTGA	360
ACCCAGATCT	GCCCGTGGCC	CATCCCGACC	ACCATCGACT	GCCTGAATTA	GTATATTCCG	420
TCCACCTGTC	TGTTTTCATAC	ATACCACCCC	AGGGCACACC	AGGCGGTAAC	AACCCCAAAG	480
GNGTCCCTAG	GGAGCGCATG	CAAAATATCC	ACNCTCCGCA	TGGCATCTCC	CNNTTGGA	540
GGGGNCCCCC	NAAATTTGGG	CCNAAANCCC	TTAAAGGNC	CCTGTGNCCN	CAANNACTTC	600
NAATTTCCCG	NTTNGGCCCC	CCCCCCCCCTC	CAACGGGATT	TAAAACAGGN	GGGNGNGGGA	660
AAAACCCNCG	AGGGGNTTTT	TTTNGCCCCCT	TTCCGAAANA	ANCCNCCCCC	CCNGGGAAAA	720
AAATATTTTT	TTTTTNGGG					

## 1228UP

GATCATGCCA	TTCTTACGCT	TTGCCACAT	GGACGCCCAA	ATGAATTTCT	GTGTATGCGA	60
GGATGCTGAC	GATGCAGCTG	AAGCAGGAGA	CGACAGCGAT	GTGACGCCTG	GTTGTATGAC	120
GCCTACTATT	TCACCTGTGA	ATACTTGTTT	TTGGCCCTCT	GTAGACATAA	TCTTGTTAAG	180
GACAAAGCTC	CTGCTGTGCG	TGTGTATCAG	GTCAAGTAAA	GTAAGCGCCT	TAAATGCCAA	240
TTTGAGAGATA	CCGAAGATTA	AGCATGCCAA	ATCGTTAGCC	GCCCTAAACT	GCCATGGGTG	300
ATGCTGGGAA	CAGGTAAATA	TGGCCTGAGG	TGCTGTGTAC	TTACCTGATA	TAAAAGTATG	360
CAGTATGCGG	GGCGCTTCGT	ACGTTCTGCT	GTAGTCTATC	GGATCCTGGA	TAGATGTTAG	420
TTTCATCGGT	AATGGTTGGA	GATAATTTTC	GTCTTGCGAG	GCCTGTATAG	TAGTTTCCCTG	480
TGTTTGAATA	TTTCATGAAAT	GGTTGGGCTA	GCTTTTCAGCA	GCTGCTTCTT	TAGTTCTTGC	540
TCATACTGAC	TTCTTTCGAG	ATCTACNCCA	CCGCNTTGGG	GCTGACCCCA	GCACACTTAT	600
GATTTTANA	AGGAATCCCC	GTAATCCAAN	GCCCTTNCNT	ACCCNGTCCC	AATNGTTNCA	660
TCAAAANGTC	ANNCCCTCNA	TTTCCNCTTT	TCTCNCCAAA	ACNCCCACNT	TAATTGAANA	720
NGNCCNTTTC	ACCGCGAGAG	GTGGCGNC				

## 1230RP

	GATCCCGGTA	GGCGTCTGGC	GGCATAATGT	CTGCCGTATA	GGTGGACTCT	GGCTGTATTG	60
	TCCGCAGGGG	AATGGCATGC	TTCTTGTAGA	AATACAACCG	ATCATAGGGC	GAGCTCATAT	120
5	CCACCGTACG	TCGCTGGGAC	ACGTACTTTT	TGACTGAGCC	ATCATTCGCG	CTGTTTCATTG	180
	CGACTCTAAT	CTGATTGAGA	ACCCTGACCT	CTAGTGCTAT	AGCGCAGGGC	GTACCTGTCT	240
	GATGATGCGC	TTTTCAATGC	TCGAGCGTGC	GCAGTGTTAC	ATCGATCGTC	GCGGACGATG	300
	TTTAAGCAGG	ATGCTGAGCT	AATATGTATC	GGTATAGGCT	ATTGGCAGTA	GACCTGGGTA	360
	TATACGCCTA	GATATGGACA	AGATGCTGCG	CCTAGACATC	CAGAACTTAA	CCAGGCTCGG	420
10	GTTAAAGCCA	CCCAGATAAC	ATTTGAACAT	TAGAACAATT	ACCACCGCGA	ATGGAGGGGA	480
	ACCCAGTCGA	AACCCACCGG	CATCCAATAG	TTTCCCCCAA	CNGCGAAANG	GCAGAAATGCA	540
	CCGCCCAATG	CTGCCCCAAC	GCCCACGGCC	ACCCTGACCC	CATTGACCTN	GAAGCCCTGG	600
	GGCNAAAACG	CATTTTACCC	CCCCCATTN	GGAAAAANTG	ACCGAATAAA	ANNCCCCCCN	660
	AAAAANAAAN	GGCCNCCCCC	AATTAATTTT	TNNCCNNGGG	CCCCNAACCC	CNGGGCANNAA	720
	AAAANNANTG	GGGGGGGGTT	TCCGNNNTTT	AAAAGG			

## 1230UP

	GATCTTCCGC	TCCACTTGGT	TGGGCTGGCG	CATGTCAAAG	GTTAGTAAAA	GCCCCGAATC	60
	GTGTACTGAC	GCGAACTTGT	TGGATCTTCC	GGAAGAACAC	AAGGACGTAT	CCGCGCCCAA	120
20	GGACGCGAAA	TCATAGGTCG	GCATCCACTT	TACATCACGG	ACGGAATCTG	AGCCTGAATT	180
	GAAATTCAGG	TCGCTGCGGT	TCACCTTGTA	AGAGTCCGAC	CGCAAGTCCC	ACACCTTGAT	240
	GCAGCCGTCC	TGGCCACCGC	TGATAAGGAG	ATGCGTCTGG	CCCATGTTGA	AGTCCACGCT	300
	GTTGATGGAA	CGCGAGTGCT	CCGACAGGGT	CCGTGATCAG	CGCGGAATCC	TTTGCCGACG	360
	CGCGGTTGAT	ATCGTAGATG	GAAACCGAGG	TCGACGTCCC	GCATATGGCG	ATGTAATTCT	420
	TGTGGTGGTG	GAACCCCGCC	CTTGACGTCC	CGAAATCCGT	GCTAATCTTG	CGCCATGTTT	480
25	CCGGCGCCAT	GCTGCTCGAA	GAACCTTCGT	CCCGCCCGCC	AAGGNTCCCC	NGTTGTTTNT	540
	GTTATTCGGT	GCACCTTGCT	GCTCCCTGTA	CCCTCCGTCN	AACTTGTTCA	GCCCCAATGG	600
	TCCTTCCCCN	CCCCNCAAC	CATGCCCCCT	ANCTTCTTTG	ATTTTTTTCC	AACCCCTGCCA	660
	CCCCCGGTTG	CCTGGAGGGG	GGGTACCCCC	CCCCAAAACC	CNCGCCCCCC	CAATTNTCCC	720
	ACGCCCNCCC	GAATTTGGTT	TNCCTNNGGG	NCCCCCNNGG	GNCCNNAAAA	CCTCCCCCTAA	780
30	AGNA						

## 1231RP

	GATCATCTGC	GTGAAGGGCG	ACAGAAGCCT	GGCGATGGAA	ACATTGGAAT	TGATGCATTA	60
	ACGCAAAACAC	ATGGGTCAAT	TCCTCAAACCT	CAACAGAAAG	GGGACGAAGC	TGCGCACACA	120
35	GTGCTGCAA	ATCTTTAGCC	GAGTTCTGAA	AATTCAAAGT	CGGTAGTTCT	CGTATGTTGA	180
	AGCCAGATCC	ATAAACTATC	TTCTCACTCG	CCGGATGCAA	AGTATCAAGG	AATAGGCGAC	240
	AATCGGTAAT	GATTGGCTCG	AGCTCACGCA	GATATTGGCG	CACCTCTGAT	ATCCGTGGGT	300
	TGTTTCGATG	ATGATGCACA	TGAATAAAAG	GAAGAAGCTT	CGAAAGAGGT	ACACGGCCCCG	360
	GGTAGCCGTG	TGATGAGAGC	TGTTAGTTTCG	GCTTCAACAT	CAGCAAGTTT	CTCTATAGGG	420
	GACGCAGGGT	CGTCAACATC	ATTTATTAGA	CACCTCCAGC	ATTTGTTCTT	GAAAAAAAGT	480
40	NGTGATGNA	CAATNGCNCC	CCCCCTTTT	GAAANGCCGG	AGAAAAATTC	CCTNNAAANAC	540
	NAATNTCTNG	GTNNAAANTGC	TTNNAAANCC	CCTTNAATTA	AACCCCTNNN	GCCNCAAAAA	600
	AATNTNTTAA	ANCCCTTTNA	ACNCCCCGGG	AAACANAAAC	CCCCCCCCCA	AAAAAAAACA	660
	NGTTTNTTCC	NCCCCCCCCC	CCCCCGANNT	TTTNNAAACC	TTTNNAAAT	CCCCCCCCCC	720
	CNAAAAANCC	CNCNAATTTT	TTTTTTAANC	C			

## 1231UP

	GATCGTCAGC	GTGCATCGAC	TTGGCATTGC	AAAGGGATGT	GATCCCTGAG	GGGAGGCTTG	60
	CAGCAGGCGC	GCTCCTTGTT	TCACATCATA	GGCTGTGAG	GCCGGACTGA	TTCAGCTCTC	120
5	AAGGCGAGCA	CCCTCCCAAC	GCCCAATAGG	GGCCCCCTCC	TGGGCTGTGC	ACGGGAATAC	180
	CTCAGACACT	GCGTTAAGAT	ATATGTATTT	AAGAGGGCAC	CAGCTGGCTA	TCAATTGCCC	240
	TCTCTGTCT	TGTTCCAACA	CCAGGCAAGT	ATCATGATGT	CTGCTGCAGG	AAAAATGTTT	300
	AAGAACAACG	GCCAGAAGGA	TGAGCGGAAG	AATGCCGGCC	AGAGAGAGGA	CGCCCACTAC	360
	AGGGTCGGCG	ATGAGCAGGG	CTTGGGCGCG	CAACAGCAGG	CTGACTTGGG	CGCCCCAGTA	420
	CCAGCAGGCG	CCACGCTCGC	AGCAGTTCTGA	CGACACTTGG	NGCTTCCCN	CATTGCGGCC	480
10	CCCCACCAAT	TGGGNCCCCA	GCAAAATNGG	CCCCNCNNCT	TTNATTTTNG	GGGCGAATGG	540
	GCCNAAACCT	ATCCCCAANT	TGNNGGNAAC	TCCCCCCCCA	GNANGAGAAC	NCATTTTTCG	600
	ATTGGAACAC	NCACCTTNNN	TTTGNNAACG	CCCCCCCCNA	AAAGCCANGG	GACTGTNTTT	660
	TTTNGAAAC	GNCCCCCTTT	NTGTCNCNNN	ANAAATTTT	CTANAAATTTG	CGNGGATTCC	720
	TCCCTTGGGG	CCATTCCNTT	TTTACCCTTT	TAACCCCCCC	CC		

15

## 1232RP

	GATCTTATTA	ATGAATTTTT	CCCCACGAAG	CTTGTGCAAT	TTTGATTCTA	TGCTTTGCAA	60
	GCACTCAACT	TGGGCTGTGG	TCATGCGAAA	CTAACACGCC	GCGAAACAGA	TACTGCCCCA	120
20	GCGTTAGCAC	TCGCTCTTTG	CGGTGCTACA	AACAAGTGTC	GAGCATTAGC	GTGTGACTTA	180
	TTTAGGGTTG	GAATATACAA	AAGTAAGCGC	TACATGCCGA	TATCTCTCTT	GTGTTGCTCT	240
	CTCTTACCTA	CATCTAGATG	TATTCAAGGA	ACTTCCCCGC	GAGATTACAG	GCCAAGGCCG	300
	TCCAGCCCGT	AAAGTGCTGC	ACCCGTTGAC	CTTTCCATCG	TTCTGGTTGT	ATTGTTCCGGT	360
	AACAAAAACC	ACCTTTCCCC	AAANTCNAAT	AATTGNTTCA	ACAGGTTGTT	CCCCCCATTG	420
	AAAGGGATAN	NCGTTTAAAC	CCGGNCNAAA	CAANNAANGG	GNNGNTTTTT	TTGGGCANAA	480
	ACCCCCCCCC	NAATTNAACC	GCGTGGGGCC	CTNCNCNAAA	TTNTTTTTTT	CCCCCCTTGG	540
25	GGNCCCCNCC	NAANAACCCC	CGNNGTTNNA	ATATATCCCN	CTTTTNCCAG	AAGNGANTCC	600
	CCCNNAACCC	GNNGGATNT	TTTTGTGNTT	TAAAAANNCC	CCCCCCCCCC	CCNGGGAGGG	660
	NNTTCCNCNC	CCCANCATTT	NNACCNAGGN	GAGTTTTTTT	TCCCTCCCGG	GGGAAAAAAC	720
	ANTGTNNNTT	TTNNNNCCNA	AAAAAA				

30

## 1232UP

	GATCAGTTTG	CCGTAATTGA	TACAAAAGGC	AAGTGGTGCG	TGGGCGACGT	TGCGAGGAGT	60
	AAAAAGAAGT	CCCGGCGACT	GCGCTTGTTA	AGGAAGTTTA	GCGGGACTAT	TTTTGACCCA	120
	GAGGAGTACT	CCAATTGGAA	TATGATAGAA	TGGTCAACATA	TTCACACAAG	ATTGCTTGTG	180
35	ATGAATAGGT	CAACTTTTAT	GGAAATTGAC	TTTGTAGACG	GATGGCAGCA	GGAAATTGTC	240
	CAAGCAAAGA	CGTGGTCTAA	CTTGCGCGAT	TTTAAACGCC	TTTCCGATGA	GAGCAGTGTC	300
	CTACTCACCT	GCAAAGAGAT	TATATTCTTA	GACCACAAGC	AGCAGGGAAC	AAAGAGGGCG	360
	CTATCTTGGA	AACACAATTG	GGATAGCAAA	GATTCATCTC	TAAAGCTTGC	TATACACATT	420
	TCTGGCAGCC	ATATGAAACA	ATATTTACAT	GCATTCTTAT	TTCCACCATG	ACTCCCTGCA	480
	GTGCTTATGT	GTCTTCTTTC	CCGGTCCGAA	AACACTTTTC	ATTTTTCCAG	CCATCCCCCC	540
40	GCTGNTTGTT	TTTTNCCATT	TACACNCCNG	NTTTTACCGA	AATTACCTCC	CCNTGTNCC	600
	NAGAAACCGA	GTTTNANAGA	ACCACACCCC	CTTTTCAATT	CCTANNTGTG	CCCGCCCCCC	660
	CCAGGGCGAG	AGTTTTGGGN	CCCCNTTTT	NTGNACCATN	TTNCCCCNCC	CCNCNAGGGT	720
	TCCCCACCNT	AAAANCCCTG	AAACCCCTTT	TCCCCCCAC	ATTTTNGGTN	GGGGATN	

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## 1233RP

	GATCACAGTG	CTGTGGGCAT	TGCTGCTCGT	CGTGCTCTTG	TGCCCCCAA	GCGCCGAAGT	60
	AGACAAGCTG	CCAGCAAGCA	CTGATTGGTA	CAGGAGCTTT	TTGTTACAGT	TCTTAAGCAG	120
	GTTTCGCGTC	GAGTCCGCGT	TGTTCAAAAC	AGCGCCCGGC	TGCACGCTCG	AGCTCGACTC	180
	CCCCGCCGGC	GACGAGCCCG	TGGAATACAC	CTCTGATCCC	GGGTCCGGCAT	CCCTCGCTCT	240
50	CGCAGTCCCC	CCGGAAGCAA	AAATTTCTC	CACGGATGTA	TTCCCGTGGT	TGCCCAGCTG	300
	CGCACCGGGC	GTACCCGAG	CGCTGTTGAC	ATTGGACGTG	ATATTCTCCA	TCAGCAGCTG	360
	CGAGCTGATG	CCCCCTCGGG	CGCCTGTCTT	GCTCGCATCT	GTAACGTCGT	CAGACCCCGA	420
	GTTTTGTTCT	GTCGTCCACG	AACGAGACGT	TCAACCATGT	GACGACGAG	GCGCGTTTGG	480
	CCTTCAACCAC	CNNATTTGGG	CCTTTCTGCT	GGAACNCCAA	CCCCGGGAAT	TTCCCAACCT	540
55	NTGATTCCCN	AANTGCCCGG	CCNCCNTCCC	AAATTANAAT	CCCCAATTGN	GNTTGAAATN	600

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GNCNAAATNA AACCCCNNTT TCCCCTNNTN CNNNNCCCNG GCCCNAANGA GCCGNTGGGG  
GNTTAAANNC CCCNACCCCC AAANTTATAC CCTTTTTTTG NNCCCNCCCC CCNNCCCTNT  
TTTTTINCCC NTCN

660  
720

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1233UP

5	GATCCAGCTT	CCATATAAGC	TCGTGTTTGC	GGTCGCGACC	TCTACAGAAG	TGGTGATATA	60
	TGATACTGTT	ACCACGAAAC	CCATTGCAGT	GGTGGGAAAT	TTGCATTACA	CCCCGCTAAC	120
	GGACCTCAGC	TGGTCTGACA	GCGGCCACCT	ACTCGTCGTG	TCATCAACAG	ACGGTTTCTG	180
	CTCCTATATC	TCAATGGAGG	ACAGCCTATT	TGGCGAGCCA	TACAGTTCCG	AGGCACAGCG	240
	GACGGATTCT	CTCATACCTT	CGACTCCAAA	AAGCAACATC	TTCAGGAACA	CCCTGCGGTC	300
	CAACCCGGTC	AACGTAAAGC	GGAAGCACTC	TGTAGGCGGC	CACAACGACT	CACCCATAAA	360
	GCGCGCTGCC	AAAAAATGTC	GCCGCTTTCC	CCTGTGGTCG	TCGATGAGGG	ATCTGCGCCG	420
	GCACACAACC	GCCTACTCCT	AGCAAAGATC	TCAAGCCTCC	GAAGGCGCAT	CCAACCCGTC	480
10	CTTGTTTAAT	GACAACAACG	GCGGCACCTA	GTATCCCCNC	ACGCCATCCT	ANAAGTTTNG	540
	ATTCCNNTAT	ACTNAAATAC	AAACCCGANA	ANCNNTTTTC	TTGTTNACAA	ACTTTTTTTT	600
	GACCTGCATC	ACACTATCCC	GGNGNGGTCA	TTCTTGCCGA	ATGCCCCCTC	CCCCTTANAA	660
	CNCCCNNTACN	TAAACCTTCC	CNCNTCCATA	TTTACTCATG	AATCNCNGCG	AANTCNCCTGC	720
	GGATCNCNCCA	NCTTTTGCCT	AGTNTTCCCC	TTTTTGTTCC	C		

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1235RP

50	GATCCTTGAG	AAGCCAGATA	ACGACGAGGA	CGAGGAGCCC	AGTGACGATG	AGGATGCCGA	60
	CGACTACGAC	TCGGATTCTC	CCCGGCCCGG	CGACAGCGGC	AGCGAACTCA	GAGACCCTCC	120
	TGCGCCGGCG	ACATTTCGCTA	CGGAAC TGCA	CGGATCCAGC	GTCTGGCCT	CCCCGTTGAC	180
	CTATTCCCTTG	CGCTCCGTCA	TCGTCCACTA	TGGCACACAC	AACTACGGAC	ACTACATTGC	240
	CTTCCGCAAG	TTCCGTGGTG	TGTGGTGCGG	CATCAGCGAC	GAAACAGCGT	ACATCGTCGA	300
	TGAAGCTGAG	GTCTTGTTCCA	CACCGGGCGT	TTTCATGTTG	TTCTACGATA	TGACTATGAC	360
	GAGGCGACCG	GGCAGTTGCG	TGACGACTTG	GGCTGCCCTAC	AGGAGCCAG	TCCGTGCTGT	420
	CAGATGGGGA	CGGAAGAATA	CGACTCATTG	ACCGGGTCCA	CCAAGACCTC	GATTCAACGA	480
55	NCCAGCTGTT	GCTCCCGCCA	ATAAACTTTG	TTTGGGGCTG	GCCGGCCATA	TNTNCTCCAT	540

GCATGTTTCAT GCCCCCACCG GACATGTTTG ATCCANATAC TTTTGTGTTN GTTNCCCCCT  
 TTCAGNGNTT CCCCCNAAGC AAGATTCTTA NNCTACTTGC CTNGTTGTTT CCNCCTGGTT  
 TGGNACCCCA AATTCCCTNTT NNCCNTTINT GGCCCANCCC NNGGNAAACC CNCCCTTTTT  
 TTTCAAACCA GGNTTNCCTT TTTNGCN

600  
 660  
 720

## 1235UP

GATCACACCC GTGTTCTTTT CAAAGGTGAC CTGCAACTTC TTGTTATTCA AGATGATAGT  
 CTCACGTGCC TTTGACACGC TAGCAGGGTA AAATACCGAC TCCTGCGCGT CAGCGTTTTT  
 TGCAGCCATG TTATCCCATT GCAAGGTGCC TATTGGGACC AAACCTTTCC CTCTGTGTT  
 CAAGGCCTCC AAAAGCTCTCT CTATGAACCG ATCTGCTAGC TGCACGACCT TGTTAAGCAT  
 TGGTATTGCT TCATATTTGT ATACCATTTT TATACATGTC CCGGGAAGGA CATCGTGGA  
 CTGGCATAAC AAGATATCTT CCCATAGAGC GTTAATATCA TTAACAGGGT ACGTGACTT  
 GTTAGGCGCT AGTAGCGAAA CCTTTGTGGC AATCCACTCC AAATCATGGA TCTTAACCTC  
 AGATAGTCTC ATCAACCGTT TAACGTCTGC CTGTGCTGTA TACGTGCCTC CTATGGAAAT  
 CAAAGTTACA ATCCGCCCCAT CCAAGTTGGC CAATGNGTTC CCANTGTCTG NCTTCNGCAT  
 AATATCACCG TAAAAACCGT TTANGGAATC CCCNACCCCC NACCTTNGGG AANAACATTG  
 CATTCCCGGT TAAAAATGAA CCGANACCCC CCATTGTGTC CACCNCCCCC TGTTTGAACC  
 CCNCCCCCGN CNCCGNACCC NNAAAAANAA CCGTTGCCNA ANGTTTCATTN AAAGTTTTGT  
 TCCCCCGGG TTTAAANCC NAATTTTNAN AAGCGTCTT TTTCCCGGGG GGGTTG

60  
 120  
 180  
 240  
 300  
 360  
 420  
 480  
 540  
 600  
 660  
 720

## 1236RP

GATCTCCCTC CGGTGCAAGT ACGTCGACTG TTTGAGACTC TGCAGGTCGT CTTTTGATAG  
 CTTGATGCC TTAGCTCCCA TGTCTACTAT AACGCTGTCC CGGGCCTCAG CTATGTGCGG  
 GCTGCCTATC TTAGTGCCTA ACTCTTGGAA GCGTGAGAGG CCATAAGCCA CGATCGGCGA  
 GCTGCTCAAA TTATGTCTCT TGAAAGCGGT TGCTGGGTCC ACTTTCCAG ACCCAAGGCT  
 ATGCCGTTA CCTGACCTCC GGTCCGGATG TGACGCTGGG AGGCGGTGCG ATGCCGGCCC  
 TCATGGCTGT CGGTGCGGAA GGACTATCTA CCAGGGACTT GGCTGCCTGC GCAATTTGCA  
 CTGCAGCTTG CAGTGGAGGT CTTGGCGAAG CTCACCGGCA GCGGCAGGCA GTTACAGCCA  
 TGGCACAGGC CAAGCCCCGC GAGTTGACCG GAGTTGGTTG CCAGATATTG GGCCGTCCAA  
 ATTCTGANTA GCCCTTTATA TNAGANCCCC NCCGTTGAAC CCCTAAGNTT TTTATGCGGA  
 TGTTTCGAAT TCNGCCCCCT GCGTTAACCC CCCCCGAACC CTTNCCCCCG GCAAAANCA  
 ATCTNCCCC NGTTCNAAAA ANCCGAACNC NNAAAATTTT AAAAGAGACA AATCANNNCA  
 CCCGNGAAAA AGAGCCCTNT CTTTGTGAGAA TTCCCGGGG GGGNGTAA TTNAACCTTT  
 GA

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 120  
 180  
 240  
 300  
 360  
 420  
 480  
 540  
 600  
 660  
 720

## 1236UP

GATCTTCGTC CGCTTGCGGT CAGGAAATTC AAGCGGGATG AGCTCTTGTT TCAGTTTACC  
 ATAAAAGAGC TGTTTTACAA GGTGGAATTG CTCGCCCTCT TCATCCAAGC TGAGCGGGAC  
 GGACGCACTC TCAATTTGGT AGAGGACGTT CCCAATGCAT TCCGTACAT CTTGCTGTCT  
 GCCAATCTCC AATGTGTTTT CTAGCTGGTC GGAACATAAT TTCGCAACAT AGGTGGAAGT  
 TTCAGGGCCT TCGGCCTCTG GACTCCCGAC CATGGTGATA TCTTTACCTG AGTCATCATT  
 CTCAACAGCC TGCCTATCCT CAAGCGGACC TGCGCTGGTG TTTTACCCN TTGGGNGGNN  
 GAANTCCAAT ANNCCCCCTT TCTGGGGTTC TTGGAAAGNA TTNGGANAAT TTNTTGGCCC  
 GGTTNTTACC NTTTNGANA GAGACCCTTG GNTNTTCNAN ACCNAAATNN TCCCNNGGGG  
 CNCCCGCNCG AATNTTTTTN TNTCCAAANT TTCCNAAANN CCNCTTTINT GCTTTTCCCC  
 NTTTTNGNGG NAGCGCCCCA GGGGGNCCCC CGAANTAATC NGGGGGNTGG AAAAAANAAA  
 NAATTTCCCA NAGGGGTNTT TTTTTTCCN TCNGAGAAGG GNGGTTANAA AAACCCATT  
 TTTCCCCCN NTAGANAACC CTTTTTNCNC CGGGGGNTCC NGCCGGGGGG ATTTNTGNGG  
 GNGCNTGNN NACCTCCCTT CCCCNCTATA NAAATNCCCC CGGGGGGGG TTTNTTTTTC  
 CCCNNAAN

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 120  
 180  
 240  
 300  
 360  
 420  
 480  
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 600  
 660  
 720  
 780

## 1238RP

	GATCACGGCA	ATGAAAAACT	ACGCAAAACGT	TACAGACTTT	GAGTGGTACA	TCGCCCTGCT	60
	TTCGGATCTC	TGCATAGTCT	CCCAGGACCT	GCAAGACAAG	ACCCCTCGCGC	AGAAACTGGG	120
5	TGAGCAAATT	AGAAACATCA	TGGTGAAGGT	TCCTGACCTG	CGGGATCGCA	CTTTGGCGCA	180
	GATTGTGCAG	CTGGTGAAGA	GCGAGGACAT	CACGGCCCGG	CTGCCCGGTG	TTCTGAAGGA	240
	GTGCATCTGG	TGCCTGGGCG	AGTATTCGTC	GTTGCTCGAC	AATAAGGATG	AGTATATTCT	300
	GCTATTGGCA	GAAAATTGCA	AATTATATGA	GCCTGAACTA	CAGCAAACTT	TGATCCCTGC	360
	CATTTTGAAG	ATTTATAGCA	ATTGGTGTA	CGAGTCGGTG	GTCGACACGG	GTCCGTATTA	420
	AATGGGTTAC	CGAGCGGATA	ATCACCCAC	TAGAAGATCT	AATAATCTCG	AAGAACTTCG	480
10	AAGTCCAGGA	GCGGTCTTCC	GAGGCTCTCG	AATTCTACCC	TTNTTTCTGG	ACNCCCCCTC	540
	CNAAATNNTC	TGNATCCCTA	NCNGCTGGCA	NCTTACNAAT	TCCTNGCCCA	NTTCTNCAAC	600
	CCTTTGAATT	NACCNCNNTN	CCNTCGGGCC	CCCAAAAANC	TCNNNNNAAA	CTNTTNTTCN	660
	ATGGGAACCC	CCTTTNCCCN	AAANGAAGCC	ANANNNNACC	GNAAAACNCN	CTTGAAGNGA	720
	TTTCCCGGAG	TTTTGANAAC	ATTTCNCCN	AATTTTCCGG	GACGGCCAAA	AAGGGTTTTN	780
	CAAAATTANTT	CGGGGGGGGA	AGGGGAANGG	GGGGGNGNNA			

## 1238UP

	GATCAGAAAC	GGCCGGCTGC	AAGAATGGAT	GGCGATGAGC	TTGAGCAGT	TGAGGCATCG	60
	CTTATGCAAA	AAAAGAAATT	CCTCAGATCA	CGTGACAAAG	TTTCGTGATC	TCTAAATGTC	120
20	GACGGTTGGG	CGAAATGTGC	CGTCCTCTGC	TATAAAATAT	AAACTAGTTT	CTCTACCACT	180
	AGACTGATTG	GGAATATCTA	AGCTTTCAC	TGATAGCAGC	AGGAGCACTT	CATAATCCAG	240
	TACCTTCTTT	GGCTTATCCA	CACTAGTCAT	CTCATCGAAA	ATGTCACAGC	CAGTGCAGAG	300
	AGCCGCCGCT	CAATCCTTGA	TATCCAAATA	TGTCAATAAG	GAAACGCTAA	AATACATGCT	360
	TACAACGCAC	TTCTGGGGCC	CCGTATCGAA	CTPTGGTATT	CCGATTGCTG	CGATTTATGA	420
	CTTGAAGAAG	GACCCGTAGT	TGATTTCCGG	CCCCATGACG	TTGGCGCTCG	TGGTATACTC	480
25	AGGTATTTTC	ATGCGTTACT	CGATGGCCGT	CACTCCCAAG	AACTACCTCT	TGTTTGGGTG	540
	CCCACTTTAT	AAACGAGTCC	CGCGCAACTC	GGACAGCGTT	CCCGCTGGCT	CAAGTTTCAA	600
	TTACTTCCGC	GAGAGCCCTG	CTGTCAAGGC	ACCCGAGAGA	CCCGCATAGG	TGCGTTTGCG	660
	TCCGCACACG	TTGCATTACA	GCGTCGACCA	CTACATAGAA	TATTATTAAG	CCGACTATCC	720
	TACACGTTTC	TAGAGCTAGT	CGAGATGCCT	TTGGCTGATA	CTGCTGCGTT	GGGCCAGGCC	780
30	GTATCTTGCT	CCTCCTGGCT	TTGCTGCGTT	GCGCAGCTCC	CANTTGNCCG	TTCNCGATNN	840
	TCCTGTGTCC	CGTATCCATT	GNCTAAATGT	CTCCC			

## 1240RP

	GATCTTAAAA	TAAGATAGAA	TGGTAATAAA	TATCATTCAG	GTACAATAGA	TGCTGGTGT	60
	ACTAAAGGAT	TACCTGGAAT	ATAATTATCA	GGATGTCCTA	AAGTATTAGG	TGAAAAGAAT	120
5	ACAAATAATG	AAAAGAAAAT	TATAAATACA	AATACTGTTA	CTAAATCTTT	AAAAATAAAA	180
	TAACCATGCA	TTGGTAATCT	ATCTAAATTA	CCTGTAATAC	CTAATGGATT	TGATGAACCA	240
	TGTACATGTA	ATAGCATTAA	ATGCATAATT	ACTATTGCTG	CAATAATAAA	TGGTACTAAA	300
	TAATGAAATA	GAAAGAATCT	TATAATAGTA	GGATTACTAA	CACTAAATGA	TCCTCATAAT	360
	CATAGTACAA	TATCATTTCC	AATAAATGGA	ATAGCACTAA	ATAAATTAGT	AATAACAGTA	420
	GCACCTCAAT	GTGACATTTG	TCCATATACT	AAACAATAAC	CTAAGAAAGC	TGCTGCTATA	480
10	GTTAAATATA	AGATAATAAC	ACCAACTGTT	CCATACAATA	ACTCTAGGTG	ATTTATAAGA	540
	ACCATATAT	AAACCTTTAC	CAATATGAAT	ATACATACAA	ATAAAGAAGA	ATGAAGCACC	600
	ATTAAGAATG	CATATATCTA	ATTATCCACC	TATTGTACTC	TCTCANAATA	GTTCCCTACCT	660
	GATGANAAGC	TATCCATATT	ANAAGAATAT	GCATACCCTA	AAAATACCGT	TANAATTGAA	720
	TACTAACATA	ACCTATAANA	CCNAATTCAC	CATAATAATG	AGAGGGTGAG	GNGAACCATA	780
	CNTACNATAC	TAATTTAATT	ATTGATTCT	TTCCCNTTTT	ATTATTAAAT	TTTAAT	
15							

## 1240UP

	GATCTAGAAT	TATTAAGTCA	ACTATTAACT	AATATCTATA	ATAATAATG	TTTATCATT	60
	AAATCATTAA	AGATAATTAT	TAATAAATTA	CCATTTAATA	ATGATATATT	ATTATCAAAA	120
20	AATTATGTTA	ATAAAATAAA	TAAATATAAT	TTACTAATTA	ATAATAATTT	AAATAATAAT	180
	AAAAAAGATT	TAATTAATTT	ATATACTTTA	GATAATAAAT	TATTAGATTT	AAGTATTCTT	240
	AATAATATAT	TATTAGGTAA	ATATTTAGTA	GGTAGTAATA	TCCAATTAAA	GGGTAGACTA	300
	TTAAATAGAA	ATATTACTAG	ACTAATAAAA	ATAAATATTA	TGAAAGGTAC	ATTTAATAAT	360
	TATATATATC	AATGAAGTAA	ATTAAATAAT	TTATATAAAT	TAAATTATAT	ATCACTTAAT	420
	ATTAATAAAC	TTAATAATCT	ATTTATTAAT	AAAAATGGTA	TATTTAATAT	TAAAATTAAA	480
25	TTAAATACATA	TTTAATAAAT	ATCTATAAGT	AATTTCTTAT	TTATTTTATA	ACATTTTAAA	540
	ATGTTTTATG	TTTAAATAGA	TAATAACAAT	TAAATAATAA	AAATTAAGAT	GCCACAAATA	600
	TTCCCATTTT	CCTTTATGAA	TCAATTACTT	ATGGTTTCCT	ATTTATTTTA	CTATTTTATC	660
	CTTCTATCTT	ATGNTTTT	CCTAAGAATT	TAANAATATA	TACTCCTAAA	TATATATTCC	720
	NAAATTATAA	TAGTTATTAA	ATTTTAATTA	ATCCANTATG	ATCCNTATTT	ATAAATATAT	780
30	AAGAANATTT	TAATATATAT	ATATGAATNT	TATATCNCN	TGAACCATTG	NAATNNATTA	840
	TAGTTTACAC	CCCCATANATC					

## 1241RP

	GATCTAAATA	TATATAATTT	AATTTATAAA	GATTAATATA	AACTTTTTTA	TTATAATATT	60
35	TAAGTATTAA	ATTATTTTAA	CTATTATTAT	CATTATTTAA	TAAATTAATT	ATTTGATTAT	120
	TAATACTTAT	TATATAATTA	TTATATAATT	TACTTAATTC	ATCATTATTA	ATATTTATAT	180
	AATTATAAAA	ATAATATTTA	ATATGAATAC	TATTTAGTCT	ATGTTCAAAT	TTTAAATTAG	240
	TTATTAAAAAT	ATTATTAGAT	ATTATTATTT	TCCTTAATAA	ATTATTAAAT	AGATTATCAA	300
	TAATTAATAT	ATTATTTTAT	AATTGTTTAT	TAAAATAATA	TATTTTATTA	TTATAAAGAT	360
40							
	TTAATTTATT	TAAATATTGT	AAATTATTAT	TTTTATTATA	ATATCTATTT	TTATAAATAT	420
	TATGTTGATT	TATATTATTT	AATCTTTTTA	TAAGAATTAT	TATTTAAAT	AATTTTAACT	480
	TTAATTTCTT	ATTATTAATT	TTTATATTAT	TTAATAAATT	ATATTTCAAT	TTATTTATTT	540
	ATTTATTTAA	TTAAATTAAT	TATTTAATTA	ATATTTTATC	ATTATTTAAT	TAATTAATAA	600
45	AATATTATAA	AGAATGTAGT	TAAAAATACT	TATAAAAGGA	TCCGAACCTA	TATTATTGTT	660
	TATGAGACAA	ATGCTTTAGC	CCATAAGCTA	TATAGTTTGA	CTATCATTTG	AGANTTGGGT	720
	NCNCCCCCTA	TGCTNNCATC	CTGNTGTCCC	CNCTAAANGA	ATTNTNTTNT	TNANANATGA	780
	AAAANTTATT	TATCAAAGAA	TTATAATTTT	TTAANAAGGG	GNANAAGGAA	AGACCCG	
50							
55							



## 1241UP

	GATCTGTATA	CTAGAGCTTA	TTTTACTTCA	GCTACTATAA	TTATTCTTAT	TCCTACTAGT	60
	ATTAAAGTAT	TTAGTTGATT	ACTAACTATT	TATGGTGGTT	CATTAAGATT	ACTAACACCA	120
5	ATATTATATC	TATTATCATT	TTTATTTTAA	TTTACTGTAG	GTGGTTTAAAC	TGGTGTAGTA	180
	TTAGCTAATC	TATCATTAGA	TGTAGCATTTC	CATGATACTT	ATTATGTAGT	ACTACATTTC	240
	CATTATGTAT	TAAGTTTAGG	TGCTGTATTTC	TCTATGTTTG	CTGGTTATTA	TTATTGAAGT	300
	CCTCTTGTTT	TAGGTTTAAA	TTATAATGAA	AAATTATCAC	AAATTCAATT	CTGATTAATT	360
	TTCTTAGGTC	TTAATATTAT	TTTCTTCCCT	ATGCATTTC	TAGGTATTAA	TGGTATACCA	420
	AGAAGAATTC	CTGATTATCC	TGATCTATTTC	CTAGGTTGAA	ATTTAGTATC	TTTATTGGT	480
10	TCTATAATAA	CTATTATATC	ATTAATGTTA	TTCTTTATA	TTATTTATGA	TCAATTAATA	540
	AATGGTTTAA	CTAATAAAGT	TAATAATAAA	TCTATTAAAT	ATATAAAACT	ACCCTGATTT	600
	TATTGAATCA	AATAATATTT	TCTTAATGAA	TACTACTAAA	TCACATCTAT	GATTATATG	660
	AATCACCAC	CTTAATCNAT	CAATTAAACC	CTCTAATCCA	ACTTTAAATA	NNCTTAATTA	720
	TAAATTANNA	ATAAATTTAG	TGGAANAATT	AATNGTAANC	AATNTTTTNA	NGGANTTTAT	780
15	CTCNNTCCAA	CCGAAACTAC	TTTTATCCTT	AANNAAAACC	TTTAATNAAT	GGACCNCANA	840
	NTCNNAACNN	GTTTTTC					

## 1242RP

	GATCACGTGC	TAAATGTCCG	GGTACATTAG	TGCACCCGTA	CACCGCATTA	CGACATTACG	60
20	ACGCTTCTTG	ACTAACCAGG	TTATCACGTG	TATATAGTTA	CATACGAACG	TCTGGTACAA	120
	GGAAAGAGCCG	GCCGGAAATC	CACCTCACCC	TTAAATTGCC	ACATTTTCATG	AGCATTTTACA	180
	ACAGAAGCAC	AGCTGTAAAC	GTTTCCTCGAA	CTCGTGAAGT	TTCATATGTG	TCCTTAAGGG	240
	CCCTTGATGT	TGCAGTTTCAA	GCTAGTTCTG	TGGGAGACT	CGTCGGTCGG	TAAGTCGTCA	300
	ATTGTTTCATC	GCTTCGTGAA	GGATTTCGTT	GATGAGTTCC	GGGAAAGCAC	AATCGGCGCC	360
25	GCATTTCTGT	CCCGTACCAT	CAAGCTGGCG	GACCACGACG	ACGCAATGAT	CAATTTGAGA	420
	TCTGGGACAC	CGCGGGACAG	GAGCGGTACA	AATCGCTGGC	TCCGATGTAT	TACAGGAATG	480
	CGAAGCGCCG	GTTCGGTGGT	TTATGACGTT	GACACAGGAG	GATTCCTCTAG	CAAAGGCACA	540
	GAGCTGGGTT	GAACGAATTA	AGAGCAGGTT	GGTGACGAGA	ATTCTGGTAT	CTTCCCTGTT	600
	GGGCATAATT	GATTNNGGGG	NGAGGANCGG	AACCNAGGTG	ATTGACNCGA	GAACNCAGGC	660
30	TCCCCAAACC	CNNGGTGANT	TCCCCNAGGT	TTNNNCCAAA	CCGGCCGGTT	NCCGGATTTN	720
	TTCCNNGGAT	TGGGGGAANN	CTAAAACNGG	GCNATTCENT	NGGGGCCCCC	CCGCNTCCCC	780
	ANNTTCCNTT	CAAGNCCCCC	CAAAGAACAC	CCTGGGGNTT	ACCCCCTCCC	N	

## 1242UP

35	GATCTTGTCG	ATTGTGAAGG	AGGAGACGAA	AAACGCTACC	ATCAGTGTTG	CCGTGAGAGAA	60
	CAAGCAGCTC	ATCCCAATTCA	TTTCGCTGGC	GGACGTGGAG	ATTTCCGAGG	ACGTGACTGT	120
	GAAGGCCTTC	CCTAACGGCT	CTGAGAAGAT	CGTTCTTATG	GGGCCACGCG	ATGAAGCGAA	180
	GGAAGCAAAG	GTGAATGTTT	AGAAITACTT	GAACACTTTA	GCAAGCAAGG	TATCTGAGAA	240
	AAAGATTTCC	ATTCCCTCGCA	AGTTCCAGCC	TCTGATCGAT	GCAGAGGATG	TCAGGGAGAA	300
40	ATACAAGGTC	TCCGTTATCT	TCCCAACCGC	CCTTGGTGAT	GATACTGTGT	CGTTCTACGG	360
	ACTGTCCGCT	AATCTTGATG	ACGCGATCGC	ATATGCTCGC	CAGTCGTCTA	AGCAGTACAT	420
	GGTAGAATCT	TTGGAGGTAT	CCAAGGCTCA	CGGAAAGAAT	GTCGCTCATG	CAAAGAATTT	480
	AATGTTCTAC	TTCGCCAGTT	ACGAACCTCT	CCAAGGATAT	TAAGGAATTC	GTTCCTAAGGG	540
	ANNTGAANTT	TTGTNCTACC	CACCTCCGGA	GGGATTTGCC	CGNTTTAAAN	AAGNTTTTNA	600
	ATNCACANTT	TTTCCAAAGG	GNGAATTTTG	GGGNACAAAA	AAAANTGTNT	TCCCCGNCNA	660
45	TNCCTTATTT	NTTAACNACC	CCCCCTCCCC	NGTTTCCNCC	GNTGAANACC	NAANTATNAC	720
	CCTTTCCCCC	AGNGATTTAC	CNNGGCCNTN	CAGGGGANTC	CNCTTTTNTN	CTCCGGANTC	780
	AANAAAGGGA	AANACCNGNN	GCTTTTGGCA	GGNTGANAAA	AAATCCNCCC	CCCCCAGAGG	840
	TAAGANCCNN	GNAAGNGNG	CCCNNTTGGG	GAAATNCCC			

## 1243RP

50	GATCGCTAAT	CCCAGAGTTT	GTTTTGAAGT	CTGTGATCAG	TTGGTTCTCC	ACATCTTTGA	60
	GAATTCCTAAT	AGCCTCCGAT	GGCAGTTCC	CCAAATCCAT	TCCGACCTGG	GCAGACTGTA	120
	TCTTTAGAGA	GTAATTTTCC	ACACACAAAG	AGTCAATCTT	GTCCTTGAACA	TCGTCAATTC	180
	TATACTTCAG	TACATCGTTC	ATGTTTGGTA	GATTTCACTGA	GCTTTTGAGT	GCGCCTTTTC	240
55	CTAGCGCCGA	AAGGTTCCCC	GCTTCATTCC	ATGAGAAGCC	TAGAAGTGAC	ATCATGGCGT	300

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	GGCAGCATGT	CTTCCGCAAC	TGTGACAACC	AATAATTCAA	GAATGCGGGG	CCTAGATAAC	360
	AGGGCCCTTG	CCCGTCTGAG	TCATAGCCTG	AAGCCTCCAA	GAAGGATTTC	CATAGGTTAA	420
	CATAATTATC	ACGCTCTATC	GGTGAGAATT	GAAGTTGGAT	TAAGTAATGA	TGCTGCTTTG	480
5	GGATTTTAAAT	CTGATATTCG	ACATCATTTCT	TTGTATGACG	GATACAAAGG	TTGAAACGTG	540
	GGATGATATC	AAGAAGTTCT	CTTGCGGTGA	AAGTCACACC	GTTGACACGT	TGGAGCTTTG	600
	CGAATTTGTT	GCGGGATCTA	GATGCATCCG	ATTGTTGCCC	AGTTCCCTGG	TATTCTGGCA	660
	GACTGTGTTC	GATATACTTT	GGAGATCCCT	TGAAGGGATG	CACTGCCATT	AGAAATACAC	720
	CTTGAATCCN	CTAGTGAATG	ATAGGTNTAC	CCGAACCCCC	ANTTTTGATA	CCCNGCAGAG	780
	TTTGTNCATC	GGCCCCCTTCN	NCTTCCTGCC	CACATTGCCT	CCCNATTTTA	TCCTGAAATG	840
10	CTTA						
15							
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## 1243UP

	GATCTCGTCC	CACCACGGGC	GCAGGAACGT	GTACTGGCCT	TTTGAGATCA	ACTCTGTCAG	60
	GACGTCGATC	TTTTTCGTCT	AAAAAGGCGG	GAAGCCGCAC	AACACGGTGT	ATAGGACGCA	120
5	GCCGATCCCC	CACATGTCTGA	CCTTCATGGA	GTAGCGTTCT	TCCTTCACCA	CCTCGGGGCGC	180
	GGTGTACCCG	ACAGTCCCGC	ACGGCGTCTG	GGTGTGGTA	GCATAAATTT	GCTTCGAGAG	240
	TCCGAAGTCT	GCGAGCTTTA	TCACACCGAT	CCCGCCGCC	CCGATGCCAG	GTCGGAACAG	300
	GCCCTCGTCT	TGTTTTGTCT	TTGGGTCTCT	CGACTGTCTC	AGCTGCTGGC	GCTTGCTGGG	360
	TATAAAATCA	ATTGGGGAGA	ACAGCAAGTT	TTCTGGCTTG	ATATCCCGGT	GGACAATGCC	420
	AAGCGAGTGC	ATGTGTTTTA	CCGCGAGTGC	CAGCTGCCTG	ATTACATGTC	TAGAAAGGTC	480
10	CTCCGAAAAA	TAAGTGAGTC	GCACGATTTT	TCCAAAAATC	TCCCCCCCCG	GCAAGCAGCT	540
	CCTGGACTAT	GAAGTAGTAT	GACTCGGTCT	CCCTGGAAGT	CGATAAACGT	CACAATGTTT	600
	TGCGCCGAGG	ACACCGCCTT	GTGGATGGTG	ATCTCCTTCA	GAACTGCTCT	CGCGATGTCG	660
	CCTGTTTTCG	CGGCTCCNCC	CNCTTNTNCC	GGGCCCCCCC	NGGTGCCCCC	ATCGTTAANA	720
	GGNNCCTTTT	GCTGATCNCC	TTGACGGCNC	CGTTTNTTAC	NGNCNAAGTN	CCCTTTCCGN	780
	CGNCCTTCAG	CGGNCCNCCG	ANNCCNCCGN	AAACCCCNCC	CNATTTNCCC	NAACTTNTCC	840
15	CNCAANCCAA	GNNCCGAANC	CCCCC				

## 1244RP

	GATCCTGCCT	TATCACGAGC	GCCATCCGAA	CTTCCCCCGG	GATGTCGTTG	AGAGGTAGCG	60
	AGCTCACCTC	CACAACTTCC	TCATCTGAAT	CGTCTTCGTA	TGTACTATCT	AGCTCTTCAG	120
20	CGTCGCGCGA	TGCAGATTCC	GCCCTGTCTT	TCACCTGTTT	CAGCACCGCC	TGTGCGTTAA	180
	GCTCAGAGAG	GCAGGCATGT	GTCGCACCCC	CGTATATCTG	GCCCAGGTAA	TACCCCGTGG	240
	CCAGCGAAGC	CATCGTAACG	CTCAGTATGA	ACGGTAAGTT	GATACCTGCC	ATCCTAGTTT	300
	CTGTTTGGTA	TTCTGCTATG	TGAGTGCAGC	AGCCAAGTTG	GTTGAAAATT	CCTTCAAGCT	360
	GACAATCGCT	GGTCCATGCG	GCAGTTC AAC	ACAGCAAAAC	TCAGAGAGAG	GTATAAACGC	420
25	CATATATAGG	AGGAGACTAC	TCTATTCACT	GCCTATCTTT	TCAGCCCACA	GTTCTCTGTC	480
	CTGCAGAATT	GTGTTGTGAT	TCCGCCAGCA	TTTTGTTCAT	CGTCTCGACA	TATTCGTCCG	540
	TTATGATTTC	GAATCCGTGG	AACATTCGCG	CGCCAGCCTG	TTAGATTAGG	CCACCCGCC	600
	TTGTGTAGAC	CATAGTCCGC	GAGTGCAGAT	ACAGGTTATC	CNTCGAACAC	CATCCGTAGA	660
	ACCAGTGGCT	ACNCTCCGGN	GTTAAACCCC	TACGCTNCCC	TTCCACTNTC	CGATAGTCCA	720
	TACGCGGAAT	TTGGGGGGCC	AAAAAAGTGC	CCNGCAGGAA	CNCAAAACGAA	GNNTC AACGC	780
30	CNTGTNTTGG	GCNGGTGCCN	TTTCCNCAAA	NCAGTGCCTA	NTTNTAANCC	NGCCNCTTAT	840
	TNTCCCCCAT	T					

## 1244UP

	GATCAATCTG	ACAGTTGGAT	TGATACCAGG	TGCTATCTCC	TTATCAGCCT	TTACAGTGAC	60
	GAAGGAGGGA	TTGGATTGGG	GAATGAGAGAA	TAAAGATATT	TTTGATCCAT	CACCAGAAGG	120
	ATTTGATCCC	TCTTTCAGTG	AGCATGCCCA	ACTTTTACTC	TCGGAACGTA	TAATGGGAAA	180
	CTTTCTCGTT	CCAAAGTCTG	GCATCTGGAA	TTATGCAATTT	ATGGGTGCTG	GATTTAACAG	240
	AGAGCTACGT	TACGAGCTAT	CTCTCGACAT	ACCACTCGGA	TTTTATGATG	AACAGCACCG	300
40	TGCAACGCAT	TTTCTACAAT	TCAACGAAGT	GGCAGCTGAC	GATACTTTGG	AAGCAGAACA	360
	GGAAGATTTA	TTCTCCTAAG	TACATATTTAA	GGATAGAGCC	AAACTTGCAA	CTAGCTTCAG	420
	TTGCGTATGA	ATCCCATATA	TGTATATATC	AATACACGGG	CCACTCATGG	CTGGTGACCC	480
	ATTTAAGCAA	ATACCATATT	TTTTAATGTT	GCGGTGATTT	TATAATCTCG	ATATCATGAT	540
	TTTATTTATA	GGAGATGACT	TTTCCCTCTA	CAACGCCACA	TTATAGAAGA	CCGTCAATGC	600
	AGCACCCAGG	CTGAAGCCAG	AACGGAAATG	TTGGAACCAG	AACAGGCAGG	TTTGAATAGC	660
45	TCGACATATG	AACCTCCCCA	GAACATGTTT	TTTTTGAACA	TCNAAATGANT	TTCTGCCAAA	720
	AACANGAAAA	TGGACNCCNN	GCATCATTTCA	AAAAAAAACCN	TCCTTGAACC	TGACAAAAAA	780
	TATGCACCCN	GATTTTTTTGA	TCACGGANNG	TTTTCTTTTAC	NCCAAATTAAA	TAGGNCCCCC	840
	NGAGATTTTTT	ACACCCNCC					

## 1245RP

	GATCAAAAAAC	AGAGTACCCT	CCGCACGAAC	TTCCCATATG	AGGCCCAGAG	AGAACAAACAT	60
	CGCCGATCAC	CTATATCAAC	AACGGAGACC	TTGGTCTGCC	GAGAACGTCA	CAGCTTATCT	120
	TATTATCGAT	CGAATGGATG	TTGGAAAGAA	GATACAAAAT	AACGCATAAT	TGCTGAATAT	180
55	ATTGCACGCT	TCTAACGCAA	ACGACGAGCC	TCACGCTCAG	ATTCCATCAA	GACCAAGATG	240

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	TCGTTCTCTC	TAACTGGGCC	CTTGACGTTT	CTGACAATGG	TTCTGGAAGT	GTCGTCCAAG	300
	AACTCAACGC	GGACCTGGGT	GACACCACCA	CGAGAACCGG	TTCTACCTAG	AACCTTGATA	360
	ACCTTAGCTA	GAGTGACTGG	GGTCTTGGAG	TCCATTTTGA	TCTATTGCTT	CTTGGATATA	420
	AAATATCTAG	TAAAAAGTGC	TGAATAGGTG	AGAGGAAGAT	ATCATGAACA	GGCGGTTTTT	480
5	TTTGATGCCC	CGAAAAATTT	TTCAGGTCTG	CGATGCCCAT	CGCAGGTGAA	ATGTGCTTGG	540
	GTTCTTGAAA	AATCACATCA	TACGATAACT	ATGCGTGAC	CCAAAGGCCT	TGGCAGCAGC	600
	GAAGTGCGCG	AAGGTTAGCC	AGCCCAGAAC	GAAACCTGAG	AACAGGTTAA	GCTCAGGTGA	660
	ATTGTTTGCT	TCTATTGCCT	TACAGTTCAT	CTTCCGGTAA	TTGCAGTATC	CGTTGATTCC	720
	CCNCAGCTGA	CCAGCCGTTN	ATTCCCCTTT	GAACTTTCAG	AGNTCNTGAA	ACCCTNGTNT	780
10	TTTCAACCCN	TGACACNTAT	ATCNCCCCCT	TATATGACTT	CCGTCNATNC	CCG	
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## 1245UP

	GATCCGGGTA	ATACAAACGCC	TCGGACCCCT	CGGCGGGCTAA	CGAGAAAATC	GCGCTAAGCT	60
	TCCAGCCTAA	TCATAATAAA	AGGGGCATTG	GTGGAAGCTT	TCTGGTACTT	ACGCGAGTAA	120
5	ACAAAAGGCG	CAAGGACGTT	TCAGAAGAAG	CCAGAAGCAG	CAATGAGCGA	GATCAACTCG	180
	ATCATTACAC	GAGTGAATGT	ACTGGTCTCA	AAACTGCCCA	AAGAGAAGGA	TGCAGGCCGTG	240
	GAGAAAGAGT	GCGCGCTGAT	CAAGTTTCGGC	GGCATGGTAT	CTAACCAGCGA	ATCGGGCCTG	300
	TTGTTTGGAG	AACTGGCGCA	GCAGATGGAT	CGCACAGCGG	TGCTACGGCA	GCCATGGATT	360
	GTCGAGTTTG	TTGTGCGCTT	GGGCAACGAG	CTATGCCCGG	GTGGCGAGGT	GGGCGAGAGC	420
	TTCTGGGGCA	AGATATTGGT	TCCGTTGGAT	GGACAGACCC	CGTTATTGAC	AGTTACTAAC	480
10	AAGAATCCAG	GGTGCGAAGT	TTTCGCGTAA	TGTTGCGGTC	CATGGCCGGT	TGGTGGAGGC	540
	GCTGCTGGAC	GGCGCCTTGT	CGCGTACGGC	TCCCTGTGCG	TGGCAGAATA	TGGCGTTGTT	600
	GCTCCAGCTG	TCCTATNNAC	CNNCCGGATT	NTCCGGAAGT	TGNTGNCCCC	CCTTTACCCC	660
	CCTCCTNNCN	AGNATGGTTG	GNGACCNTTT	GNMCGNTTNC	CAACTTCCTT	NTNCCCCNCT	720
	TTTTTTGNAC	NTTGAANCNA	TTTTTCCCCC	TTNAANTCAA	CCNACCNGTT	NTNNCAACCC	780
	CCCCCCCCTT	TGGGAAAANN	AGNAAAAAAN	ACCTTTTCCA	CCCNGGATNC	CCTTTGGNCA	840
15	NCTGGAACNG	NNNTNTTCNC	CCTC				

## 1246RP

	GATCAACAAT	GATTGTGGCG	ACGGGCGGGC	GGGCGTTCAA	ATTCTACGAC	GTGCTGCTGT	60
	CGGAATTTCC	GGGCGTGTCA	GATATCCTCC	GGCTGGACGA	GATGGACTGC	CTGACGAAGG	120
	GGTTGGACTT	CTTCATCCAC	AAGGTGCCCT	ACGAGGTGTT	CACATACAAC	GACCTGGACG	180
	GCGAAGGCAC	GGTGGATGCG	GTGGCGGATG	ATGAGATGTA	CCCGTACATG	CTAGTGAACA	240
	TAGGATCCGG	GGTCTCGATT	CTGAAGGTGG	AGTCGCCCCA	CGAGTGCATG	CGTGTGGGCG	300
	GCTCGTCATT	GGGCGGCGGC	ACGTTGTGGG	GACTACTGTC	GCTAATTACT	GGGGCGAAGA	360
	CGTACGACGA	GATGCTGGCC	TGGGCAAAAC	AGGGCAATAA	CGCGAACGTG	GACATGTTGG	420
25	TAGGCGACAT	ATACGGCACC	GACTATGCGA	AGATCGGCCT	GAAATCCAGT	AATATTGCAT	480
	CGTCGTTCCG	GAAGGTCTTC	CAACGGGAGA	GCGTCACCGC	GCCCCTCGGC	GGGCCTGACT	540
	TCGGCGTCTG	CGACCTCGAC	GTGTGAGATC	CGAGATTCCA	AATGAGAAAT	CCNNACGCC	600
	GAATNTTCCC	ATCCCTCMTG	TACCCATCTC	CAACAAATCG	GCCAAATGCT	TNCTGCAGCC	660
	AAATCCCCAA	CTCCAAAAAA	NNTCTTTGCG	GTCNTTATNT	CCCCGCCTTT	TACCCCTGTA	720
	CCCTTTACCC	CCCCCTAACT	CNGGTCNAAN	GNTTTTAAAC	NCCNCCCCC	TNAGGNTTAA	780
30	GGTNNTGGCC	CCNNGGCCCT	TNTTGCCCCA	AAAATTTCCC	NNCGNTTCTN		

## 1246UP

	GATCGTAGAG	CGTGAGACGG	CACCGGCGGA	GGCGCCAGCG	CCGGACGGTG	TGCAGCCACG	60
	GGGGTTTCCT	GAGCTGTACC	GCCCCGCAGC	GATATCTAGC	TGGCGCCAAC	GGCTGCAGAA	120
	GAAGAAATGG	CAGCGCAGGC	CGCCCCGCGC	GGCCCTCGCC	GCAAGCGAGG	CGGAGAAGAT	180
	CCACAAGGAA	AACATGGCGT	ACATCGAGGG	GCTGTGCGAG	GAGCAGCGGA	CGGCAGAGCG	240
	CCGCGAGCTG	TTAGAGAGCC	TGGACCCCAA	GGTCGTGCAG	GCGTTGTACC	GTCGGTTGGA	300
	TGCACGTGCA	GCAGCGGACG	GAACGGCGCC	CTTAGTGGCG	GAAGTCGAGG	GAGCGGCAGG	360
	CACGTGGGTG	GGCGGCACCC	GCGAGGAGCC	GATGATGCCG	CGCCTGGATG	ACGCGACCGT	420
40	CGACGCCGCG	CTAGGCGCGC	CACAGGCTTC	GATGCCAGAG	GCCGCGCCCA	CGTACGACCT	480
	GCCAGCGCCG	CTGGAGGATG	CGGACGACAT	CGCGCCCCAG	GAATACCAGT	TCATCAGCAG	540
	ATGGACCATA	TGAAGGACAG	GACTTGCTAC	GAGATATCCA	CTTCCTCCGC	AATGAGACTG	600
	TGGCGCCCG	ACTGGACATC	AACGACCCCA	ACTTTATGAG	CAGCTGCACG	AGAATACTTC	660
	CGGATNTTCC	GAAAGAAANA	AATAACTNGA	ATGGATGAAG	GCCACTGAAC	CCTGACACTC	720
	TTCTNCTAAC	TCNCCGATTT	TGCCGAATGC	CCTCCAACCT	AGGGCCCCATG	TCCCCCCCCC	780
45	CCGGAATTTN	NTCCCCNNAA	CNGCCTCNNC	CCTTCGAAAA	CCCCCTTTTN	CCGGCNTTCC	840
	TCCCATTTGC	ACNTTCCCCA	C				

## 1247RP

	GATCTGGCCG	CGCAGCTGCG	GCCTCGTATT	GCTCCCCGTC	GTTACTGTGG	CGCCGCCGGC	60
	GTGTCTTTAT	CGGCATCGCG	TACGCGTCAC	TAAGCCCCCT	CAGGACGGGC	ACAAAAAGCG	120
	CAGGGCGCTC	ATAGAGCACC	ACAGCGTCTG	GGTCGGGAAG	CACGTGCATC	CGCGGCGTGT	180
	GCTTGCTCAC	CGCCTCGTGC	GCCTTGCCCC	GCTCTGCCAC	CGGCGCAGCC	GTTGCAGCCC	240
55	CGCGGGCCGC	GGGCGCCCTG	TGCACTGTAG	CGGCACGGCC	GCGGCGGACG	CTCCGCTTGC	300

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5 GGACCGCCTT GATGACCCGC TTTGCGCCCG GCCCGCGCGC GCTCGCCCGA GCGAGCGCCA 360  
 GCGCCCGCTG CACACGCATC AGCATCCCAT CCACCGCTTT CCTGTGCTCT TCCACCACGC 420  
 TGTCGCCTGA AGCAGACTCT GCGCTATCTC CTCCGCTCTG GACGAAAGGC CTCGTGCTG 480  
 CTCGACTCGC TCTGCCCGTA CTTCGGTCGA AGTACGCGC CAGTGCCGCC GCGCGCTTCG 540  
 CCTCCGCGGC CGCCGGCGGC GCGAAGGGCA CGTTAGGGCG CCGAGCCGCC GTCAGACCC 600  
 CCTCATCGAA TCCGAACCGC TCGCGCCGTC GCGCCAATCG CCCACGGAAC CANCCCCCG 660  
 GGGGGTTNCG NGGCCCGGCC GGCCCCCTCC TTTTNAAAAC GACNACCNT TGNAANCCG 720  
 TTACCCNCN CNNTTCAAAC NCCNGGAAAA ATTTTCGN CN ANNNNNNNNN CCCCCCCCCT 780  
 NTNCTNNGAA ANAANGNCCN GGCCCTNNGG

## 1249RP

15 GATCATGCAA CATTTCTTCT TTTCCCGCTT TCTGCCTGTG CCGGACGGTG TGTCCCCGCC 60  
 CCGCACCTCT GAGGAAGAGC TTGCGGACTG CAGCGAGCAT GCCCACAGTA CCTGGGGCGA 120  
 CTGCTGCGGC ATTCCGATAC CCAGCGCGGT GGCCGCCCTC GAGGCCACTC GCAAGCATT 180  
 TAAACCACTT CCATTGCAAT GAATCAAATT ATATATACCA TTAAGTAGAG CTACCATGCG 240  
 AACCTTAGCT GGGACGCAGT AAAGATTGGC GGTTCACAGA TCAGCTTCTC GGGGTGATC 300  
 20 GATCGCCTTT TCTTCGCTAT CAGCTTCTCG TACCTTAGCA GCACGTCTC GTTCAGGTAC 360  
 AAGATGTGCT GGCCCTTGTA ATATCGCAGT ATGTTAAGAG CCTTGGCTGT GTGCAGTATG 420  
 TCTGTAGTCG TGAGCGATGT CATGCTACTG ATTTTCATCGA TCGTGATCTC GGTGCCGTTT 480  
 TCGACTAGCA GCTTGATCAG GGTATCGGAC CAATAGGCTC TGTAGAGAGC AGCCCAAGAT 540  
 CAGAGAGCGG CTTCTCCGGC ACCCAACTTG TTCTCCTTCT TAGAGAGCTC CATACGAAAC 600  
 TCAATCAGCA GCCTGCCGTA CCCCATCCGC TGGTACTGAG GGAGCGTCCA GAATACACGC 660  
 CACATTGTAC CCGTCCGCCA NTCCCTTCCN TTGGANAATN CCCACCAAGT NGGTGCCCCA 720  
 25 CTCACCTCCC TGTGTCTTG CANTAAAAA AAGGTCAANT TCCTATNACT CNTGTGNTCC 780  
 AAAAACTTT GANAAAGNTN GTTGCNACC ACTTCCTNNT NCCCCGTCAA TTCAAAT

## 1249UP

30 GACCTGCCGA TGGACNGCCG TTGGCAGGTG ACTGCCCTAC GGTCTTTAGT CCCCAGAAAG 60  
 CGGATGGCCT TTGTCGGCAC ACGCAAGAAC TTGGCAATGA TGTGACCAC GTCCATGGTG 120  
 TCCTTATTCT CTTTGTACAT TGTGAAGTGC ACGCAGTTCT TGGAGGGGCC GTACCCAG 180  
 TTAATGACAC CGTTCTCGTC TCTTGTCTGC TCCACATAGT CCTCTTTGCT GACTCTGGTT 240  
 TTACGGTTGG CCAGGGCAAT CTGGAATGTG TTGGACGCCG AAGTGACCGA TTCAAGCTCA 300  
 35 TTGTTGAACG CCTTTCGTAG CAGCTGGTGG ATCTTCGTCC GTGCAGCTTT GTCGTCAAAG 360  
 CTCCTGGTGG TTTCCATTTT CGTGACGTTT CTGTACACGG CCTCAATCTG CTGCATGTCC 420  
 TCCTCGCCCA GTAGCTCTAC CAGCTGGTTC CGCAGCTCTG CCTCCACCGC GTGGTTGTGG 480  
 CGCCGTTCCG GCTCTTCAGC CTGCTGTGCC TTCACCTGGT CCGCAGAGGT TTGGGTTTAG 540  
 CAGGCATTTT GAACCCATTG TCCCAGCAAGT ACACCACTGT TCCATCCTTC TGGATCTCAT 600  
 TGACCATGAA GTCGGAATAG CGCTGCTTGA TCTGCCCGCT AAACCTGGT ACTCTGCTGA 660  
 40 GAGGTACTCT GTGATCCAAC GTCGATTCTT TGAGTCCATC GGTCTCCGNT TTGGCCCCCT 720

45 NCCNCAAAAG TTCCTGGCTG CTCCNNANCC GCTCTNTAAT CCCCCGAAAN TCTGTACNNT 780  
 TCNCNATTTT CNNTNTNNCC TACCTNAACC CTTGTTNAAC CTTCCACCCN ANAANTCATA 840  
 AATATTCCCC NCC

## 1250RP

	ATCTTAATTT	AAAATTTTAA	TTAACTATTT	ATAATTTAGA	AATATATAAT	CTAGAGATAT	60
	ATAATCTTAA	AATCATAGGT	AAAAATACAT	AAGATAGTAA	GAATAAAATT	AGTAAAAATA	120
5	ATAGAAAACC	ATAAGTTAAT	TGATTCATAA	AGAAAAATGG	AATTATTTGT	GGCATCTTAA	180
	TTTTTATTAT	TTAATTGATT	ATTATCTATT	TAACATAAAA	CATTTTAAAA	TGTTATAAAA	240
	TAAATAAGAA	ATTACTTATA	GAATATTTAT	TAAATAGTAT	TTAATTTAAT	TTTAATATTA	300
	AATATACCAT	TTTTATTAAAT	AAATAGATTA	TTAAGTTTAT	TAATATTAAG	TGATATATAA	360
	TTTAATTTAT	ATAAAATTAT	TAATTTACTT	CATTGATATA	TATAATTATT	AAATGTACCT	420
	TTTATAATAT	TTATTTTTAT	TAGTCTAGTA	ATATTTCTAT	TTAATAGTCT	ACCCTTTAAT	480
10	TGGATATTAC	TACCTACTAA	ATATTTACCT	AATAATATAT	TATTAAGAAAT	ACTTAAATCT	540
	AATAATTTAT	TATCTAAAAGT	ATATAAATTA	ATTAAATCCT	TTTTTATTAT	TATTTAATTA	600
	TTATTAATTA	GTAAATTATA	TTTATTATTT	TATTAACATA	ATTTTTTGAT	AATAATATAT	660
	CCATATTAAA	TGGTAATTTA	TTAATAATAT	CCTTTAATGA	TTTNATGATA	ACCNTATTAT	720
	TATGANATTA	GTTAATAGTG	ACCTTAATAT	CCCNATCCNA	ATATATNTAT	TTATTTNTAA	780
	NAACANANAA	CTTCCTTATNN	CATATTTANT	TTNANTATTN	ACCNTTNCCN	NNNT	

## 1250UP

	GATCAAAATT	TCAACAATTT	CCATTTTCATT	TAGTACTACC	ATCACCATGA	CCAATTGTTA	60
	CATCATTTAG	TTTTATTAGGT	TTACTATTAA	CTTTAGCTTT	TACTATACAT	GGTATTATTG	120
20	GTAATATTTA	TCCTTTTATTA	TTATCTTTAT	TAGTAGTTTT	ATTACTAATA	ACTTTATGAT	180
	TTAGAGATAT	TGTAGCTGAA	CTTACTTATT	TAGGTGATCA	TACTTTAGCT	GTAAGAAAAG	240
	GTATTAACCT	AGGTTTCCTA	TTATTTGTTG	TATCTGAAGT	ATTAATTTTT	GCTTCTTTAT	300
	TTTGAGCTTA	CTTCCATTCA	GCTATAAGTC	CTGATATTCT	ATTAGGTAAT	GTTTGACCAC	360
	CAGTAGGTAT	TGAAGCAGTT	CAACCAACAG	AATTACCATT	ATTAAATACT	ATTATTTTAT	420
	TAGCATCAGG	TCCTAACTATT	ACATATAGTC	ATCATGGTTT	AATTGAAGGT	AATAGAAAAC	480
25	ATGCTTTTAT	AGGTTTACTT	ATTACTTTCT	GATTAAATGT	TACATTTGTA	TTATGTCAAT	540
	ATATTGAATA	TAGTAATACA	TCATTTACAA	TTACAGATGG	TATTTATGGG	TCCAGTATTT	600
	TTGCTGGTAC	TGGTTACATT	CTTACNTATG	GTTAGTTTAC	TAATTAGGTA	GGTNC'TATTA	660
	NGAANAACAA	GAAATTNCCCT	TTAACNCCCN	CCCCCTCCGT	NGANATNNAA	CCNCACCTAT	720
	TATTACNNTT	TTTNAAAATA	CANNATTGTT	NTAANGAAAG	GNNTAACGTN	GNNTAACGTN	780
30	NACNCACCCN	TAGNNTTTNG	GTCCCCCCCC	NTGCTACCCC	ATTTTGNCCC	CCCCCACAAN	840
	AACCCCC						

## 1251RP

	GATCAGGAGG	GTTTTGCGGT	GCTGCGCGAC	GGCGGGTTAG	AGGTAATGCT	CCTGCGAGAG	60
35	GATGACAAGA	CTGTGCGTGT	GTACCGGGAA	GTGGCAGAAAT	AGTGTATACT	ACATAGTCAT	120
	AGTTATAATA	AACAAGCCGC	GGCGGGCTCT	AACGAAATGG	GGAGTTGCC	ATGCCACCGG	180
	GGCCGCCGGG	GCCGCCGGGG	CCGCCAAAGG	GCGCGTTCCA	GCGCGCACCG	GGGAGGAAAC	240
	CGGGCGGCCT	GCGCGGGTCC	GCGGGGTCCG	CGGGGTGCGA	CTGGCCGCCG	TAGGGCAGCG	300
	GGGCGGTGGG	CCGTTGTAGC	CGCGGATCGA	ATATCATGCC	GCCCTGCGGG	TTGGGCGCGG	360
40	GAAAGGGGTC	AAACGGGTTT	GGCCGCTTCT	GGCCGCTTGG	ATACAGGTCT	CTGTGCGCGT	420
	AGCCTGCAGG	GCTGCCAGGC	AGCGGCTGCG	CGGCGCCGGC	CGGGGGGGAG	AGAACCTCGT	480
	ACTCGTCCTC	GAAGCCAGGC	ATGTCGTGCT	GCAGCCTGCG	TGCAGGAACC	TGCGCGCGGA	540
	TTGGCGGAGG	CGCGCCTCCG	CTGAGGGCGT	CNTAATCACC	GGGCTGTGCT	TTTGCGCNGG	600
	GCTTCTCNTC	CGCCCACCAG	GGNAATTTCC	CTNGNAAACT	TNCCGAACCT	CNCCCCCTTA	660
	AAACTGGCCN	CNCCCTTTTN	CCTNNCNGCT	NTCCTCCTGC	NNCCCCNTTT	CCCCCTCAAN	720
45	ACCCNCCTAC	CCNTNTCTNT	NGNTTCNNNC	CCTACANCCT	TTCNNCCTNC	TCCCCCNCC	780
	ATNTCCTCNT	TNTATCNNA	AATTTCTNTN	CTTTTACCC	CCCCC		

## 1251UP

	GACTGTTTCG	TGTTGAGGAA	GATAATCAAT	ACCGGAATCC	TCTGAGCTTT	GCTTCGGCCT	60
50	CCATTGCGCT	ATTACGAAAT	TCGCGTGCTG	CTCCTAACGA	TGTTGTACCG	TTTATACAAC	120
	CGCTTGTTGA	TCGCTTTTTA	GCAGAAAGCC	GTTTTTGAC	CGACAGAGAT	GACAACCTTT	180
	GCTACTTCTC	CGATCCAGTA	TTGTTTCAGT	CTGTAGTCAT	CTTGCGATCG	TTGGTAAACA	240
	CATATACCCC	ATCGCAGTTG	GAGAAGATCG	ATACCACGTT	GCTTTCGCTC	TCATTTTACC	300
	CATTAATTTT	GCGCCTTTTA	TTGTAAAGGT	GCAGCACCAC	AGAAATACTT	GATAAAATCT	360

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	TAGGCAATGG	CCATATTGGG	AAGTTTATAT	TACTAGCAG	ATGGTTGCTC	ATCCCGGCCT	420
	TGTGCTGTT	GTTCTAGGG	GCGCTGTTAC	TACCTTTAGT	CCTGTGTTAC	TCACAGCTTG	480
	TTACCGGCC	GGGCTTCTAT	GCAACTATTA	TATTTGCTTC	TAATATATAA	GTACTGACAT	540
	TTTCATACGC	GCCTAGCTAC	CGCTGCTTTG	TCTTCGGTGA	CTCTCTTCAG	AACAGCTTCT	600
5	TGGAATTATC	TTGTACTATC	AACCATGGAG	ACACTGTTAC	GCCACACCCC	GACCAAAAGG	660
	AGAACCGAAG	GACAATTTTG	ANCCCTCCCTT	TCCCCCGAAT	TANGGNTTNT	GAANATATNA	720
	ACCGGGACCG	GGTTCCCTNN	TCCCCCGGGT	ANTTNCCCNT	TAAATTTCGTN	TAAANTTANN	780
	AANGGTNTAT	GGGGNGAANG	AACCCCANCT	GACCCNAAAN	GTNGNTGGG	GTTTAACCTN	840
	CTNNINCGCC	GTNCCG					

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## 1252RP

	GATCTCCTAT	TAGTGGGTAG	CTAGCTAGTC	GGCCCGGCTG	GCCGGGGCCG	AACTGGTACC	60
5	GGGTGCGAGG	CCGAGTGACT	AACACTCCGG	GTTCTTCTGT	CTCTTGCCAT	GCCGAACATA	120
	ACCATGGCGA	CTTATATAAG	TTCGGGCGGC	GTGCAGTCGT	ATGAGCCCGT	ACGAGCAAGA	180
	CGTCCAGCAG	TTTGCAGCGC	GGTAGTCGGG	GCGTTGCAGT	TGTGTATATA	TTGCCACCCT	240
	TGCGAACTTG	GACAGCCGTA	TGCTGGAGGC	GGTCAGTAGT	AAGCAGGAGC	CGGTGACTCA	300
	AAGTAGAAGT	CGGATTGTAA	AGGACAACAG	ACCAGTGGCG	GTACGGACAG	CAGCGGGCCA	360
	ACGTAGTAAT	AAAATATGAC	GAGAGATATA	CAGAACCACC	TACTCTTCGA	GACGGCCACG	420
	GAGGTAGCGA	ACAAGGTCGG	GGGCATCTAC	TGCGTGCTGA	AGTCGAAGGC	ACCGGTGACC	480
10	TGCGCTCAGT	ACAAGGACCA	CTACCACGTG	ATTGGGCCCC	TGAATCCAGA	CTCGGTGCAG	540
	ATAGAAGTGG	AGGCGCTGGA	CTGGGAGGAT	GACAGCGTGT	TGGACCCGGG	AGATTGCTGC	600
	CCGGTAAAAC	GTCCCCCTGCA	GCACATGCGG	AACCCCGCGT	TGAACTCCGT	ATATGCCGGT	660
	GGTTNGTGAA	GGTNCCCCCG	GTTATCTTGT	TCAACCTGTT	CCCGTACCCC	CCTCCTCCAC	720
	AATTGAAGCC	ACCTGTTGAA	CACCTGCGGAT	CCCCCCCCCC	CAANAACCA	NAAACAAAAC	780
15	CCATCCGTTA	GGTNCCCCNG	NCTGTCCCCG	AAATTAANGC	CGANCCNCNC	TCAN	

## 1252UP

	GATCTTTATC	GCAACNTTTT	GGTTCTGTTT	CGAGTTACGG	GCCTGGCGGA	CCACACCGAA	60
20	AGCGCCAGCT	CCGAGTGTTT	TGCCGAATAT	GTAGTCGGCT	TTGTTACAT	ACGAGGCTGG	120
	TTGACCTGTC	ACCTTGTTGA	AGAACTTCGT	CAACATGTTG	GCCTGAGACG	GAGGACGATC	180
	CTGGGGCTTC	GATGCGTCTT	CGTCGTGCTC	CCCTACACCC	TTACCGAGTT	TTCCGGTGGA	240
	ACTAGTGAAC	ACTGCCATAG	CCTCGCAGTT	AAAGTGATGT	GGCAATATTA	TATTGTAGTT	300
	TTGTTCTTTT	CTTGATTGTT	TTAGGCTGCC	GATAGCCAC	GAGGTGAAGT	TTTGTACACT	360
	TCACACATCC	CAGCACTGCC	ATCACGACAG	ATGTTGAAGA	TCAAATTTTCG	CAGCTACATG	420
25	CTGCATTGTG	GTGCTTGGGT	TAGCAGTAGC	GGCTAAGTTG	CAACTACATT	GTCCCCATTC	480
	ACTCAGAAGT	ACCTCGGTTA	AGCTCACTAT	CGCCTTATTG	CCGAGCGAAG	CCGAGCATTG	540
	TTACAGCAAT	GATGAGAAGA	GGCTATTGGT	ATGTTAACAT	AACGCCAGTA	GTGTTATATT	600
	TACCACTAAC	CATAGAAAAA	GTACAGAATA	TCCGTAGCCT	ACGAACTGAA	TGAATATNTT	660
	GTCTCCCNCC	CCCGNCCNTA	TACCAATGAA	TAATAAATTG	GATTTGCTAA	TATCTNCCCC	720
	ATATCCNGCC	GGGCCCCCGA	NNCCCTNCAA	CTTATTGGTN	CACNCCNCCN	TGCCNCCN	780
30	TTTTNTTTTN	TCNNGGAACC	CCCCCCCCGT	CATCNTCGNN	TGNNTNAANA	TGANTACCCT	840
	CCCTTGNTCC	CCCNCCCT					

## 1253RP

35	GATCCTAACC	AAGCTGATTG	ACTCCAACCT	TCCACTTGGC	ACATTGACA	AGCTGTTGCA	60
	GAGCTCGACG	GCCGTGGGGG	GTGGTGGCTC	CATATTGGGA	TCAGATGGTG	GGTGACAGA	120
	CACGGAGGCA	TTGGGACATG	ACCGAAAACG	CAAGAAGTTG	GAGCCCCGCT	TCCCGGCGCC	180
	TCCGCGGAGC	GTGGCACTCG	GCCCGCGCCA	TCGCCGATAT	AATTCTGAAT	TGGGCCTCAA	240
	CTACTTGCGC	GAGAGCAACG	CGCAGCCGAG	CGTGATGCTC	CCGCAGGTGC	AGCAGCGCTG	300
40	GAACACAGCT	CCTCGACAAC	AACCCAGACA	ACAGCATAGA	CAACATGGGC	AGGCCGAGGA	360
	AACGGGTTCA	CCACCAATGG	CTCTTCGCTA	TCCCCCTCCA	ATGTTAATGA	ACAGCAATTA	420
	TACATTCCCT	GCCGGCCCCC	AGCAGCCGCT	CGGCCCGCAT	CCACAATCGC	GTGCCTCGAC	480
	GCAGCAATCT	GATGTCCCAG	CTACCCCTCC	CGGAATATCG	GCGTAGCACC	ATCGTCCCAA	540
	CTTCCCACAG	CCCCCACC GC	TGACTAGTCT	TTTGTCTAAA	CATCAGCCTC	ATCACTCGCA	600
	GCCTAATGAG	CTGCCTACCT	CCCATGCATA	TGTACAACAG	ATTTGCCTAC	TCCAATAGCC	660
45	CAGTTCTGAA	GTCTGCTTGC	TTACGTTGCG	CCCTCTCCCC	TTGGCCAATN	TATCCTTGTN	720
	NNNAAAACCN	AACCCNNGTT	CCCCTGTGCC	NGAATTTCTA	CTTTTACCGT	CCGTTATTCC	780
	NTAAATCATA	ACCCGGTTCA	ANAACCCTTT	CTTTGACNAT	ATCNCATTGN	GCNANCCNNT	840
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## 1253UP

50	GATCGACGAG	TTCGATGTTG	AGACGTTCAA	GAAGCTGTTT	GCGAACTGCA	TTCCGAAGGA	60
	TGTGGATGTG	CGCGAGGTTG	TCGCGGAGTA	CCGACTGATA	GTGCCGTGTG	AGGAGCCGGG	120
	TGGGGTGGCG	CGCGCGGCGG	CCGGTGACGC	GGCGGAGGCG	GAAACGGAAC	CGTTTTCCGA	180
55	GGAAGAGAGC	AAAGAGATTA	GGATCATTCT	GCCTCCAAAG	CCAATTGCGA	TTGAGTTTGT	240
	AAAGAATGTG	TGGGAGAACT	GCTGTGTGCT	GTACCGTTTC	TATCACCGCC	CGACTTTTCAT	300

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	CAGGAAGCTG	GACGACCTGT	ATGAGACAGA	CCCGCGTGAG	TACACGCACG	AGCAGCTACG	360
	CTTCTTGCCG	TTGTGCTACG	CTGTCAATGGC	AGTGGGTGCG	CTGTTCTCTA	GCTCCATGCT	420
	CCCTGGTCGG	GGAAGCGAAG	ATGCGGGCTC	TGCAGGCAGA	ATAACAGCGG	CTACATTGGC	480
	GGATACGGAC	ACACGGCACG	CTTATCTGCA	CGACGAGGGC	TACCGGTACT	ATGTGGCTGC	540
5	GAAAAAGCTA	GTGATCTCAC	GAACGCCCGT	GACACCGAGG	CGAATCAAAC	CTTGTTCCTG	600
	TTTGTGTTCT	CCCAAGTTCC	GCGCGGTCNC	CCCGGCATCC	GTTTTTCTGC	CCNGCTATNA	660
	ATTCCNCCCN	CCTNNAGANT	CCACCCACCC	CCCCCGANA	ANTAAAAAAA	TTTCCCCCCC	720
	CAACCGGAAN	TCCCNCCCCG	NTTTACCCCC	CTTANAAANG	AGGTTTTTTTA	AACAAANCGG	780
	GGNGCCCCNC	NCCCCCGGNN	CNNACATCC	CCCCCTAAA	TCGGAANATT	NNCCGAAACC	840
	GC						
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## 1254RP

	GATCGGCCAC	ATTGTCCCTG	AGGCCTATGA	AGGCGGCCCA	ATTGCGCTCG	TGCAAGACGG	60
5	TGACGACATT	GTCAATCGACG	CCGAGAACAA	TGCCATCAAC	CTCCTTGTGC	CAAAAGAAGA	120
	AATTGAGTCG	CGCCGCGCTC	GCTGGACCCA	GCCGGCTCCA	CGCTACAAGA	GGGGCACGCT	180
	CGCCACCTAT	TCTAAGTTAG	TCTCCAACGC	CTCCAAGGGT	TGTGTCTTGG	ACAGCGACGA	240
	CTAGCACCTC	GACGCAAGTC	ACTATTTTAT	AACAAGATTA	TGTATATAAG	CACCCCGCCA	300
	TGTCCATTGA	ATGGACCGCA	TATGTAACAA	AAATCGAGGA	TGCTTCCCTA	TCGTCTACAA	360
	ATCTCAGGAT	GTGAGTACC	TTTCAGGTGT	CTGACTGAAA	TAAATGTTGA	ACTTTGATAG	420
10	TACTTTTATG	TTTGAAAAAT	TTTAAAATTT	TATTGTATGG	CTGTCAACAC	GAGTACTCAT	480
	CTTCAACCGA	CATTACGGGT	ACCTGAAGAG	CTTATCTATC	GATAACATGG	CGACTCAGGA	540
	GGCGGTATTT	ATCGGGCGCA	ATAGGCAGAC	GAAGGTTGCG	GACTTCTATT	TGCCGACCAA	600
	GACTGACGAA	GGAGTCGGG	AGTGCAATCC	CTATGGAATC	CGTTGGACGA	ACNCATGCNG	660
	GNGTTTNGC	CATTGAAGGC	CNCAACCCGA	GNTACTCGGN	AATTTATGGG	GCNAAAAACT	720
	TTTGGTCACN	CTCNCNCGAAG	CACAAATNCTT	CGGCAAGNAA	NAAAAANGGA	ATTGNCCNAT	780
15	TTGGAGCCCN	AAACCTNTAC	NTNGCNTGGN	GNNGGGTANC	TCCNNTTCCN	ANGTCN	

## 1254UP

	GATCTCTGGT	ACCCAGCAG	CCCTGGCGGG	GACGTGGCAT	TGGTGACTTC	TCCCCAGGT	60
20	AACCGGGTGT	GCCTCAGCC	CCTTCCCCAC	ATTGAAGTTA	AGCTTGTTAG	CGGTACTCCG	120
	CTTCATTTTC	TGTGCCCGGT	CGACCGGTAG	CGTCATAGTC	CCGCCGTGTG	GCCGACCGCG	180
	GGCCGCCATC	ACAGGTATCT	ACAGTTCAAC	GGCCGCGTCG	CGATCCCAAG	CGCAGTCTGG	240
	AATCTCGAAC	GGTGCTACAA	AGAACGGATG	CGTGGCAGAT	CGAAGCTATC	GAGAAGGTGG	300
	TGGGGGAATT	GAGTGAAAGT	ACACGAAGGC	AGGGTGTCAG	ATCTCGTACC	TCTCGCATAC	360
	AGTACGAGAA	GGAGTCGGCG	ACGGTGTTCA	GAAATCAGCG	CAGTGTCCAG	TGCGGGGAAG	420
25	CGTGCAAACG	GAACTCGGAA	ACAATCCGAC	GGACCTACTG	CCAGGTCCAA	GCCCTTTCCA	480
	CGGTGTCACA	GCTAAGATGG	TGACTGGCCA	ATAATTTGTC	ATGCTGGTAT	TCGTGTGTCTG	540
	ACGATTATCT	ATTCCGGTTCA	GCCGTTTATA	TTTAGGTGCG	CTGCAAACGT	GGTGACATCA	600
	CGATTGCAC	GTATATATGA	TGGAGTAATT	CGCATACACT	GAAAATCMTA	ATAATCAATA	660
	ACCCATGCCN	CNACTCGNCA	ACTTCNCCNC	TTTNGCTCCN	GGTGAAATCC	CCTTCACTAN	720
	TTTTTTTTCAT	TGCCCATTTN	ACCGAATTTT	ACNAATNATG	CAATGANAAC	CNCCCCCTCC	780
30	AAACCTANAT	CCTTTTNTTN	NGGGTCCCN	ACNGTTNCCN	TTCCNGNCNA	NCCNCTTTN	840
	ATTCCAANAC						

## 1255RP

35	GATCGTGTG	TCAGGGTGCA	TTGCACTGGG	CCTGAAGACG	GTGGGGACTG	ATCGGCGGCC	60
	GAAGAAGCTG	TCGCAGCTAC	AGGCGATTGC	GGCTGTGGGT	CAGGGCCGCG	TTATTGCGCG	120
	GTGGGACTCC	CTCTTCAGAC	CGTTCAACGA	GAAGATTGCG	CAGATTTTGT	TGACACGGAA	180
	CGACATAGTT	GACTGGTCGC	AGTATAAGAA	CGCGCAGAAT	ACGTTCACG	AACTGCTGGC	240
	GATGGGCGTG	ACGCCGATTG	TGAACGAGAA	CGACACGCTC	TCAATCAGCG	GAGTGAAGTT	300
40	TGGGGACAAC	GACACGCTGA	GTGCGATCAC	AGCGGGGCTG	ATCGGCGCAG	ACTACCTGTT	360
	CCTGATGACG	GACGTGGACT	GCCTATACAC	CGACAACCCG	CGGACGAACC	CGGATGCAAA	420
	GCCGATCTTG	GTGGTGCCGG	ATCTGTCAAC	GGGACTGCC	GGCGTGAACA	CCTCTAGTGG	480
	GTCCGGTTCA	GGTGTGGGCA	CCGGCGGCAT	GGCGACGAAG	ATCCTTGCTG	CAGACCTGGC	540
	AACGAACGCC	GGGTGCATAC	GATTATTATG	AAGAGTGAGC	GGCCGTGCG	ATGGTGCGGA	600
	TCGTGGAGTT	CATGGAATGG	CGCAGCAGTG	CACTGCAGTT	TCTGCTGACG	CGAGACTTGC	660
45	AGACGGACGA	GCTGAATTTG	TTGCAGAGCA	CGGCGTCCCA	CTACACACGC	NCTTCNTGCA	720
	ACTTTGCACC	TCCTGAACNA	CNGATTCTNTG	ATCCCNCGTC	TGTGACNCGG	NCGTATCTAA	780
	CAGGGGCTNA	GGCCCCCCCC	AACAACGTNT	CCCACGTNTT	CCGTGAG		

## 1256RP

50	GATCTAATGG	CATTCTCCCT	ACCAAATGGG	CCCAATTGTA	TATTGCCGAT	CTTCCTACAG	60
	GGNACTGGTT	TACGGATCCA	GCGAAGATCG	GGAGAGTTCA	GCTCTTGTTA	TTGCCGACAT	120
	TGTGTGCAAA	ACACCAGCTG	CAAACTTGAG	GCCATATGTC	ACTGTCATCA	CAGGTCCACT	180
	TATCCGTGTT	GTTGGCGAAA	GGTCTAGCAG	TGATATTAAG	GCTGCTATCC	TATATGCCCT	240
	AAATGTTCTC	TTTTCGAAGG	TTCCACAATT	CCTGCGGCCA	TTCTATACCT	AACTACAGAG	300
55	AACATTTGTT	AAATCTCTTT	CCGACTCAAC	CAATGAGACC	TTAAGATTGC	GGGCCGCGAA	360

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	GGCACTAGGT	ACTTTGATAC	AATATCAACC	AAGAATTGAC	CCTCTGGTGG	TGGAGCTAGT	420
	AACAGGCGCT	CAGCAGGCCA	CTGAAAGGGG	AGTAAGGACG	GCTATCTTGA	AGGCATTGTT	480
	GGAAGTTGTC	TCCAAAGCTG	GCAGCAAGAT	AAGCGAAGCT	TCCAAAGCTA	ACATCATTAG	540
5	ACTTGTGGAG	CAAGAGATGG	CATCCACAGA	CAGCAAGTTT	GCAGTCGCTT	ACGCCAAGCT	600
	TCTAGGTGCA	CTTTCTGAAA	TCATGTCTCC	GGAGGAGGCG	CAGACCATAC	TTCACGAAAA	660
	GTGCTTGATC	CAATTTTGAA	GANGCACNGT	AAATTGCCGT	CNGACCCAC	TCTATCCTNC	720
	TACCCCTGTA	CNTTCTCCCG	CCATNCACCN	ATNTTGACTN	TTNGTGGTGC	ACGGATCNCN	780
	ATCCTTCCNN	CACACGTTTN	CCCN TN GNAT	TCCCCCNAA	NGAAAGTNAN	CCCCC	

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## 1256UP

	GATCAACTGG	TCGGGCGGGC	TGCACCACGC	CAAGAAGAGC	AATCCTTCGG	GGTCTGTGA	60
	CGTGAACGAC	ATTGTTCTGG	CGATTCTGAA	TCTGCTGCGC	TACCACCCAC	GCGTTCTGTA	120
5	CATTGACATT	GATCTGCACC	ACGGAGACGG	TGTCCAAGAA	GCATTCTACA	CTACTGACCG	180
	CGTGTTCACG	GTCTCGTTCC	ACAAGTACAA	TGGTGAGTTT	TTTCCGGGAA	CGGGGGATTT	240
	GGATGAGATC	GGATGCTCGC	GCGGCAAGCA	CTTTTCGCTG	AATGTGCCGC	TCAATGACGG	300
	CATCGATGAT	GATTCTGTACA	TCAACTTATT	TAAGAGCATC	ATAGACCCGC	TAGTTACATC	360
	ATACAAGCCA	ACAGTAATTA	TTCAGCAATG	TGGAGCAGAC	TCTTTGGGGC	ATGACAGACT	420
	GGGGTGTTC	AATCTAAATA	TCAGAGCCCA	CGGCGAGTGC	GTCAATTTGT	GAAGTCGTTT	480
10	GGGATACCTA	TGCTATGTGT	CGGTGGTGGA	GGTTACACCC	CCAGGAATGT	GTCGCGGCTA	540
	TGGACGTACG	AGACAGGCAT	CCTTAATGAT	GTGCTCTTAC	CTTCAGATAT	CCCAGAAGAT	600
	ATTCCGTTCC	GCGAATGGTT	CGGTCCAGAC	TATCTCTGCA	CCCAGTCCCT	GGATGANTTN	660
	TCCAAAATAA	ACNCCCAAAT	TACTGGANAA	NATACGTNCG	GNTTTAAAN	NTAAATTNTG	720
	CNCGGGCCAT	TTTGNCTTGA	NNCGAATATC	CTCCAGATTT	CCGTTTAAACN	AAAAAAAAT	780
15	GATCGGAANA	ACCAAAANAT	NCCTTGNTAA	CANTNAAGAA	NTTTGCCGNN	ACTTNTTANT	840
	C						

## 1257RP

	GATCACTGGT	GTCACCAAGG	GCTACAAGTA	CAAGATGAGA	TATGTGTACG	CGCATTMTCC	60
20	CATCAACGTC	AACGTTGTCT	AGAAGGACGG	CGAGAAGTTC	ATTGAGATCA	GAAACTACTT	120
	GGGTGACAAG	AGAGTTAGAG	CTGTGCTGCT	CAGAGAGGGC	GTCAGCGTCG	AGTTCTCCAC	180
	CAACCAGAAG	GACGAGATTG	TTTGTGTCGG	TACCTCCATC	GAAAACGTTT	CTCAGAACGC	240
	TGCTGACATC	CAGCAAATCT	GCCGTGCCAG	AAACAAGGAT	ATCAGAAAGT	TCTTGGACGG	300
	TATCTACGTT	TCTGAGAAGG	GTGTCAATTGC	CGAGGAAGCC	TAAGTGCTTT	ACTGACCGTA	360
25	TCTTGATAAA	TAATATGAGT	ATTATGTAAT	CAAAGAACTC	ACTGCTTTTT	ATTGGTGGTG	420
	TTTTTCGTCAA	ACGCTCTTAT	TAGCGCCGGG	GTTAGAGTGT	GGGAATACTG	GCGTTATATG	480
	CTTTAGAAAT	TATGTTAAGT	AAATTTAATG	TCCTATCAGG	GCCACAGCCT	TAGCAACTAG	540
	GTGCAGGTAC	TCCTTTAGCT	TGCCACTGTT	CTGGAACAGA	AGATATATTT	TATCTGTCTC	600
	GTTGGCACCA	TCGTAGACAG	GTTCAACGCT	TCCTTGACAG	AACGATGGAA	CGCCAGCTTT	660
	CCGCGGTGGA	AGTTATAGGA	ATTATGGATT	CCAATGACAG	TTGGTGTGTT	AACNANCTG	720
30	ATTTGTCCAN	TTTCCCGTCT	CNGAAGCTNC	ANTGNTTCCN	TGACCNANCA	AACCCGGGAN	780
	ACCCCTAGGG	CTGNNAGGCT	TGAATGCNTT	AAAANANTTT	CNTTGANAAA	NCATTGNTAA	840
	T						

## 1257UP

35	GATCGGGCCG	CTCACACACT	CAGGTACCTC	AAAGGAATAC	GAGTTTGTCG	CACGCTTCCC	60
	GTGTCCAGAT	GCACAGAAAA	TCGATATGTA	CATCAAGGAG	CCGCAAAACA	AGTACCTCTT	120
	TTCCGGGAACA	GAGTACACTT	TCCAAATCAT	CTGCAGCCCT	GCAGACGGCC	TCACTCACGA	180
	TCCATACGAC	GCGCAAGCCG	CTGCGCCAAA	TGTGATAGTC	GTCCAGTCCC	CATCCGGCAA	240
	GATCTACCGT	CTGAAAAAGG	CGGAATCCGA	TGTCGAATTT	GGCGTATGCG	AAGCTAGGCT	300
40	AAAAGTGCAC	GAGCCAGGCG	TCTGGCTGGC	CCTAATTACC	TCTGAGGCAG	GTGCTGGTTG	360
	GTGCACTTTC	GCGAAGTGGA	TCTGTGTTTA	ACACCTAGAT	GCTACACAGT	CATCCACCCC	420
	ACGAAATTAA	TAGATAGTAC	GGGTACATAC	AAGCCCTATA	GTTTCTTAAT	ACACTTGCCC	480
	TATATTGAAT	ATGTCTACGA	AGTATATGGG	CGAGGCACCT	TCAAAATCGG	TGAAAAAANA	540
	TGCACCACTT	CGAAATCCAT	GTTTTATGAG	CTTAAACAAC	AGTGGTTGTT	GAAGAACCAAT	600
	ACCCTGCCAA	GGAAATGTCA	GGTACTCGAA	CCAGCTCTCA	ACAGATTCTT	AAAGATTGCC	660
45	AGTGTGTGTA	CCGAATCCAC	GTTTCGCTGAA	TGCTGGGACC	GACATCAGAC	CCTTGCAATTG	720
	GTACAAAATC	AGTCTATACG	GNGAGCGCCT	GTNTGCCCN	AAAANAAANA	CCACGGAAGG	780
	ACNCATTGTC	ACTTGAACNG	AGNCAATGTG	TNCNGTGACG	CGGNTNTTTC	GNTTCAAGCC	840
	CCAAGGACAA	NAACGC					

## 1258RP

50	GATCCAACCT	TCTACTAGGG	TATTTTTCCC	TACCTCAGCC	TGCAATTCCA	TGCCATCGCT	60
	AACCAAGATA	ATATTCTCCT	CCAGTAGATC	CATATTCTCT	CCCGACTTCG	CACTAATCGG	120
	GATGATGGC	ACGTTTCCAC	CCAGATCTTC	AGCATGTATT	TCAATGCTGTA	GCAAAATCATT	180
55	CATTATTTTG	TTGATCACAG	TTTCCTTTTC	TTTTGCCGAC	CGGAGTTTGT	CCACCTTGGT	240

TATGGCGACA	ATCAGCTCAT	TCCCTGATTT	TTTGACATGC	TTAATCGCTT	CAATGGTCTG	300
GGGTTTAAAT	GAGTCTTCGG	CAGATACTAC	CAAGACAACG	ATATCGGTAA	TATTCGCGCC	360
CCGTTCCCTC	ATCTTCAAAA	ATGCTTCGTG	CCCGGGCGTA	TCCAAAAACG	TGATCTTCCG	420
CTTCGAAACA	GGTGTGACAA	CCTGGAACGC	ACCAATGTGT	TGTGTAATGC	CACCAAACCTC	480
CTGCGAAACG	ATGCTCGACT	TCCGCAGATA	GTCCAATATG	GTGGTTTTGC	CGTGATCAAC	540
GTGACCCATA	ATCGTCACAA	CAGGTGGCCG	GTCTTTCAGG	GCCTTCGGGT	CTGCAGGCTG	600
CTTCAATTCA	TCGTAAACGT	TCTCCGGAGT	GACAATTCCC	TGCCGGAGGG	CAGTTGGTAG	660
CTATCTCCTC	CCAATATAGC	TCGATGTAGT	CTCCTGGAAA	TATGTAGTCC	GCCTGGCTTT	720
TCAA						

## pAG1258up

1 GATCCTGTTT ACAACTAAGT TCGCATCCCT ACCAGGGGAA AATATGAAAT  
 51 ACCAAGTGTT GTATTCCGAA CGCTAGAATT CTTGTACAAA AACC GCGGCA  
 101 TTCAGGAAGA AGGTATATTT AGGTTAAGCG GATCCAGTTC TCTCATAAAA  
 151 TCTTTGCAGG AGCAATTTGA CAAAGAATAT GACGTGGATT TGTGCAATTA  
 201 CAACGATAAA GTTCTGTCA CACCAGGAAA CGAAAATCAG GGCGGTCTCT  
 251 ACGTCGATGT GAATACCGTT TCAGGTTTAT TAAAACTATA CCTAAGAAAG  
 301 CTTCTCATA TGATCTTTGG GGATGCTGCA TATATGGATT TTAAGAGAAT  
 351 CGTGGAAAGA AACGGAGATG ATAGCAAACCT AATAGCACTC GAGTTCAGGG  
 401 CATTGGTTAA TTCCGGACGA ATTGCCAAAG AATATGTGCG CTTAATGTAT  
 451 GCATTGTTTCG AGTTATTGGT GAAGATCACC GAGAACAGCA AATATAACAA  
 501 GATGAATCTG CGGAATTTGT GTATCGTATT TTCGCCAACG TTGAACATAC  
 551 CCGTGAATAT ACTACATCCG TTTATCACTG ACTTTGGCTG TATATTCCAA  
 601 GATAAGGCGC CGATGGAGAA CGGACACGGT CAACATACAC ATCCCGCAAT  
 651 TTAGTTCATA CTAAGTAAAA TACTATTAAC TTAGAATATG TGATAAGTGT  
 701 TTTAATTACN TAACTTGGTA TTAGTCCNAT TGTNTAATAA TTGAATATGA  
 751 ATGCNTTATT NTCTCTNANT CAATNTGTCA CGATTGGATT TACACCNGCG  
 801 TCTGTAANGA CNTCTAGCTT GGTCATCCCA NTTCTCANTT NCTCCCGCTT  
 851 NCA

## 1259RP

	GATCACACGA	ATATTGCGGG	AGTATTTCTC	CATCGTTCGC	CGCAACGCGG	CCTGCGCATC	60
5	GCGCGTGAGC	GATTTCGGCCT	CGTTGATGAT	CACACTCTTG	TACCTCCGCG	CTAGCCCTC	120
	CGATCCGCTC	TGGAAATCCA	CCTGCTCCAT	CTGCGCAATC	TCCTTCAACA	ACTCCTGAAT	180
	CACGATCCGG	TCATTGTGCC	CCATGTGCGT	CGGCGTGATC	TCGATGTGGT	ATGGGCTGCT	240
	GACGACGTTG	AGCTCGAGCT	TCTTGTTAGA	TGGCGTAACA	AATTGCCGCA	CATCAATCTT	300
	TAATTTGTAT	ACACCTGCTC	CAAAGATACT	TGCAAGGAGC	CCCATGCACC	GTGTCTTCTT	360
	CCCACCTTCCA	TTGGGCCCCGT	AAAGTAAAAA	ATGCGGCAGG	CCCTTCGCAG	AACCTGCTAA	420
10	AGCCTCGAGC	TGCTTGGTAA	GCGATGCCGT	ATGTGAAAGG	CTGGTCAACG	ACTTCGGTCT	480
	ATGCTTGTCA	ACCCAAAGTG	ACATATTCCT	GTGTATCCTG	AGATGGGCTT	TTGTGTGTG	540
	TAGGGAAGGT	GAGCAATTCA	GTCGCAATTA	AATTCATTTA	GATTCGCGTT	TTAGCACAAA	600
	ACGATATGCC	CTCAGTAAGG	CCAGAATACA	TACACGTACT	TCGCCTACTA	CTTTTGACAG	660
	AAGTAAAGCT	CTCAGGAGAT	CGCTCGAGGA	GATGGCATGT	ATATAACCCN	CAATTACTCT	720
	GATGCNAAAA	ATGTTGCACC	CNTGCCTTTT	TANPTCNGTC	GACAACTANN	AGAGCCTNTA	780
15	TCNAGTCCAA	ATTTTNCCAA	ANCTGGGAAA	ACCTTNTNCC	GTGGTNTATN	AACACA	

## 1259UP

	GATCACCCCC	CAAATCAGCA	ATAACTCGAA	AACTGTGCCC	AGTACCTTTC	AACGCGCATG	60
20	AACCTAACGG	CGCGCAGCGG	TCATGGGTAC	TCGACTGCCCT	TTGTATCCCT	CACACTGCGC	120
	CTCTTCGTGT	GCCGCACGTG	CTTGTTGATG	GTAGCGGCGC	GGCCCCGTGG	ATCTAAGCGC	180
	ACGTCTCTTT	GTACGTGGGT	CTCACGTGCA	CATCGTCATC	CATCCGCTTG	CGAATGAGTA	240
	GATCAGCACG	GAGACCATGC	TAGGCAGGGC	CGTTGGGCGA	GGTGGAAAGG	TTGCAGCAAT	300
	GAGGTGGAGC	AGCAAGATGA	CATCACAGGA	TAGTAGTCGG	AAGAAAGAGC	TATGTGCAGC	360
25	GTACAGCGTA	GTGGATGAGC	GGGTPTCGCG	CAGCATGGAA	GAATGCGGAC	GTAGAAGGTC	420
	GGAGGTTCTA	TTGCTTGCCG	TTTCTAAACT	GAAACCTGCG	TCGGATGTGG	CGATACTGTA	480
	CGAAGAAATG	GGGCTGCGGC	ACTTTGGAGA	GAACTACGTG	CAGGAGCTGG	TGGGGAAGGC	540
	AGCAGAGCTG	CCGGGCGATA	TCCAGTGGCA	CTTTATCGGG	GCGCTGCAGA	GTAACAAGTG	600
	CAAGGACCTG	CGGAAGGTAG	TGAAC TG CAT	GCGGTGGAGA	CCATCGACTC	GCTAAGAAGG	660
	CGCGGAAGCT	GAGGAGGCCG	TGCGAAGTTC	CAGCCGAGCC	CCCGCATCTG	TGTTACATTG	720
30	AGTGAACNCT	CTGGCAACNC	AAAGNNGTTN	CNCGATGAGC	NACNGTGAC	TGTGATTCTT	780
	CTNCCAAAAC	AAACCTTCCC	TGCCCAGCGA	TAAATGGTCC	TGGACCCTCC	CCGCGAAGGG	840
	AACCGATCCC	C					

## 1260RP

35	GATCCTCAGA	GGGCCCCGAA	GAAGCTTCGG	CCGAGACAGT	AACGATGTTT	GGCGAGGTTG	60
	TGCTGTATCA	CAGTTGAGCT	CTAGGTTGCA	CTTTCGGAAA	GAGCGCTACC	GTAGCTGCAT	120
	GAAAAAAAAG	TAAGGCTCAT	CAGTTTATGC	AGAGGCAAGA	ATAAGTTTGG	TAGAGCCTTA	180
	CTTCACAAGC	GTCGCTCTAG	CGAGCCATAT	TATTTCTATG	CCGGCAAGAG	AAGACCGAAG	240
40	AAGGCCAGAG	CTCCATATCG	AAAGTACGTG	GCGGGTCAAG	GGTTTGTGCA	TACCTACGGG	300
	GTTTCCAGTA	CTGAGAGTTC	AGCACACGAT	GAAAGCGGTT	TGTTCCCCGC	AGACAGTGGG	360
	GTGCAGGTAT	CTGACGATGA	TATTGCGAGA	CGACTTGTTG	ATATGACACT	TTCCGCAAGC	420
	GCAGCGTTTG	CCGGTGGAGC	GGCACCCATA	CCGTATCCCG	GACACTCAAT	GGTGCTTCCC	480
	TGGGAGCTGC	AGTTTTTGTT	TCTGTCCAAA	TGCAAAACTA	TTGAAACACA	CTTCATGCAA	540
	GTGTGCAGGC	GGTGGTATAT	CATGTGTCTG	CCATTGATCT	ACCGAGCACC	AAGGCTCTCC	600
	AGCAAGACTT	CTACAAGTTT	GTGGAGACAC	TGGTGGCAGC	CCGTAAACAG	AATTACCGGC	660
45	AATATTCTTC	GATCTCGACC	GTCCATGAAT	ACCNNANCGC	AAACCTTTTC	CAAGGTCTCT	720
	CCGTGCTGCC	CACCTTGAC	ATTCCGGCCC	CAAACACTCG	TATCCCCNTG	AATCTTACGG	780
	CNNCCCNNTT	GCAACCGATT	TGTCNTNTCC	CAACGTTANC	GAACNCNTTG	AG	

## 1260UP

50	GATCGACCGG	CCGCCACGCG	CGGTGCCGTC	GGTGAAGTCG	CCGCCCTGGA	TCATGAAGTT	60
	GCGGATGACG	CGGTGGAACG	TGGAGTTGAT	GTAGCCCGCG	GAGGCGTCCT	GGCTCTTTGC	120
	GAGCGTGACG	AAGTTGGCGA	CGGTGCCGCG	AGCGACGTCG	CCGAACAGCC	CGAGCACGAC	180
	ACGGCCAGT	GGCTCGTCGC	CGTGCTGCAG	ATCGAAGAAG	ACACGGTGTG	TGACGGTGGG	240
55	GTCTGCGAGC	GCGAACGCGC	AGAGCAGCGC	CTGTGCGAGA	ACGAAGAGGA	CCTGCATTGG	300
	GGGTGGCTGC	GGGAGGCGCG	GGACGCCGCG	GGAAAACGCC	CGCTTTTATA	CGCGAAAAAG	360

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	CTGCTTCGGC	TACGTAGCTA	GAGATACAGA	GCGGTGGACT	TGAGGCTCTG	CAGCATCAGG	420
	CGGTCCATCA	TCTCGGGCGT	CAGCACGTCC	GAGTAGCCCG	CGGTGCGGCC	GTCCAGCGCC	480
	GCGGTCAGCG	CTGGCGCAGT	GGCGCTAGAC	GCGGTGCTGC	CACTGGCCGG	CTGCACGGAG	540
	TTCTGCTCCA	CGGGCACGAA	GGCCGCGCCC	TGGCCAGGCT	GGAAGCGCGC	CAGACGCTGA	600
5	TGCGCGCCAG	CGCGGCCGAC	AGGTGGAAGC	CGGTGACAG	CAGGCCGTTT	TGCACCACGC	660
	TGTACGCCGT	GGCGCCTGTA	CCTTCCCCNA	ANANGTNTAT	CTTGACGCAT	CACCGTTCCG	720
	CCCCCGCTGC	TTCCGAACCA	AATCCGTCCC	NCTTAACCAC	CNTTTCANGC	CNTCACTTGC	780
	ACNCTGNCCA	CACNCTTCNC	GGTTACGTCC	CAATGCCGTC	TCCCCNNGGC	GCTTAGCNCG	840
	GCTCGT						
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## 1261RP

	GATCATAAAC	GAAGAATTCC	TAATTAACAA	TTTGTCTCTGC	ATGTACTTCC	TCAGTGAGAA	60
	ATAGCGATAT	AATCATTAGA	AAGCTTCCCC	GAGCACTTTA	GCAGCACCGC	ATGCCAGCAT	120
5	AACCCCTGG	ACTCAGGGCA	GTATGCCGGC	TGGCACCTCG	GCACCTCATC	GCAGGCGAGA	180
	CAGTCCACCA	CTGCGAGCAC	CGTAGTATTT	ATACTTTTCC	AGGTTGAAAA	ATTTTCGACC	240
	GCCCCACGCC	GCAGAGGGCT	GGACGCGCAT	TAGGGCTCAC	AGCGGTCGAC	TGCCACTGCT	300
	GCCCCAACAG	CGCCGCGCAT	GTAACGTGAA	ATGATATATT	ATACCTTCTG	ACTACAATGT	360
	GAAATATACA	AAGGTGGCTC	ATAGGCGCAT	TGCATTTATT	CAGACGCAGT	AGCTCTGGTG	420
	TAGATAGCCT	GCTTGGAGTG	CTTGGAGATT	GGCTTGATGA	TGCCCTCGGT	CTCCAAGTGT	480
10	CTCAAAGCAA	CTCTGGCCAT	GGAACCGCCG	ATCTTCAATC	TGTCGACCAA	CACGGACACA	540
	GAGACGTATC	TGTAGGTTGG	GACCTCCTTT	AGGATTCTGT	CAAGCTTGTC	CTGGTCCAAG	600
	ATGACGGCGT	GCTGGGCCTT	GTCCTTGTGG	GACTTCTTGG	ACCACTTCTC	TTGGACTTCT	660
	TACCACCGGC	CATGGCGCGC	GCGCCTTCTG	GGCCTTAAAN	ATNTTGTTTT	TGGTGCATAT	720
	ACNGTGTGCC	CNTATACTGT	CCGCACCACT	GGCNTCTCTG	CGNAGGGTGG	TGAGCTTCCG	780
	TACTCCNCCC	CCTACCCNCC	CCCCCNNGNT	TGTCCNTTTC	NNCNRNCCTA	ANTCT	

## 1261UP

	GATCTGCAAC	AACACCATTTC	CATCGCGAAG	TCTTTCCAAT	TTCTGTTCTG	GAATATTATG	60
	AGGAAGTTTG	AGAACGATAT	TGGGAGCGAT	GATGAGGAAG	ATCCCTTCCA	GATCAACGAT	120
20	TTGGACGAGG	AGAAGACCTT	GCGCATGCTT	TCTAACCAAG	CCTGTTTCTT	CGGCTACCTG	180
	ATGGCCGAAG	GTCAGGTAAA	GTTAGATGTT	TTAAACATG	TATCCATTAT	GGGGTTGAAC	240
	TCTGACGGGA	GACTTTTCTT	AGAGAATCTT	CTATTTTCAGT	TTCTGTTGGC	CTCAGCCAAA	300
	AAAGCAGAAA	CTAAAAAGAA	GGTGGGGAAT	ATCAAGGAAT	GGTCTTACAG	AGATGACTTG	360
	TTGCAGGGCG	CCCTGTCCGA	TGGGATCCAG	GCCGAAAATA	AAAAGATAAT	CTGCAAATCG	420
25	CTCAGGATGT	TTATGAGGAA	TTTTAGATAC	ACGAACTATA	TTCTGTTGTC	GCCTGGCTCG	480
	AAGGAGTATC	AACGTGACAT	GAGAAGGTTG	GACTGGGCCG	TTAAGCGTTT	TTTGGAACCT	540
	ATAGATGATG	AACTGGATAG	TGCAGATTGT	GAAGAGCTTC	TTGTCACTAG	TCTGAATGCA	600
	TATTACGTGT	AACATTGAAC	ATACGTACTC	TATATTAAAG	TGGTGAAAGT	GATGAGAGTA	660
	TGACGTCCNT	GCTTTTATTG	CATACCACTT	NTGAATTACA	GTTATTTCGGT	GAATGACNAC	720
	AAACANGTTT	CATTACTTAC	TTGTTGACNT	CGCCNCGACC	ACCACCCGCG	CCACACCTTT	780
30	GTTTACCTTA	TAAAAATCTC	CACNTCCGNC	GTATANAGCC	TNAANAATTC	NTTCGCTCAT	840
	GCGGTTTGA	CN					

## 1262RP

35	GATCTTTGCA	CACGCTGGTA	ATGTTTCCCA	CTAACTGGTA	TTTTTCCTTG	TCTAGATAGT	60
	CTGCCGTAAA	GACTCCCGAC	GTGATCGGCC	GGGCACGGAC	GCCCATCTGC	TCCAAGGCCG	120
	TCACAAGTTT	CAGGTTCTGT	TCCAGAAAGC	ACTCGCGAAC	TACTGTCATG	GTCACAGGAT	180
	CAGTTACGCG	AATTCTTCT	ATATATGAAG	GCTCGATACC	CTGAGCCTCC	AATTTGTTAT	240
	TCACCTGCGG	ACCCGTGCCA	TGCAGCACAA	TCGGATAGAG	CCCCACATGG	TACAGGAACG	300
40	CCAGGCATGA	AGCCAGTTCC	GGCAAGTTGT	CGCTGATGAT	GGCACCTCCA	ACTTTGATAA	360
	CCGCGAATTG	CTGCTCCGAG	ACGGAAGTAA	AGTACTTCAG	GTA CTGTTCT	ACTTCACGCT	420
	TAGAGCCAAT	ACTGTTGAGA	AGCTGGATCA	CGGTGGACCG	TGCTGTCAGA	GACCCAACGC	480
	CCTCGTTGTT	CCCGGTTCTT	GCATAGTTCA	GCTTCTTTAT	AGCGGCAGTG	CTGAACAATT	540
	CGCGCTTGTA	TGCGGCACGG	ACAGCCCATG	GCGTCCGGTT	TTAGATCCTG	CTACCAGCGA	600
	AGCTCTACTA	AACAGTAGAG	AGTGCTCGCA	AGCATCTTGG	TACTCCGTTT	ATCCCAGTCG	660
	CGCGAGTTCT	AGCTCTCGAA	AGCAGTCCGT	GTGGCTTATA	GCCTAANTTC	TCTTCGGTTC	720
45	CATAACCACA	AACCGTCTCN	TGNCNTTCC	TGANTTTCAA	GACCCCNANA	TTTTTACAAT	780
	TTNTGCATTT	NTCCNNGNGNA	AGGGTG CNAT	TTATTTNTTG	ATNCNTTTAA	A	

## 1262UP

50	GATCACAAGC	TTGTTGAAGC	CAACTGCTGA	AAATGTCTCC	TACGAGAAGA	AACGATTCCCT	60
	TCCACTAGGA	GACGTGTGGC	AAATTTTAAA	AGGAGCCAGT	AAGACGCAGA	CTAGCCCCAG	120
	CAGAAGCGCC	AGTAGTTGTT	AGGAAGCATT	CCAGAGCGTA	TACGACACTT	TGAAGACGGA	180
	CAGCGTTTCA	AGAAGACAGA	GACAATCAAC	ACCAAACAAA	CATGGAGAAT	CCTCACGTAC	240
	ATGATAATTT	ACAACACATC	CAGGCGGTGT	TATCGAACTA	CGACACATCG	TTTCTCTCGG	300
55	ACGATGAAGA	GGACTACTGT	CCGCTCTGCA	TGGAGCCTTT	GGACATCACC	GATAAGAACT	360

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	TTAAGCCGTG	TCCGTGCGGG	TATCAAATCT	GTCAGTTCTG	CTACAACAAC	ATCAGACAGA	420
	ACCCGGAGCT	AAATGGGCGG	TGTCCTGCGT	GTCGGCGAAA	TATGATGATG	AGTCGGTGGA	480
	GTACATTGTT	TTGAGCCCCG	AGGAGCTGAA	ACTTGAGCGA	GCGAAGCAGG	CGCCGAAGGA	540
	GCGCGAGCGC	AAGCAGCGCG	AGAAGGAGCG	AAAGGAAAAC	GAATATGCCA	CCGCAACATC	600
5	TCGCCGGCAT	GCGCGTTATC	CAGAAGATTG	GTATACGTTA	TTGGCCTGAA	CCACCCGTAC	660
	CGTACGAGGA	GGTTGGTGCG	CTGTTGCGCT	CGGACAGTTA	CTTTGGCNGT	TNCGGGANAT	720
	TTACNNATCN	TCCGTGAACC	GCAAAAAGCC	CCATGACCCC	NACGGTNTGG	ATNTNTTTCC	780
	TTCCCNAAAA	AAGAGCGGCC	CNNTTNCGGC	GTGGATGTNT	TTTNTGANGG	CGNGGTGAGG	840
	GGGTACGACC	NATNTGCCTN	TTTTG				

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## 1263RP

	GATCGCGCCA	TTCGCTTCTG	AATGGTTCCT	CACAGAAGGA	TTCGTCTACC	AATGGCATT	60
	GTTCAGCGAG	GTCCTCGCTA	CTAACAGAAT	CGTCTGTGG	AACTCTCTTT	AGGAAGGTGA	120
5	ACAGTTCAATC	TATCCTTTCA	AAATTGATAC	TCTGAAAGGG	TTCATTTGCG	GCGTTAAACA	180
	TACTAGATGC	AGTCATTAGG	GCGGCACTTT	CTTGGTTAAT	ATCGTCAGCT	ATCCTTTTTTA	240
	GTGCTTCTTC	CTCATTTTCA	TTGGGCTTGA	ATAAACCTCT	AGCTATCAAA	AACTCAATTA	300
	GTATCTTCCT	GACCTTAGTA	GTTGGTCCGT	CTGTGGGCTT	AGTCATACTC	ATTAAGTGAT	360
	GACGGAGCTT	TTGCACACCT	TTGCCAGAAA	ACACACAAAA	TATTTGACGT	TGGTTAACGG	420
	TAAATTCACT	AGGAGGAGGT	CTGCAAAATT	GTGTGATATC	TGGCCTGAGA	AAAGAAGTAC	480
10	CGCAGTCAAT	GACAAATGAG	AGAGCTTTGG	ACAAGCCATT	ACCAACTCAT	ATATTGGATA	540
	AATAGTCAAA	TTAGTACAAT	ATGATAGGTG	AACTCTTTCC	AATGTGTCTAT	TCCTACCACG	600
	CAAAGCAATC	ATATTTAATA	ACCTCATCTG	TCATCTGAGA	ACATTCACCA	ACCTTATCTT	660
	TTTAGTTTGT	TAATTCCCCA	ATCATATAAG	TATGAATTGT	CCATTTTGTA	CACAACNATC	720
	CNCTTCTGAT	CNNGGANATC	CTGATTCAAC	CTTATCCCN	CCNGAATGA	ACNTGGCCAA	780
	NGANATTNTN	GTTTTTCCCN	CTTGAAANCT	CNAAATNCAT	ACCCCGCTTA	CC	
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## 1263UP

	GATCTTAAAA	GCTGGCCTCC	GCAGATAGAC	CTTCGCGCA	GAGGCTGGAA	ACCTCAACTA	60
	GCAAGTCGCC	ACCCGAATCA	GATAAGCACT	AGAGTCGTTT	CAGTAACAGA	GGAAGCGATC	120
20	AAGGAAGATA	GTAGAAGAGG	ACACTGCTGC	CAGGCTTGAT	CGGACAGAGG	GTTTAGCTTT	180
	CTGTTGAATT	TTAGAGTTTC	GGGGCTTTGT	TTACTTCGTT	TCATTCCTTC	GTGTAAGAA	240
	GCTGTTTGCA	GGCTGCCATC	ATTTGCCAGT	CGCCAGGTAG	GGTATTGCAG	GGCGACGGAG	300
	TCCGTTGAAC	AGAGCAGGAC	CGAGAACGCC	GATAGACAGG	CGTTTGTGTT	TAAGCGGTGA	360
	GAGCTGAAGC	AGGTCAAGAG	GCCGGCTTGG	GCAGGTTGTG	CGGCGGCGGC	AGAGCACAGC	420
	AGGGCATCCG	AAGAAGGCGG	AGCGTGCGGA	CAGGAGCGCA	GGCGCGCGAA	CAGGGGGGTG	480
25	TGATGACGAG	CGAGACGAAC	AACAACAACG	CGGCGAGCTC	GAACGGCGGG	CAGCTACCCG	540
	CATCGGGGCT	TCCGGCGGAG	TGGTTTACGA	CGCCATTCCCT	CGCGGCTCGA	CCACAGACAG	600
	ACAGCAGTAC	TCCCAGAAGT	TTCCGCGAGCG	TGTTTTCGCG	TGACGCCAGC	GCGCCAGAAC	660
	TATTTTTCCT	CTTACCAACC	GGCCGNAATG	CCCCCCTT	TNTTGNCCAA	ANACCATTTT	720
	TCCNCCAGCN	CCCNCCCTNC	TAAAACCAAT	TCTTACNCGG	NCGAATGAAA	TGGGTTGNNT	780
	TTCCCGCCCC	NGAGAACACA	TTTTTCCNCA	CTGTGACCCG	ANTNNNTANT	CTCCCNAAACA	840
30	TTATTTTTTTC	C					

## 1264RP

	GATCTCGTTT	TTGTAATGCT	CTAGCTCATA	TTTGTTGAAG	GAGAAGGGTG	AAAACAGCTC	60
35	CGAGGCTGCA	ACTACTGCAA	AGAATAAAGA	GCAAAATATG	GCACATAAGA	TGCTTTCCCA	120
	ATTCATTTGG	TACAGCTCTA	ATACTGTGAA	CCCTTAATCT	CGGGTAGGCG	CAACAGTTAT	180
	GCGGCCAACC	ACGTTAACGT	GATAATGATG	TAGGTACCCC	GGTGAAAAAA	AGAGTATGTG	240
	GAACCGCCCA	GCTGAACCAA	GCGGATGAGA	CATGCCAACC	ATATCCAAGC	ATACTTGACC	300
	ATGATGACGC	AAAACATATC	AGCATAGTTA	GTCTTGACGC	TGAGACAGGC	TTCAATCGTA	360
	AACCTCCCA	CTTCACTATT	GTCACGTGAG	AGGCAACATA	ATTGATCTTG	TGACTACCAC	420
40	CCATACATTT	TGCTACCACC	CATACATACT	AATTAATGGG	GAAAATAGCG	GCTGGTACAG	480
	ATCTCTGCAT	CTCCCTGCCC	CAGAGGGCCG	CGGGCCTCTC	GTTCCCCAGC	GCGCGCAGGC	540
	GGCCGCAGGC	CGACTGTCTT	ACTACGCTCT	CCCTGTTGGC	CCGTGGTTAC	CGCGCTCAA	600
	ATTACCAANC	CTCCAATTTT	TGANATTCCC	CGACAGTTNT	GTNCCNTNTT	TTTACCCCAA	660
	TTCCGGAATT	TCCCTATTAA	ANGGTAAGAC	CCNNNTTAC	TTTTGTGGAN	TAACCTNNGG	720
	CGTNCCTNNG	GGNNTNCCCT	TNTTACNNG	CCCCNTTCNA	GGCCTTTTGG	TTCCCTAAAA	780
45	CCGGTNAAAA	AAAAAAAGAT	T				

## 1264UP

	GATCTCATGT	ATCACAACCA	GACTATGATG	CGACTTGGGG	TGACTATGTC	TCCTTTGCCC	60
50	AGCGGTTTCA	AGAACGAGTG	AAAGACAAGG	ACCTTATTTT	GATCGACTCT	GGTGACAAAC	120
	GTACCGGTAA	TGGTCTCAGT	GATCTCACTA	TGCTCGATGG	TTTGAAGTCA	AGCGGTATCT	180
	TTAACCTTCA	GAAACTTGAC	TTGTTAACTC	TGGGTAATCA	TGAACTGTAT	ACGGAAGATG	240
	TGGTTCGCTT	GGAATACTAT	GGAACAGCAA	TGGAGCCTGA	GCTAAGTGAT	AAATATGTCA	300
	CAAGCAATGT	GGAATTTATC	ACAGAAGATG	GGGACGTTGT	ATCCGTTTCG	CAATAAATAT	360
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	AGGTACTTTG	AAACGCCAAA	CCAGAATCTA	CGTGTATTGG	CGTTCGCATT	CATGTTTCGAT	420
	TTTCCCGTGG	GCTGCTAAAA	ATGTTAGGTT	AACCCCTCTG	GCCGAAGAGG	TTAAAAAGGA	480
	CTGGTTCACC	CAAACTGTGG	AAAAGTACCC	GCTGACAAGC	TTGATATTAT	AGTTGTCTTC	540
	CGTCATTTAC	CAGTCACCCG	TGGCGAAACG	AGAGCTTCTG	CAGTTACACC	AACGACTAAG	600
5	GGAAATCTTAC	CCCGACACTA	TTATCCCGTA	CTTCCGAGTG	NNTACTCAGT	CNGAAANTCC	660
	CTNGTTTNG	ANAAAACGAN	TGCTTTACCA	ACGGCGAAAT	TCCTGAAACA	TGGAATCCNA	720
	TCAANANNNG	TTTCNCAAGA	AACCAAATTT	TCCATTTCNAT	ATGACTTACC	CAATTCCTTT	780
	TCCCTCCNG	NTTNANACTC	CAAATTCNT	CCAAGGAAGA	ANANTNACNC	CC	
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## 1265RP

	GATCTTGCTC	AGAAATAACT	TGCATTGTCT	CCACTATTTT	CTCAAGATTA	GCATTTATGC	60
	ATGTCAC TAG	GCATTGCGTT	TCAGGTAATG	CATTCCCAAC	AAGTGGCTTA	CGATCTGGAA	120
5	CAGATTGTGT	TCTTTGTGAT	TCTGGTGGAG	CCGTACCTCC	AAAAAGTTGAA	TCTTCGTTTT	180
	CCGCCGAGCA	GGAATTGCAT	GGACGAGACT	TCTTGTCAGA	CATAAACTCA	AGTGGCGCCG	240
	CTCTATCTGA	CATATCTTCC	TGACTCTCTT	CTGCATACGT	GCGGTTACCT	GGCTCTAGTT	300
	CGTCCCTCAGT	CCCTACGTCT	CTTCTTG CAT	GCATATCCCT	TGTCGTCAGA	TATGTTTCTC	360
	TCTTCGGGCT	AGAAGGGTCC	TCATTTGTAG	GATCTTGAAC	AAAAAGTAGT	TTGTTATTCT	420
	CCAGCTGCGC	AGTCTCTTCC	AGGTTTTACT	TCCGATGCTT	ATTAATACTG	GTTC'TTTAGA	480
10	TGGTTCCCTG	ACTTTGGCTA	TAGGCCATTG	GTTCCGGCGA	CTTGTAAGG	TATGCATTGA	540
	GAGTCCTCCT	GGTTAAACGT	GTNGTCCCCC	CGTTATTTTA	NCACGGCTTG	GCCGGAATGG	600
	TACACNGNTG	AGTTAATCNC	NGCGGGTTGC	NGTTCCATCC	TGTGGGGGGC	CCACCCAGAA	660
	CCCNAACTTN	GGCGCCACNA	TTTCCCNTCN	CCAAACNNTT	TGGCCNAAAA	AANAATTNTT	720
	CCCCCAAGGN	NGGANACGC	ATACCCCGAN	ATGNNGTATN	TTGTGGGGGN	AACCCCNNA	780
15	ANCCCCNCCC	CCCNNGNGGAA					

## 1265UP

	GATCCGGTCTG	CCGCTGGTGA	AGGCAGCGAC	GTCGTTGTAC	CGGCAAGGCG	GCCTGCGCGC	60
	GTTCTACCTG	GGCAACGGGC	TCAACGTCAT	CAAGGTGTTT	CCGGAGTCGG	CGATGAAGTT	120
20	CGGCTCGTTT	GAGCTGGCGA	AGCGCGTGCT	GGCGGGCTTG	GAGGGCTGCG	GCGAGACGGG	180
	CGAGCTCTCG	CGCCTGTCTGA	CGTACGTTGC	GGGGGGGCTT	GGCGGCATCA	TGGCGCAGTT	240
	CTCGGTCTAC	CCAATCGACA	CCTTGAAGTT	TCGCATACAG	TGTGCGCCCC	TGGATACGCG	300
	CTGCCGGGGT	CTGCCGCTGC	TAATCAAGAC	GGCGAAGGAC	ATGTACCGCG	AGGGGGGTCT	360
	GCGACTCTTC	TACCGCGGCC	TTGGCGTTGG	CATTTTGGGC	GTGTTCCCCG	TACGCGGCGC	420
25	TCGACCTCGG	CACCTTCTCG	GCCCTCAAAC	GCTGGTACAT	TACCCGTGCG	GCAAATGCGC	480
	TGGGCATCTC	CCGAGAACGA	AGTGGTCATG	AGCATCTCCG	TGTGCTGCGG	AATGGCGCCT	540
	TCAGCCGTAC	GTCCGCGCCA	CGTGCTTACC	CTATCAACCT	TCTACNGANG	CGNTCCCAGC	600
	CCAGGNAGT	TNTCNCNCCC	CCCTCCTACA	ANGNTTCAAN	TNTTTCCGAA	AACACCNCNN	660
	AGGCCCCCCC	GCTTTTACAA	GGTTGGTTCC	NACATTGCCA	GGTNNCCNC	ATCCACNCT	720
	NTTTTTTTNC	NAAANTTAAA	NNCCANCCCC	CCNAATAAAG	GCCCCCTTNTC	CCCCCNACCC	780
30	CNGGAATAAN	GGTTCGGNCT	NNAAAACCAA	NACNCCCCC			

## 1266RP

	GATCTTATCT	GGAACACCCA	TTCAGAACGA	TTTATCTGAA	TATTTGCTCT	TACTAAATTT	60
35	TAGTAACCTT	GGGCTTCTCG	GTACGCGGGC	ACAATTTAGG	AAAAATTTTCG	AAATACCCAT	120
	TCTACGGGGT	CGGGATGCTG	ATGCTACTGA	CAAGGAGATC	GCTGCTGGTG	AGGTGAAGTT	180
	ACATGAGTTA	TCCCAGATTG	TGTCGAAATT	CATTATCCGG	AGAACCAATG	ATATCCTATC	240
	GAAGTACTTA	CCTTGTAAGT	ACGAACATAT	TCTATTCTCT	AATCTCTCTC	CGATGCAAAA	300
	GGCAATTTAC	GAACACTTCG	TGAGGTCACG	AGAGGTTGCC	AAGTTAATGA	AAGGTACAGG	360
	GTGCGAGCCA	CTGAAGGCGA	TAGGTTTGCT	GAAAAAGTTA	TGTTACCACC	CTGACCTGCT	420
40	AGATCTCCCG	GATGAGATCG	CCGGTTCTAC	AAATTTAATT	CCAGATGACT	ACCAGAAGTG	480
	CTAGTGACAC	ACACTCCGCC	GCCGAAGAA	TTCCCCTTTT	GNATTCCAAC	GANACATTCC	540
	ATCNAAATTT	GCNATTCCTA	GAACGTTTTT	NGTTTTAGAA	TCCAGCCNTG	ATTCTNAATGA	600
	AAAAAATGTC	CCNGATTTCT	ACNNCCCCC	ACCTTGGATT	TTNTCCAAAA	AATNTNNCCN	660
	CCNCCCCCN	GGTTTNTTCC	CANCTGAANG	NNCCCNNGAA	ATTAANNANC	TTTNAACCTT	720
	TTGAAAATTC	CAAAACCCCC	GGGAGAATTT	NTCNTTTNTT	TCCCCCNNGN	CNGGGNNGGG	780
45	NTCCCCCTTT	NGGCCCCCGG	NGAANTTTGA	CCCCAAAGN			

## 1266UP

	GATCTGTCAG	CATTCACAGA	AACCATCGCT	ACGAAAAGTT	TCCTACAAGT	AATCCCAGCC	60
50	AGCCGAAGGA	CTCCCCGTTG	GGTCCTGTAG	CCGTCTTGGC	AGCGCACAGT	TTCCAGGACT	120
	TGTCTTCTGT	TGGTCAGAGT	ACTAGGCAGG	ATGCGTTTGC	TTATTCCAAT	CACAGTGTG	180
	TGGCTAATGA	TCGCCAGCCC	TCTTTACCGC	GAAACCCTGC	CCCAGACTCC	ACGTTCACTG	240
	CGGAGTTTAA	CCAGCTGCTA	TCTGAATCCA	GCAACTGCCT	TGAGCTTGAT	TCTATATTCT	300
	CAGGCAACTC	AGTTCTCTGG	AATGGCGAGA	CCTTAACCTC	TGAAGCAAGA	GCTACCTCTG	360
55	AGGGCGATGT	GCCATCTGTC	TCGGAAGATG	CCCAGCACGA	CAGCCAGGCA	AATTCTGCA	420

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	AGAATGGCCT	GAAGTATTGA	GTCTAGCGGA	CACTGAGTAT	GCGGACCTGG	ATAGTTTGAT	480
	CACTAATTTG	TACTTCTACC	ATGCGAGGGT	TCGTCCCGCG	GGTCTGAACG	TTTGTTATA	540
	ATGATCGATT	TTAGAAAATA	TAAGAACCCC	CTTGAATATG	AATACNGNCN	NTTAACCCCC	600
	GGGGGTTGCT	GATACCCCCC	CTNTCCCCCN	CTNGGNTGAA	TTNTTACCCC	NCGGNGGGGN	660
5	GANAAANAAT	TCCTGCCNNC	TTGGGTTCN	AANCCCCATT	CCCTTTNNAA	TNAAAANTGC	720
	TTCCNNGNCN	TNTTAAAAAA	AAAAACCGTG	TTGCCCCNAT	AACCAAATCC	CCNCGCANGN	780
	AATTTCCTGG	GTTCAACANC	CGCTCAC				

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## 1267RP

	GATCCATTCC	ACCGGATTGC	AGCAGCTAGT	GCATTTGGCC	ATACGCCCGA	TTGCCCTTTC	60
	TTATAATGAA	TCCCGGCTTG	TAGAGCATCA	TCCGGCACTT	CACGTGGTAT	TGAATAGCTC	120
5	CTCATAACCG	CACCGGAAGA	TTTCAGGAAT	ATATCTGGTT	GTGTAGTGTA	GAGGTATATCA	180
	CTGTGGATTTC	TGATATGGCT	GTTCAGCTT	GAACATTCCA	CTAACCTCGG	TTCGAATCCG	240
	AGCACGAACA	ATTTTGTGNC	TNAANCCNA	NATTTTNCC	CCTANAATAN	TGGNCTNNCC	300
	AAAATCNTCN	NNTTTNAATT	TTTCCAAAA	CTTTGTCCGT	GACCGGANTN	GAAATGNGGG	360
	NAAGTGGAAT	GTCCAAGNCG	GGNNCGCNA	ATTAGAATTC	CAGGGAAAAT	TCCTACANTA	420
	NANAGGTGNC	ACCCNCGGNA	ACCCCGGGN	GGNNNACTG	GNCCCTTTNA	ACCTGNGAAT	480
10	GCGGTTNTCC	AACCTTTTNC	CGGGNGGCTT	GGCCCCCN	TTAATNCNAT	TACCCNCCCC	540
	TNCTTTTCCC	NAAANNNGATN	CCCCCCNCG	GAAAGGTTCN	TTNNNNNANCN	TAGGAGGCC	600
	CTTNGGTCCG	GAATTNGNNN	CTTTTCNNC	TCCCCCCCCA	AATCCNGGAC	CCTGNAANNC	660
	CCTTNTNCCC	CCNTTTTAC	NNTTTTCNN	GNAANTNCTT	CCCTTGGCCC	ATCCCCGGAC	720
	NNNAATTGGG	GNTTTAANGG	CCCCCGGNC	CCCNCTGN	AAAAAGNTNN	GGNNCCCCC	780
	CCCCCCTTN	GN					

## 1267UP

	GATCCGCATC	GTTTTGTGTA	GTCATACTAC	CTGGACGCCA	TGTTCCGCCGA	GCTGGCGCCC	60
	CCGGCGAGTC	TCGGGTCAC	GGTCGGCTTG	TGCAACGCGG	ACTGTGCCCC	CTCCTACTGG	120
20	TTGGAGCTAC	CCAAGGACCG	TATCCTGTTC	CTATGTGCGA	TTGCGAACCT	CGTAATCACG	180
	CACCTCGTGA	ATGTAGACCC	AGCAGCAAGG	GACATGCACG	CCTTCTGGGA	GAAGGTGAAT	240
	GCGCTCTTCT	TGGAGAACCG	CTCAGGGCGG	ATGCTGCAGA	AGGAGGCTTT	GGTGCCGCA	300
	CCGAAGAGCT	GCGAGAACGA	TGGCGGCGAG	GCGAACGTTT	CTGCGTCCCC	GATTTCCCGT	360
	TCGCAGACAC	AATACACATC	GGACCAGGGC	AGCAATTACA	TGAACCCGCA	CGCATTCCGGC	420
	ACGGCGGCCC	ATGCGGCGCG	CACAGGCGCC	TCGTCTGTTG	CGCCTAACAG	CGACACCCTC	480
25	TCTGTGCGAC	TGGCTTCACA	CAACGCCTGC	GCCCCAGAAG	CGTCGCGCAG	ATTCCATACC	540
	AGACTTGCTG	ACGCAGCGTC	GAGGACGCCA	TCAGACAGGG	AGCTTGCTGC	TTTGACCAGA	600
	AGGGCTTGAG	CAGGATTCCC	AGGACGACAC	GACCGCNCCTG	TAATGCAACT	GTTGTCTCTC	660
	CNATTTGCGC	CCTATCCCCC	AATGGAACGC	CACCTCCCCNG	AAAAAAAAAA	AATTTTCCGN	720
	TGGATATTTG	ATGAATTGAA	TTAGAAAAAT	TACNTTTC	NNATTCCTGC	GGTGCCACAA	780
	CAATTGCGAN	TNCTAGACCC	GCGNCCTGGC	NTTNGGTTTT	AAAT		

## 1268RP

	GATCCTGAGA	ACACTTTTTTC	TGTGGAGGCT	TATCAATGCT	CTTTCTATCC	GCAGCTTCTT	60
	CCAGGCAGAT	GAATACTGGC	AGTCGCTGGA	GCCTGCGCAT	GTTAAGGCGT	TTGGATATGG	120
35	TGGGCTGACT	TGGGAGTGGC	AGCATGGGCT	GCGCAGCTAT	GCATTCCCGA	TGCTCTTTGA	180
	AATGTCGTAC	TATGTGGCGT	GGATACTGGG	TGTGGCCACC	CGGATGGCGC	TGCAGGGGTT	240
	GGCACATGCC	ACGGCGCTGT	GTGGGGCGGT	GGTGCGGAGC	GCGCGGCGCG	GCGTGGCCGC	300
	GATGAAGGCC	GTCTGGGAGC	TGCCGGAGGC	AGCGCAGGAA	CTGGTGAGGT	ACTACGGGGT	360
	TATTGTACGG	GCCGCGAAGT	GGTGATGGCG	GCGGTAGCAG	CGTTCCGGGA	GTTCTACAGC	420
	GTGCTGCTGG	TTGCGCAAGC	TGTATCTGCG	AGTCGCGGAT	AAGGGGGACA	CCAGAAGGGC	480
40	GACGCGCGCC	GTCAGCCGTT	GCGCTGATGC	TGACCATGAC	AACTTCTTCA	ACTGTTTCTT	540
	CGCGACGCGA	ACGTTTCATCA	CTCCTTCGAG	ATGACGCTCA	CGCGTCGCGC	TCTACCATTG	600
	ATTGAACGGG	CCTCACTTGG	TTCTCTNGCT	TCNCCCAACT	TGCGGTGGCT	CTTTTGCCTG	660
	CCTCACGCCA	NTACTTTTTTA	TCTGGCNCCT	TGCTNTTCTT	GGTGNGANCC	TGTTCCCCCN	720
	ANNGTGNCN	CCTTTTAACC	CGNCCCAAGT	TGCCCCGAGC	CCCTGCGGTN	TTTCAATCCA	780
	ANNANNC						

## 1268UP

	GATCCAGGTA	TACCCGCCTC	CGTCGCGCAG	CGAGCTGCGC	AGCCGCTTCA	TCGCTGCAAC	60
	TGAGAATGCC	CTCGACCTGA	TGTGCGGTAT	GCTGACGATG	GACCCGCACA	AACGGTGGGA	120
50	CACGACTCGT	TGCCTGCTCA	GTCAGTATTT	TGTAGAGCTT	CCGGAGGCGA	CACCTCCTAC	180
	GGAACTTCCA	AAACTAAATA	AGTAATGACT	ATGATAACCT	AGATGGTATA	CTCGGACGTT	240
	TTGTGTTTGT	GCTTTGAGGC	GATGACATTG	GCTTTTATGG	TATCGCAGAC	GTTGCCTGAA	300
	AAAGATTCAA	CGTCTCGGTA	ACAGATTTGC	GCAGACTACT	TGTTGAAAGA	ACAAAGACCA	360
	GAGCGCTGGG	ATGCTCACCC	CAATGACGAA	CCCCTCCGC	CTTATTGGCG	CTGGCTGCAG	420

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	GTTCCCTTAGC	ACCAACAATA	GGCCGCCACT	GCACAAGATC	TTTCCCTCCC	AAGAAGCTGG	480
	TGAACAGGAT	GCTGTTCGAC	CTTGATAGCC	GACTGACCTT	CCCGGAAATT	ACTGCCTGTA	540
	TACGAGCAGT	TGTACACCCC	AATTAGACAG	TAGTACGGCG	ATTTGTAGTA	CCCCGCGCGT	600
	TGAGGGCGCC	ACGACGTTTA	TGATTCATGA	AAAGGTGCTG	AGAAGACTCG	CCCCCCAGAA	660
5	CGAGAGCTCC	CATCGCCNTC	TACTTGCNCC	GGANAACAAC	TGCTTTACTT	GCTGCCCANT	720
	GGANACNAAA	ATGCACGNGC	NCTNCCCTTG	ANCCCGTGCA	CCGNTTCGCC	NAAGGNNCGA	780
	AATGAATTTG	CAATTTAGNT	CNGATTTTAC	NCTCTGGNTC	CCCCCCCCCA	CTGANNGANC	840
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## 1269RP

	GATCCCACTC	TTGGCAAGCT	ATACGGTGAC	ACTATCATAG	CTCGCGGTGG	CCTCTACGAG	60
	ATGGAAGACA	ACCTGGGCGA	GTTCTTGGAC	AGAGAACCCA	ATAACGAGGC	GTACCTCAGA	120
5	GATCAGGGCC	TAGCCTAAAT	GCTCCTTCTT	TTTCGCGGCCT	TCCTGCCCTC	CTATGTATAT	180
	TCCAGCTAGA	GAATCGCAAG	CAAGCCATAC	TTAGAAATAG	GATATTGTTC	CGGGAACACT	240
	GATTTACTGT	GCGTTACTGC	TCCGGAAACT	CACCTGTTCG	GTATCGAATA	ATTAGCGTTC	300
	GACTACCGCC	AGTGTGATGC	TTTCTTTATA	CCGGCATACT	AAAACAGGGT	CCTCAGTCGA	360
	ATCGTGTGTC	ACTGAATATG	AGCCCCCTCCA	TGAGTTCCCA	TCGCGTAGAG	CGTCTATGT	420
	GCAGACCATA	TCAACACCCT	CTGTACACGC	GTGGAGTTCA	ATATACGCGT	ACGACGCACA	480
10	TACAATAGTA	CGTGTGCGCA	ACCGTTATAC	GAAGAGCTGC	GTTCTGATTG	CAGCATTTCC	540
	CAAGCCCCGG	AAATACAAAA	CCGCATTTTT	AGCCCAGTGC	GATAGATGTC	CTGAACCANG	600
	GAATTACANC	GAAGGNCGAT	TGCTACTACN	ANCATCANCC	AGGGCTCGNG	TATTTCTCAT	660
	CCATCCCCCT	CNAACNAAAA	ATCCGGANTT	TTTAAATTTT	CATGCAAACC	ATNCANATCC	720
	CCNTTTNGAT	ATTNCCCCAC	TGGCCCCCCC	NCCCCCANNT	ANCNGTCGGG	ATCCNGNATT	780
	CCCCGGT						

## 1269UP

	GATCGAACTC	CATGAAGGAG	CGTAATGGCC	TCGTGGAGCT	GCACCGCACT	GGGTGCGTAC	60
	ATAGCGGGAT	GTAGGAATGC	GGGGATAACG	ATTCGGAAAA	GCTGACTGGG	CTGCGCCTCT	120
20	AGCTTCAGCT	CAAGCTGGCG	CAGCAGCGTT	GCTATAGGCT	GTTGTGGCGA	CAAGGTCGAC	180
	ACTTCAGTTG	CAGTAGGAGC	AGGTAGCATA	CGACTAGTTA	TATCGAACTG	GTGCCGGTAA	240
	TGAGGATGAG	GGTCAATTTT	TGGCTCCGAG	CGCTGGCTAG	CACCACAATT	ATCACCAGT	300
	CCATACCTCC	GATCAATTCT	GAGATCTTGG	CTACGTGCGA	CCGGTTTTTG	ACCCCTCCG	360
	GCTAAGTTTT	GCACCGTGAC	CTTCGATTCC	TCCTGGGAAA	TGCGAGATTT	CTTTACCTCT	420
	TTACGTGTGC	CCTGGAATAT	CCCCGGCAGC	TCCTTCGCAT	ACTGAGTGTT	GAGCGTGTAT	480
25	ACCACCACAT	GCGTTATCCC	CCCCCCCCTGN	GGGCCCCNAN	TTTCCCCCCC	GGTTATTTCT	540
	GTCCCTGCGC	CTGCAANAAC	TTCCANTTAC	GANGCAATCT	GGTCCCCCTG	TTCTTCCCCC	600
	AAAACATCTG	GCCCATTGGA	NCCCATATGC	CCTAGAACCN	ATCCAATCTG	CANCCCCNGA	660
	NTTTTGTGAA	ANNAATTACC	GGNAAGGANC	AACCCGGAAG	NAAAGCCCGC	CCCCCCTGTG	720
	GAGCCNACTT	CCCCCCCCC	NAAAACCNCA	ANTTNNTTTT	TNNTTTGGCC	CNANCGNCCN	780
	TTTTTCNGCCC	NGCCGGGGANG	GCCTTAAAAAN	TTCTNTCCCC			

## 1270RP

	GATCATATGG	TGAACCTGGC	ACATACAGTT	GAATCATCCC	AATAGCAAAG	AGAACGTAAG	60
	ATTTACCTAG	CGCGGCATCA	CCTGGAATAT	CTAGCATTTG	CAGCGCAGGT	GAAAAGAATT	120
35	TCTCATGAAT	TGATTGGAAA	TGTGGTTCCG	TGTGTTCCAT	TGCTAAGCCC	GCTAGTACAC	180
	GATAATCATC	ATTAGACTCA	CAGGTTAGAT	GGGCCCTTAC	TGTTGCCTTA	TACCAGTCTA	240
	ATAGAACCCTG	CCTGTAAACGA	GCATATTGAT	CCTGAAGAAT	AACCACCGAT	GCGTCAACCA	300
	TCGAATTGAG	CAACAATGTC	GCGTCAATCA	CGGTTTGAGT	GATGTGACTT	CCGGTGAAAT	360
	TCTCAAAGGA	ATTTAATTTT	GGTATCAACC	CCTTCAACAA	GGAAGCTGTG	AAGATATCAT	420
	CAACATGCGA	TTTGTAAGCT	AAACCTTCCC	GCATCCATAG	GAAATCAAAA	GTGGCTGGGA	480
40	AAGCATAGTT	TGCGCTATTG	GCTTTGACTA	ACTGCGAAGT	TAGAATACTA	CTTGTGGGCG	540
	CCAGTTTGAA	TAGCAGAGTT	AGACATTCAA	CGGATTCTNA	GAATATAATC	CTNGCGAATT	600
	TATCCATCCN	CCTANAAAAAT	TNTTTCCNCC	TTGATCCANA	ACNANAAAAAT	TCCGTTGACC	660
	NCTGAAGACC	TATTCCCTNCC	TTTNAAAGAC	CTGCNCATTC	TTCNATTTCC	CNAANGNNTC	720
	CCGTTCTACC	NAGAAANTTC	TTGCATGCCN	NCATGGTTTN	AACCNAACCN	TCCTTTGANG	780
	NTANTNACTT	CCCCCINNCC	AATTTA				

## 1270UP

	GATCCGATTG	TCAAATTTTC	TGAATGGTAT	GGTAAGAAGT	TTGGGGCTGG	AAAGGCTAAC	60
	AGTGGTGTTA	TATCTTTGCG	TGATATTTTA	GCTTGGGTGCG	AGTTCATTAA	TAGTACCTAT	120
50	AAGGCATTGG	CTTGCCCTTA	TGCTTCATTA	ATCCATGGGG	CGGCAATGGT	ATTCAATTGAC	180
	GCCCTTGGAA	CCAACAACAC	AGCGTACCTT	GCCGAGAGTG	AGGAACGATT	AGAACACCAG	240
	AAGCAAGAAT	GTCTCAAATA	TCTGTCTGAA	CTAGCAGGAA	AGGATTTAAA	CAATACATG	300
	TCTGGTCCAT	TCGATGTTAA	GATTGACGAT	GAAACTCTCC	AATCCGGGCT	TTTTAGCCTA	360
	CCCAGAGTTT	CTTCCTCATC	TGTCCAACCG	GTTTTCAATC	TTGGCGCACT	ACTACAGCCT	420

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	ACAATCTCAT	GAAAGTTGTC	AGAGCAATGC	AAGTACAAAA	GCCATCTTAC	TGGAAGGATC	480
	ACCTGGTGTT	GGTAAAAACCA	CATTAATTTT	CGCATTGGCT	GACTGTACCG	TTACGAATTA	540
	CCCNTTTTAA	TTATCCGAAC	CAACTGATTT	GAATGAATTA	TTTGGATCCG	AAGCNCCCCG	600
	AAAAAAAAAAN	GGNAATTTNT	TTTGN GTTGA	TGCCCCCNTT	TTTNAAACTA	TGCCAAAGTG	660
5	GATGGTTTTN	TTTAAATAAA	ANNANATTGC	NCCCCANCCN	TTTTTAAGGN	CNNACCCTGT	720
	TTGTNNCCNT	GGNGAACCCA	NTCCCAAATT	TAANAAAATT	TNTCGCCCCC	ATCCGCTTTT	780
	TTGNTNCCCA	AACCCANACA	GGGGNGGTGA	AAAGGGNTGC	CAANCTTCCC	TC	

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## 1271RP

	GATCATTATA	TTATAAAATA	TAATAAAGAA	TATATTTAAA	TAATAATAAT	AATATGAAAT	60
5	ATTATATTAA	TTCTCCATTG	GAGCAATTTG	AGATTAGAGA	TTTATTAGGT	TTAACATCAC	120
	CAATAATAGA	TTTTAGTTTT	ATTAATATTA	CTAATTTTGG	TTTATATCTT	ATAATTTCTT	180
	TATTAGTAAT	TTTACTAATG	AATTTAATAA	CTAATAATTA	TAATAAATTA	GTAGGTTCTA	240
	ATTGATATTT	AAGTCAAGAA	ATAATTTATG	ATACTATTAT	AAATATAGTT	AAGACACAGA	300
	TTGGTGGTAA	AGTTATGAGG	TTATTATTTT	CCATTAGTTT	ATACATTTT	TATTCTTATT	360
	TTTACTATAA	ATTTAATTAG	TATAATCCTT	ATTCAATTGC	TATAACTTCA	CATGTAGTAT	420
10	TTGTAGTATC	AATAAGTATA	ATTATTTGAT	TAGGTCCTAC	TATTATTGGT	TTTTATACTC	480
	ATGTTTAAAT	CTTTGTTTAT	TTTACCACTA	GGTACACCAAT	TAATTTAGTA	CCATTATTAG	540
	TATCCATTGA	ATTATATCCT	ATTTGCTTNA	ACTTATTCCA	TAGGTTTPTA	AAATACACTA	600
	ATATATACCG	GTCCATTTAT	AATGGTTATT	TAGNNGGTTT	AATATTNAAT	TNAAAACCAN	660
	AATATTTACA	TTTTATGGTN	NCCNCCCAAN	AAGGCATTGG	TTTGGTTNTT	TAAAAAGGCN	720
	ACCTATATCN	CCTANTTGAT	NTTTTTTATN	CCCCCTTTTA	AANANCNATT	TTNNCCTTAT	780
15	TAAANTAAAT	C					

## 1271UP

	GATCAATCTT	TCGATCATTG	TCCAATATTC	CCCCTGCTG	TATCATATAG	ATATTGATTA	60
20	TAATTTCTAA	ATCAACGTGA	TTGTTCTAAC	TTTAATTAAC	AATTATGAAT	TTTTGGCTAG	120
	TTATTATTTT	TTAATTAACT	AATACCTAAA	TCATTATAAG	CTTGACTTAA	AACAAATAAT	180
	TATTACATTA	TTCTTTATTT	ATTATTTAAT	ATTTAGTTAA	ATTTTAAAGT	CATTATTCTT	240
	AATTTTACT	CACGAGTACA	CCACTTATTA	ATACTATTAA	TTAATAATAT	TAACGTTTGA	300
	TTGCGATGTG	TAATGTCCTT	AGTTAGCGCT	TAATCTGAAC	CAACATCATG	TTCTCATTAT	360
	TATTAACATG	TTTAAATAAT	TATTTAATAC	TATTTAATAC	GAAAGTTATA	GGATTTCGAAC	420
25	CTATGAAATC	ATAAAGATTT	ATAATAGCTC	AAATATTACA	CTTTAAACCA	CTCAGTCAAA	480
	CTTTCTTAAT	ATATATACCT	TATATATGGT	TTGATAATTT	ACTTATAATA	TATAGTATAT	540
	AATTTAATGA	TAACCTTTAT	CATTTAGGTG	CGTAGGGTTC	ACCCCCCTAT	TGCTAGTCAG	600
	CATATGAGGT	ACCTCCCCCC	AATGATAAAA	GTTATAATAT	ATAATATTAT	ATTAAGTATT	660
	TAAAGAANAT	AATATAATTA	TTTAATAATA	TTTTTATTTA	GGNNAATAAA	AAAAANTTTC	720
	ANNTTTGAAA	NANGGTGCNG	AGAATTANAA	AAAGCNAATA	ATATGTTCAA	TTTGACCCAT	780
30	TAANAATGTA	GTNCNCTGAC	ATCNCCTATT	TCCTATANAA	ANTTTTANAAN	AANA	

## 1272RP

	GATCAAATCT	AGGTTCTCCG	ACGGCAACGG	TGACGAGTTC	GTGAACGCGC	TCAAGCTCTG	60
35	TGGCTTTTTT	CATAAACACA	CAGACAACAG	CAATAAAATG	TTACACGAAGT	TTGAGTTCCT	120
	CAAGCCTCCA	AAGGAGATCC	TAGAAGAACG	CAAAGCCAAG	CTCGAGCGTA	AGCAGAAGTT	180
	CATCGAAGTG	GAAACAGAGA	AGGAAGCTCT	AGAGTCTAAG	CGGTGCGGAA	ATCCAGAAGG	240
	AACTGGCTA	CTAAAGCCAT	GTATATATAA	ACGGAGGTGA	TTGCCTAGTC	TCTTCTCAGC	300
	ATGCGATCAT	ACCTTATTCT	TGTAATCTTA	TCAAACTATA	TATAGGGCGA	CCGACAGCTT	360
	CAACCGTTCC	TAAAAAAGGT	TTGGAAGGTG	AACAGCCGCT	GGATGTTCTC	CACATTTCGT	420
40	AATGTAGGCA	TTTGTGGCCA	TATGCTGCTT	GTCTCCGAGC	TTTTCTTGTT	GGGCTCCCAT	480
	CTGTGCGCAG	GAGCGGAATC	CCGTACGCAT	TGTACCTGTT	ACCCTGCTGC	GAACAGCACC	540
	AGAAGAGGCT	GATAATTGTA	GTCNCAGCAC	ACCATAGACG	CCGAACAATG	CCCCAAGCGC	600
	AGTGCTGCGT	TAGTTTGAAA	TCCCAAAACA	CTTCGAATCA	TCGGTTCCCC	GGAGGCCCAA	660
	TTATCCGAAN	TTGGCTTTTA	AANTCCNAAT	ACAANGANTG	CGCCCCNTGT	CCCCTGTACA	720
	TTGTGCCCCN	CCTAGGNNGC	CCACTCCCN	CNCGAANTTT	TTATTTCATTT	AATTCTNCNG	780
45	NCCCCNCTTT	GTGANAAATNG	AATTCANTTT	TTN			

## 1272UP

	GATCGACCCC	GCGCGCATCG	GGCCCTCCGG	CCTGCTGCGC	CCCTCGCGCC	TCGGCTGGCA	60
50	GCTCGTCTAC	ATCCTCACCG	TGCCCATCTT	CACCAACGAC	TTCTTCATGT	CCGGCTTCTG	120
	GCTGCGCACC	TTGCGCGCGC	GCTCCAACCG	CGACCTGCTG	CTCGGCTGCT	CGCTGGCCGC	180
	CGTGCTGCTC	GCCGTCGTGC	TGCTGCTCGT	CGGCGTCACC	GGCCTGCTCG	CCGTGTGGGC	240
	CGGCTACGCG	CCGGTCGCGC	ACCTCGACAG	CGCCAGTTTC	TTCTGCTGCT	TCGCGCGGCT	300
	GCCCGCCTGG	GCCAACGGCG	TCGTGCTCGC	CCTCGTCTGC	GTGCTATCCA	CCTGCACGCT	360
55	CGACTCCTTC	CAGAGCGCAC	TCGTCTCCAC	CATTTCCAAC	GACCTCTTCC	CGCAACCGCC	420

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	TGCCCCCGCT	CTACGCGCGC	GCCGCGGTCG	CCGTCGTCAT	GGTCCCCGTC	GTCGTCGTCG	480
	GCCTGCTGGC	CACCCGACAT	CCTGGCCATC	TACCTCATCG	TCGACCTGCT	GTCCGCGCGC	540
	GTCGTCCCCG	TCATGCTGCT	GGCTTCTGGC	CGCGCGCCCC	CGCGCCCTGT	TCTGCCCTGG	600
	AGCTGATCGG	CGGCGGCTCC	GGNGGGCTGT	CTGCGTTCTC	NTCTTTCCGG	CCATCTATAA	660
5	CGCTNTNCCN	CNANGGGGNC	GCNTGCTATT	TATTGNAANG	NCCCTACTTN	AATAANGGGG	720
	NNCTTNNGGN	GCCTNGTCNT	TCCCCCCTN	GGGAACTGTT	TTTCCCGGNA	NAANTTCNGC	780
	CTGGGNNCCC	GTGGGNCCCN	CCCGGANANT	CANGNTAACC	NCAGGGGAAN	TCCAAANCTT	840
	CTNC						
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## 1273RP

	GATCCCAATA	CAAGCAATAT	TGTCGCTACC	AGAATGCCCC	ATTTGCGACC	CATATAATCA	60
	CAAGCGAATC	CCATCCCCAC	CTGCCCTATG	ATAGTCCCTA	TGAGTGATGC	ATTTGAAACC	120
5	CTTGTAAGATA	CATCTGCACT	ATATTCTATC	TCACCGTACT	GATTTCTGAA	TACACGGTTT	180
	AACATCGACA	TGACATTATT	TTGGTAACCA	TCTGAAATAA	GCGCAAATCC	TGCCGCCAGG	240
	ATACTGAATA	GATGTAGCCA	TTTGCCCTTC	TTCCCCACAG	CAAAACGTGC	TTTGCGAGCC	300
	TCCGCGTCAT	ACTTTAGTAA	CCCTGTCGTG	GACATCGTAT	TTCTGCAAGC	CCCGGCTATC	360
	CGAATAATAT	CTAGCGGGTC	AAGCGTTAGG	TTGCTGCATT	CTATATTATA	TATTTCCCTCT	420
	CTCTACCACG	TGCAAATTTA	CCTGTATGAT	TATGCTGCAA	TCTCCGCGTT	CTACTTCCTT	480
10	TCTTTGGAGAC	CGCTACCGAC	TGCTTTATGA	TTATCGGTGC	ACCATATGGC	GTCAAGCAGC	540
	ACTAGCTTTT	ACCTGTGATA	CCTTCCTTTA	CTAACTGNAT	TCCGAACCTAN	TTTGNNCCCA	600
	TACTATATCC	TTCCCTTAGA	GTGAAATAAC	CCTCCATTTA	GGTTNNTCCC	ATTCCTCNGAA	660
	ACAGTTTTTA	AANAAANACA	ACCTTTATCC	TTNAACCCCA	AACGCCCCAA	AAANAAAAAT	720
	TCCCCATTTN	CTAGGTTTTT	TGNGCCNGGA	GGGAAGAAAC	CCCCCCTAAC	CCCCTAAANA	780
	ATTCTCTTNC	CC					

## 1273UP

	GATCGGCGTA	TAAAACTGAA	AGTTCATGTA	TGCTGTCTTG	AATGCAGAGA	CGCGGCGCAC	60
	TTTACACATC	GGCAAGCCTT	GTGTTGCGAA	TGAAACATTA	AGCTTATGTC	AAATACCATG	120
20	AACTGTATGC	CAAATTTAGT	AAAACTCGTA	CGTGCTGGCA	GCATAGATAG	AGCTGTTACC	180
	GATATCTCCC	TTGAGGCTAA	AGCCGAGCAT	TGGGTATTAA	CTTGCTTGA	CTATTCCGAA	240
	TCAGAGCTTT	CAGATTCGTC	TTCATCATGG	TCAGTCATCA	AAGTCGTCGA	TGTAGGATGT	300
	TCTATTTTCC	CACCGCAATA	AAGTGCAGTA	TTCAATGAGT	ATTCAATAAG	CTTACCTCTC	360
	ACCTCGATAT	CTAGCACATC	AGCTGGAGCG	GAACCTAACC	AGACACGAAG	TTTAGTGGCC	420
	AGCTCTTCGA	ATAGCGGAAT	TATTTCTTGG	TCCGGCAATG	ATCCTCATGC	GCCATTATAT	480
25	GGCGTAACGT	TAGGTACATA	CCTGTGACAC	CCAACAAAGT	ACAGTTGCTA	ACGTCCCAAT	540
	ATCTTAAAGG	ANCCGTTTAA	ACCNCATATT	AAGGTGAAGT	TTATGAACCT	TTGANAGTAA	600
	CTGNNTCNTT	ATAGCGGAAT	ACCANANNAA	TAACGNCTTT	GTTANGGNAT	CTATCGAAGG	660
	NTTACTTCCN	NTTCGANCAT	TTTATAGTTC	NTNCTATTAC	CCCCGANAAA	TTTGAACAAC	720
	CNTGAGAAAA	GTNTNNCCN	CNGGGAAANG	AAAANTNTNC	TTNTGANTCC	CCCCGTTTAC	780
	CTTGAAGNTT	CTCCATTTCN	GAGATTCAAA	TTTTTNTAAN	AAGGANTTTN	TAA	

## 1274RP

	GATCAGAACC	AAAAAGCAGT	TCGAGTATAT	CAGTAAGCAC	TGGGAAGTTT	GGGAAATAGC	60
	AGTGTGTAGA	GTTACGGGAC	AGATTGGCAA	AGACACATTT	GCGATGGAAT	TTAATTCGCC	120
35	GCAGCCAGAG	CACGCACAAT	TACACATTCA	CCCTAAAGGT	GCAGCCCGGC	TGCTGGGAAA	180
	ACTGCACGCG	GAGGGTCGCG	TGATGCACCA	CGAAGATAAC	CAAGAAAACC	GGGGCCGGGA	240
	AGGACCGCTG	ATTCCGTCAC	CGCCGCTGTC	ACCACGAATC	GGGCCGGGAG	AGAACCGGGG	300
	CGCCGTNGGA	ACGGAATCCC	CGAACCTTTT	TTNTTACCCC	AAC'TTGGNTC	CCNGCCTTAN	360
	TTTCAAACCG	NTTNCAAACC	CCNNCCCTGG	GTTTNTTNGC	CCNNTNCCCA	NTANTTGGGG	420
	TNCGGGGGGG	GGGGCCNGN	CCAAAAAATA	ANGGGGTNTN	CCNGGGNGGC	CCCCNGTTTT	480
40	ANCAAAANAT	TTNCCCCCGG	GGTTCNCCCC	CNNAAAAGGT	TTTTTCCCCC	CCCGGGGTTT	540
	ACCAAAAANC	CNGCCCCCCC	PTTGGANGGT	TTCCCNNTCC	CCATGGGGGG	TTTTTCNCGG	600
	GCTCCCCCN	GGGGAACCCC	AAAAAAGGGC	CCCCCCTTTT	NTGGGGCCCC	NAAANNCCCC	660
	CNTNNTTTTC	CAGANGGGTT	NCCNCCCCCC	TTTTTTTTTCC	CCATTANNCG	GGAANTCCCN	720
	NTNTTCCCCC	CTTTNNCCCC	CCCCCCTAAA	ANNAATTTTT	TNNATTAAAA	GAGGGCCCCN	780
	NGAAAAANAA	NACCCNNCCC	CAC				

## 1274UP

	GATCAATTGC	GGATACACGA	GGCACAGGGC	GATAGGCCAA	GCTTCCAAGA	ATGGGAAGAG	60
	TACCTAGTCA	GGGTGCTCCT	GGTAAGACTG	AACCGCTGCA	AGCAGCTCTA	TACACAAAAT	120
50	GTAGAGATTG	TATTCGATAT	ATATCCGCAG	ATAGACCGCC	CATAAACACT	AATGATACGC	180
	TAATTGCATC	ACCTACAGCG	TGTACATCAA	ACACACACAC	AAGTTTGATG	CACACGCTTT	240
	ATTTGTTTCT	TGCACACACT	TGATTTAGAG	GGTCAACACC	CTCAAGGTGT	TAGAGTGGCC	300
	AACACCAGAC	GCGAAACCTT	GAATAGTGAC	AATAGTGTCA	CCCTCGCTCA	GGATACCAAG	360
	CTCTTGGAC	TTCTCCACAC	CGAAGTTCAA	TCTGGCCTCG	ACGTATCTCG	TCCACTCATC	420

	AGCTGCCTCC	TGTTCTGTAGA	CGAATGGGAA	GACACCTCTG	TGCAAGTGGC	AGTATCTGGC	480
	CGCTCCTTGG	TTTCTGGTCA	CCATAACGAT	TGGAACGTTT	GGCTTGTA	TGGAGACCAT	540
	CTGTGGTGT	CACCCGAGGT	TGATACACGA	ANATGCCTTG	GCTTCTGCTC	GAANTNCCGC	600
	GAAAGCAGCA	CACAAGNCCC	CGAGGTTGAA	TTGGCTTGNT	CATTTCTCTGA	GTCACCGTAT	660
5	TTGAACGTTT	GGAAGGCCTG	CNCCACNATC	AAAATCTCGC	CAGNCNTAAA	CGTNAATGGT	720
	TGANACCCCTG	GGGNTCCCCN	AAAAATAANA	TCNCCC GCCN	GAAAAGTTCC	ACTTCGAACN	780
	CCCCNGTNGT	CTGGTTTTGN	TGGTANCCCA	ACCG			

## 1275RP

	TGACTCGGCT	TCGTGAGGAA	CTGACGCTTT	TACTACATGT	AGATTGAAAC	CCGTTTTCTCT	60
	GGATCGCCTC	GTCTCGTTGC	TTGGTATCTT	TGCCAATCCT	CCTGAGTGGA	CGCTGCCTGT	120
	AGAGGATCTT	CGCGATGGGC	CAAACACGCC	CCACCAGCCC	AAAGACGTTG	GAGAGAGGGC	180
	TGAAGAAGGT	TCATTGACCT	CCTTTATGGC	TTCAAATGCT	GACGGAAGTG	ACAAATCGTT	240
15	CCCAAGACGC	ATGTCCGACA	ATTCTCTGAC	GGTGGACTCC	AAGACCTGGA	TGCGCTCTGC	300
	CCTGGTCTTT	GATATTCTAT	GGATAGTGCC	AATGTCCTTT	GAGAGTGTC	TGTTCTCGTT	360
	TGTGAGGTTT	AGGTTATCAA	GTTGGGCAAT	AGCGAGCTGC	TCTGCAAGTT	GGTGGTTTTTC	420
	TCCACCAGCT	GTGCCCTCTGT	GTGTTTCAGG	TCTGTCTATCA	GTTTCTTTAA	GCCTCTCTCT	480
	ATCGGCCGAT	CGTCCACCTG	GACTGNTATN	TTTTTNCCAC	NCCCATNNNN	CCATAATTTG	540
	NTNAAGNAGG	TNCCCNCNCG	GAATTTNGNT	CCCGTTTCCA	NAGNTCGGNC	CGGGGATAAT	600
	TTAAACNTTT	AAAAATTANC	CCCGGCCCTA	NTTCTTTTIN	CCNAATNNNN	GNNCCCCCN	660
20	GNAANNTTTT	NCAANNCTTN	TGNNCCNTAN	CCTTTTINNC	CCCACGGTTT	TTNNTCCCCC	720
	CCCNTCCCCN	ATTNNGGANT	TCCCCNTTN	CCCC			

## 1275UP

	GATCGCCAC	ATTATGTCTC	AGGGTACTTT	GTACGTTAAG	AAGACCTGCC	GCTCGATGCT	60
	GCCTCAGAGC	ATCGTCGAGC	ACTACAACCT	GGACGTCTCT	ATTGTGATG	CCGACAAGAA	120
	CGAGGAGTTC	GAGAAGAAGT	TCCCATTGAA	GCGCGCTCCA	GCGTTTTCTCT	GTGCGGCTGG	180
	AAATCTAACT	GAGACCATGG	CCATCACCTA	TTACTGTAAG	TTGCCACCGA	CTACACACCG	240
	AAGCATGGAG	CCCTAGTGTG	ATGAGAAAAA	CTTTCGAAAA	AACAGTTATC	CCTGTCTGAA	300
30	TGGGCATAAT	ATCTGGTTGC	ACATGTGTCTG	AGAGACCATA	CTCTGATTTA	GAGCTACATG	360
	CGAGGTTCCTG	AGGAACACGT	ACTAACCAGAA	CAACAGTGGT	CAACCTAATC	CAGGACGAGA	420
	AGGCCAAGGC	TGCTCTGCTT	GGCTCCACGC	TAGAGGAGCA	GGCACAGGTG	TTGCGCTGGG	480
	AGTCTTTGAC	CAACACCAAC	TTTCTTGACG	ACGTGCTGCT	TGCCTCCTAT	ACCTAGAGAG	540
	GGTGTGGTCC	CNTTNCACCA	ANNCNACATG	GAAAAACGN	TTCCCNGNGG	CGAAACNTTN	600
	CCCNAGNGTT	TTNNAAAAAA	GAAATAACCN	CTTCCCTCCC	TTACCCCCCG	AAANTTTTNT	660
35	TTNCCGGGAN	NCCNTGNCNN	TNGGGGGGTT	GAACNNANTT	CCCCACANTT	NGGGGNGNNN	720
	NTGGGNCNG	GCCCCCCCCC	CCCNNNNANG	GTTACCCCTT	GGGTANCCCC	NNNTNAAAAA	780
	CNNCCNCCCC	CCCTTNGGTC	GGACCNAAG	GGGGGNGCCC	CAAANGAAAA	AAAAA	840
	AA						

## 1277RP

	GATCCGTCAC	GGACAGACTG	AATGGTCAAA	ATCAGGTCAA	TACACAGGCT	TGACAGACCT	60
	TCCGCTGACC	GAATATGGTG	TCGGCCAGAT	GCGGCGCACT	GGTGCTGCGA	TATTTAGCGC	120
5	AAAATACATT	GATCCTGCGC	ACATAACATA	CGTATTTACT	TCCTCCACGCC	AACGCGCGCG	180
	GAAGACTGTG	GACCTGGTTT	TGGAAAGCCT	CAGTGAAGAT	GAACGTGCAC	GCATCCAGGT	240
	GGTGGTGCAC	GAGGACCTAC	GGGAGTGGGA	GTACGGTGAC	TACGAAGGTC	TGCTGACAAG	300
	CCAGATTATC	GAATTGCGTC	GTAGCCGTGG	CTTGGACTGC	AAGCGCCCAT	GGAATATATG	360
	GCGCGACGGC	TGCGAGAACG	GCGAGAGCAC	CCAGCAGGTG	GGCCTGAGGC	TATCACCAGT	420
	GATTGCCCGG	ATCCAGGCAT	TACACCGGCA	GCACCAAGCT	GAGGGACGGC	CGAGCGATAT	480
10	TCTGGTGTTC	GCGCATGGCC	ATGCTCTCCG	TTATTTTCT	GCGCTCTGGA	TGAAGATGGG	540
	CGTCGAAGCG	CCGACGCCAG	ACTGCGCCAT	CCCCTCGAGT	AACCGGAATG	ACGATCCGTG	600
	CCCTTGGTGC	GGCTGGAGCA	ATCCGTACCT	GCAGGACACC	CCACTTCTTG	CTAGACGCAG	660
	GTGGCATCGG	TGTGTTGTCC	TACCCCNCCN	ATTTGAGACC	ANTCTACTCN	CCTGGCCNTT	720
	CNTTGCCCCC	CCGAGATCCC	CCCACGGTNA	GTCCACCGA	AAATTTTAT	ATCTACAAGN	780
	GNGTCCCCC	ATGAATATAC	CNTATCTTCT	TAATCGTCCN	CN		
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## 1277UP

	GCCGTCTCTC	TGCGGCCAGC	GCGAGTCCAG	GTGCCGCAGC	ACGCCCCACG	AGCGCGACCT	60
	GCGCAGGCGA	TAGTACCGGT	ATGCGACCAG	GCCCGCCGCC	AGCACGTTGC	TTGCGCCGAA	120
20	GAACCAGAGG	AACCGCGAGC	GGCTAACCAG	CTGCACCAGC	TGTCCGTAAT	CGTGCCGCAG	180
	CGCGTCCCCG	GACGCCAGCC	CCATGCGTGT	GCCCACAGTC	CCCAGCATCA	CGCCGCCCCC	240
	GCAGATCAGC	ACCGTCCCCA	CGCACGTAAG	CATACAAAAC	GGCTCTGCGA	GCAGCCAACA	300
	CGAAAACCA	CTGTTGAACA	GCACTCCGCA	CGCCTGCAGC	GGGGCCAGCA	TCACCAAGTG	360
	TAGCGTGGCA	ATCTGCATCG	TGCTTCCGAA	CACGTTGCGT	AGAATGAATA	GCGTCAGACC	420
25	CATCTGCCAT	AGGCGGCTAC	GGTACACCAC	CTGCACAGTT	CCCCGTGCCA	CTTGCAGCGC	480
	AGCCTTGCGC	TGAAAGTACC	AGGCCCAAAA	GACTGCATAC	GCTTGAAACT	ACCGCCACCA	540
	CGACCCATAA	TAACCAGTTG	ATCGACCATT	CGCTTGATA	CCCTGCACCC	TTGCTGTCAG	600
	AGTACTCTAC	TGTGGGCGCC	TTTGGGCTCT	AGGTCTCTAC	GCTATGCCAA	ACATACTGGC	660
	TCCGGTGCCT	CATGTTTCGAT	GCTGTATGTC	ACGTGACCGA	TGACAGGGTA	CCTGTGCGTT	720
	CTCTTCCGGT	TCCAGGGNAT	GATACCGAAA	NCCGAAATTA	NCCGGATGAA	TTTCCCAGCC	780
30	CTGCGANTAC	GACNCCAACN	GGAGACGCNG	TTTTNTGT			

## 1278RP

	GATCTTCAAC	CTGCTTCCGC	CTATGAACAT	TCTGTTGTGA	TTGAGAGGCG	ATACCGCCTC	60
	CACCTTTCTT	CGAGCCTGCC	CGGTPTTGGT	AATCCATACG	TTCTTCCCCA	TTCTTTTGGT	120
35	ATTGGTATAA	GCGATGCAAA	TGAAAACAGC	CTCTTGAATA	CAAATCGACT	TGCCTACGTA	180
	TAAAATTATA	TTTTTATCAG	AAACTTGCGG	AGCATCAAGC	TCGGCTTCAT	TGATTATAT	240
	ACTAAACAGA	ATACACTACA	TGCTACCGTC	CGAAAACGAA	TAATCTATTT	CCAATATATA	300
	TATATATATA	TATATATATA	TTATAGTTGT	ACTTTATAAA	TCTGAACTAG	GTCATACAAC	360
	TCTCAAATCA	AACGATATTT	ATTCTACATA	TAGCACGGGC	GACGCACCAA	TTGAAGACTC	420
40	TAGGGCGCCT	GAAC TTGGCG	CTGCCCTGTA	TCTTTAGCCT	GTTCTTTTAC	AGGGTCATAA	480
	ACATAGTACA	TACCGCGCTC	TAGTTGCTCA	TACTGGATGT	TCCTCTGTTT	CAGCTGCGGC	540
	CAATTTTCGT	GAGGGATATC	CCACCCACAT	TTCTGAGCTA	TGAAAGCTGC	AACGTGCTCG	600
	CACAGCCCCA	GTAAC TTAGG	TCAATTCGCG	TGCTTAACGG	GTCTCCTATG	ATAGTACTTG	660
	TGGTACGTGA	GCTGGACCNT	GTTTACATCN	CGGAACTGTC	GCNCCTTCAN	CTNTTCNATC	720
	ANCNCAATCG	CATNCANNTT	CTGGCNANTT	TTTTTGANTC	CATGACCCCC	CCNAAANTNT	780
45	TTCCGGTNG	ACCCACACCC	CCTTGAAATN	NCTGATNTGN	AGANGCNC		

## 1278UP

	GATCTTGGAT	GTACTGGGGG	CTCATACTTC	GGCTTCTGTT	TCTTGTCTCT	TTTGCCCTTC	60
	TGGCCCTTGC	CATACGTCGA	TGCTCCTTGG	CCCATCTTAG	AGATATCTGC	TGTGCGCGTA	120
50	TGGAGTAACG	CTTCTGCTTG	CGAACTCTAA	GTAAGTGTAT	CAACTTGTGT	GTATCATTTT	180
	TGCCACCTGG	AATCCATCAA	TTTCACCTAG	CCCAACCCAA	GCTGCGACCT	ATCAAAAAAC	240
	AGGAGCAGGA	AGCTGCCTGA	AGAAGCGCTC	CAGGGGTCTA	CCGACGGGAA	AAACTACGAG	300
	GACTGGTGCT	ATGACATCCT	TCCCGGGATC	CATCCCGAGT	TCAGTGCTTT	CGAGCTGTAC	360
55	AATTGCGTCC	GAGCGGTTCG	AGCGCAAGCG	TCGTGACAAC	ATCAACGACC	GTATCCAGGA	420

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	GCTGCTCAAC	GTGATTCCAG	AGGAGTTCTT	CCAGGACTAC	TACCAGAAGA	AGAAGGACCA	480
	GGAGTCCGAG	AGCGGGACGC	CGGGCGCTCT	GCCCAAAAAC	AAGGGAACTG	GGACGCGCGA	540
	CGGCAAGCCC	AACAAAGGCA	GATTCTCACG	CAGGCCGTCG	AATATGTGAC	CTATCTGCAA	600
	ACCAAGTGGAT	CTGCGCACCG	CGAAGAGGTG	GAGCTGATCC	TGAAGGTCAG	GAGCTGTGTC	660
5	GGCAGACGGG	CAGCATCGTG	AACGACGTGA	ACTAGAAACA	CCATTGCCGA	CTCGCGCTGG	720
	GAAATCGCGT	TGGGCNCTGC	AGCGTGCTCC	GGAATTNTGC	GGCCNCAGGG	CAGCACACCC	780
	NGGCAGCACA	CCGCCCCAGA	CCACACACTC	ATTTGGGTCC	CATTCCGACG	CNTAGATTTT	840
	CNCCTGGNCT	GTTTT					

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## 1279RP

	GATCCTTCTG	GATGCTGGTA	GCTCCGATGA	GGAAGTCGTA	CTTTTGGTAA	TGTCAGTCTG	60
	GCTTAAGCAT	CTACTTTCAA	AGCGTGATAT	ACAGAGAGCG	TTTGCTAAAA	GTGGTGGATA	120
5	TACGTTACTG	TTCTCCATAT	TAAAAGATAT	CCAATCCGGG	CTTACAGGAA	AAGTCACGAA	180
	TCTATTGTGC	ACCTATGCAT	TTGGAAATCA	TATTGTCCCA	ACACACAGCG	AAAGCACGTC	240
	CCTTCTTATT	AGACCGCAAG	GCGATGGGCT	ACAAAGGATA	GTTTTCGAAC	TTCATTATTT	300
	GGCAATTGCA	TTGTTAGAGA	TAGCGGTGAT	AAAAGCCCCA	AAGGAGGATC	AACAAGAGTT	360
	GAGTAAAAAC	ATTATTACGT	ATATCAACGA	GTTGGCGTTA	CTTCATAGTA	CTCACTCTCG	420
	AATATCGCTT	TTTGATCCAA	GCGTATGCCA	ACTTCATGAG	AGATTGTTAA	CTTTGTTATT	480
10	AACTTTGACA	GATCCCAAAT	ATCAGGGTTT	CTATATACAG	GCTATTCTGG	ACATTGAACT	540
	TCTATTGAGT	AACAACATAT	CTTTCACCTA	AAGAATGATG	ATCCACCACC	TTTTCGAACT	600
	ACTTGCAAAA	TATTTTGGTA	ATGAAAGGGA	CATCCGATTA	GTCCTAGCAG	ATTACAGTTA	660
	GTAACAAAGG	TCCAATTATA	TTGAGACCAC	TATATTNTAA	AATTGTCCCC	NTGTTATTGA	720
	AAACTTNTGC	CCNGGGTACA	CTTATTGCTN	TTCNACACCG	TCCTGNAAAA	ANTGTGNTTT	780
	GTTACGATTA	ACTCGTTTCC	TTGATTGAGC	AACTTTTGNT	TTTTATCATA	G	
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## 1279UP

	GATCAAGAGT	ACAGTTGATG	AAAAGGAGTT	CCATGATGAA	ATATGTAAGA	TGGACTTGCT	60
	TAAGAAATTG	ATAATATAAA	AGGCTACGAG	CTTCAATATT	ATAATACGCA	TTGCATAATT	120
20	TATTACATTA	AATTGATATA	GGTATATTTT	TCTTCGAAGA	ATTAATTCTA	ATCATTTCCTA	180
	TGTGAAGATA	TCGCCCTCTG	TGTTACCTGC	GGATATTTTCG	ACTCTTAGTA	TATCTACATA	240
	TTTTGGCGAG	CCATTATTTA	AACTCGCCAG	CTTGACTCTG	GACCCAAGAG	CCGTAATGGC	300
	AGCAGCTCTT	CCTGAGCGCA	ATTTCTTCAA	GCAATTGAGG	CACCATGTGC	CGTTCCTTAA	360
	TTCAAGCACA	TATAAACAGA	CCGTCCCGTC	AATAAACCTT	AGCACAATTA	TATCCTTTTC	420
	TTTCCAATAC	ATGTGCCGAT	ACCTGGACAT	TTCTTGAGAT	GCAAAGTTAA	CAAAGCTTAT	480
25	AGCAGTGATA	TCTTGCGTTA	GAGACATGCT	TGCAAATTTT	GAACCGTTGA	GGTCATAAAC	540
	ATGAACGTTA	TTTGAGAATA	TCAACCACCC	ATTAATGAA	CTGTACCTGT	TTGAAACCGC	600
	AATGCACTGG	NNTNNTCTGA	AATATTCNCC	AACCCNCCCT	TAAAAGNGTC	CCCCTTTATT	660
	NNGNCCTNGC	TATTTCCAAA	AACNTACCCG	NTTCTNTGTG	NCNCCAAGGN	NTTTTNNCNT	720
	TNTTGGCAGC	CTTTTAGAGN	TTTAAANATN	TTCCAANCCC	CAAATCCANT	TTTTAAAGGN	780
	CTCCCTTNA	AANNCTNTGA	ATGANCAGGN	GAATTCTGTT	GCCNTTTAAC	TTCCCAAGTNA	840
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## 1280RP

	GATCATCAGA	CCTGTCCGGAG	GGTTCGGTAG	TGGAACCTCT	TCGTAGGGGG	GAGCCGCTGT	60
	TGTGAGCCTT	GAGCCGCTCT	GGAGACGGCG	GCCTCGAGTG	AAACGGAGCT	CGTATCGGGG	120
	ATCGCGAGAT	GTACTGGGGC	GACCTTAATG	CAATTTTCTT	CTCGAAGGAC	TTTGTGGGGA	180
	CGGAGGAAAG	TCTTTCAAAT	ATTGACGCAG	AGCGGCCCTT	TGAGATTTGG	CTCTGGAAAG	240
	ACGGTCTTTT	CAAGGCCGCG	GGCAGCTTTT	CTCCCGTGCT	TGCAGCGCTT	GCCGCGAGTG	300
	CAAGCACGGC	CGCCTTCCGA	AGAACGGGAC	TCTGCTTCAG	TAGGCTTGTC	TTGGTCATCA	360
	TCGGCTGCAC	CACCAGCGGA	TCCTTGTTTCG	GCAGCGGCAC	AAACATGTTG	GACCGCCGGA	420
40	GGGTGCGGTC	ACGGCTCGGC	GGAAATCACGG	CTGCCGTCCG	AAACGTGAAC	GTGTTCTCGG	480
	GGCTCTTCGA	CATCGAAACC	TTCGTCTCGT	TGATGCGACT	TCTCCGAGTC	CACCTCCTGT	540
	ACCGTCGTCT	GCTCCCGCTC	CTGCGTGCGC	TCCGGCTCCN	GNCCNCCNGT	TCCTGCCTCC	600
	CTGACTNNTT	CCCCCCTTTT	AGGGGAACAC	GGGAAGAAAA	NAANTNCCCT	TTCTNNCCCG	660
	GCCCCCTGTG	TCGCCCCCN	NNNNCCCCCN	CCCTNNNNNN	NNNNNNNNNN	NNCCNNCCNN	720
	NNNNNAAAAT	NTAGGGGNGG	GAAAAATGNG	GTTAGNGTCC	CCCACNGAA	CCCCAAAAAA	780
45	AACCNCCCAT	GTNTCCAGGG	NCTTNATGAN	CANCTTCNCN	NTGGGA		

## 1280UP

	GATCATAATG	CGACTATCGC	CCATAAGCAG	GGCAATACGC	CTATCCACAT	CAAAGTCCCT	60
	GACCGTTCCA	TTCTCCGCGA	CCGTGACGTG	CTGTGTGACA	AAGGCTCAGC	GCTCCAGGCG	120
	CGCGATGTCA	TCCCGTATCA	CGAACTATCA	AACTCGAAGT	ATTTCACTGT	GAATCTGGGT	180
	GAAACACTAA	CACCTCTCTG	GTATGAACCG	GAGTTAAACA	TCCAAGGCAA	CATTGTGAGG	240
	GGGCGGCAGA	TTACCAATTT	AACTCAGGGT	GTACCAGGCG	ATGTCCCGAT	TTCTATTCTA	300
	GACGGGAACA	ACTATACCCA	CTGGCAGCCG	TTGACAAGT	CTGAGAGGGC	ACTCTTGTTG	360
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	ATTGATTTGG	GTTCCGAAGA	GGAGTACGAG	ATCACAACGG	GTTAAAATTT	TGTGGGGCGC	420
	TCGTCCCGCG	AAGAACTTCT	CCATCTCTAT	TCTCCCCAAC	TCAAAGCACA	TCACAGAGAT	480
	ATTGACAAAA	CTGACGGCCA	TGATGGACGG	COGGAATACG	GACTTGTCTC	CTGCTCAAAG	540
	TGCCACGCCG	TCTCTTCCTC	GCAGCATCTG	CTCGGCGGGC	TGGCGAATGT	CACCGATTCC	600
5	AGGGAACCTCG	CGGCCATTGA	TGAAAACGTG	GANNITGTTT	TAAAAAATTT	CNGTTGGACT	660
	TTCANCTCCN	NCNNTTCACN	TTTCCCNAGG	CGCCAATNCN	GANCTCCTNA	GGCCCTGNAA	720
	CACCATTNAN	CNTCGACCTA	CTCAAAAGTN	TTCTATCCCC	CAATNTCNTT	TCCAACACAA	780
	CGATCTGCTA	ATTGNGCGNC	CAACCATCAC	TTNNTGCATC	ATTTTGCCAC	AACAATGNGA	840

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## 1281RP

	GATCCGACGT	TCAGTGGACT	CTTCCCATTT	AAGGTTTTC	ACAAATTCCA	AACTCATGTG	60
	TTTAATGCCT	TGTACCATAC	CGATGAAAT	GTATTTATTG	GAGCTTGTA	GGGCTCGGGT	120
5	AAAAC TGCAA	TGGCAGAATT	AGCTTTATTG	AGTCACTGGA	GAGATGGTAA	GGGACGTGCC	180
	GTCTATATAT	GTCCATCTCA	GGAGAAAATT	GATTTTCTGG	TGAAGGATTG	GCGAAACAGA	240
	TTTTTAAATG	TGGCAGGTGG	AAAGGTTATT	AATAAACTCA	CATTGGAATT	AACTAACAAAT	300
	CTTCGAACGC	TAGCCCAGTC	GCATTTAATC	TTAGCGACTC	CAGAGCAGTT	TGACCTGCTT	360
	TCTCGTGGCT	GGAAAAGAAG	AAAAAACATT	CAGACATTAG	AGCTGTTGAT	TCTAGATGAT	420
	CTTCATATGA	TCAGTAGTGA	CTTGCCCTGGC	GCAAGGTATG	AAAATATAAT	ATCCAGAATG	480
10	CTGTTTCATT	GGGGTCAACT	TGAAACGGCC	TTGCGTATAG	TCCGTTTATC	TACCTCCCTC	540
	GCTAATGGTG	GCGACTTTGG	AGAGTTGGCT	CCGAGCTAAA	AAGCTACATT	TTTATTTCTC	600
	CTTTCACGAA	GGGTTATGCC	CTTACAGATC	CNCTTACATC	CGTTCCTAGA	NGCATGAAAN	660
	TCTTTAATTG	AACTATGGCC	AATCGCTTCC	TGACGNACAA	CTCTGTGATA	CTGCCANTNT	720
	TANCTTTTGT	TCCATTAGAA	ATGTTTCAAT	TCTGTCTNCTG	CACGCCGCGC	GGANGAAATC	780
	CTGGTCNCCN	ATTAGTTGGA	ACCATTCTAG	GNNAAGAC	TCTTATCCTA	ACN	

## 1281UP

	GATCTGAACG	TATGAGAGCG	GGTTTTTACT	AATTATAGAA	CCATATGAGA	TAGAAAATGC	60
	GGCAGTTCCA	AATCCAATAA	TGCGATTAC	GTGCCCTGAT	GCCTCCATG	CAATCAAACC	120
20	AGTGTTTGAG	AAGTTTTCGT	CAGTTATTAT	TACATCGGGG	ACCATTCTCT	CGCTTGACAT	180
	GTACCCTCGA	ATGCTGAATT	TTGAGACAGT	TCTTCAAAA	TCTTACTCCA	TGACGCTGGC	240
	GCAGAAGTCC	TTCTCCCAA	TGATTATAAC	CAAGGGGTCA	GACCAGGTAG	CCATCTCTTC	300
	TCGGTTTGAG	ATCAGGAATG	ATCCCTCAAT	TGTCAGGAAT	TATGGTTCCA	TATTGGTTGA	360
	ATTTGCCAAG	ATTA CTCTG	ATGGTATGGT	AGTGTCTCTC	CCCTCATATT	TATATATGGA	420
	ATCCATTATT	TCAACTTGGC	AGACAATGGG	GATCTAGACC	AGGTTTGGAA	ATACAAGCTC	480
25	ATCCCTCGTG	GAAACACCAG	ACGCCACAGG	AAACCTCCTC	TACCTTTAAA	AACTNACCNA	540
	AGGCCNGCCC	NNAATGGGNC	GGGCCANTTA	ATTTCTNGTGG	CCGNGGGAAA	ATTCTNAGGA	600
	ATGGATTING	ACNCCCTCGG	NGGGAGTGTT	TGAAAATGGA	TCCCTCCCTT	NACCGANAAC	660
	GTTTTNTTAT	GGAGGGTTNT	NTCCNTNANA	AAANATCCAA	ACCGGGAATA	CTTTTCTCTT	720
	NNAGCATGAA	NCCCCCCCC	TTTGGGAAAA	TTCAGGGGTG	AGGAANATAT	GGTTAATGTN	780
	CCCCCCANCN	GNNNCCNNAA	AAAAANCACT	CCCAATGTCC	CAGGNCCTTN	NGNACCACCT	840
30	CTNNNNATTG	GAT					

## 1282RP

	GATCCGGAAT	TATAGAATCG	ATGAGCATT	CATTTAGCAA	CCTTCTTCCA	ATTCGTAATG	60
	GTTTCATAT	AAACTCCCTA	GCTTCCTCTT	GATAAATCCT	TTCAAGAACA	GCACCGTCGC	120
35	AGTCTGGGTT	TATCTTTATA	TTATTTCTTG	TTATGCAACT	CGCATGGTCT	ATGAGGTCCC	180
	TACATACATT	TAGGTCGCCC	ATCAGTACCA	CCCTCTTCCC	CAGATTCTCT	ATGTTCTCTA	240
	CACGTTTGAA	TAGAGTTTTC	AGGAAACGCA	CCCTAAAAAC	TTCACCCTCC	TCAGTGTTCA	300
	TAGAATTAGC	AGGGCAGTAT	ACGGAAATGA	CCACCACCTT	ACAGGCCAAT	TCGACTAGAA	360
	GGCATCTCCC	CTCACTGTCT	AGTTCTGTGT	CATTAGCATC	ACTCCCATAG	GGCAAGCCAT	420
40	CATAACCACC	AATACCAATG	GTCGGGTCTT	CGCAATATGC	TACCAAGGCG	CCATCCTTTT	480
	TTAATTTTTT	AGTCTGCCTG	TAATACCTCC	TCCCGCCTTC	AATACTTGTA	ATGATTATCG	540
	CAACGATCGG	CTGCTTCAGG	GATTCGTGTT	CACNCCACN	CCNATACCCT	TCTCCTGN	

## 1282UP

	GATCTGCGCA	AACACCCCCA	CTCTGTGTAC	CTCCTCGATG	CTGTCAATCG	AGTCTTTGTC	60
	CATGCTTCTA	TCCTTCAGCA	GGAACGCGCC	TAGGTACGGG	ATGTTCCGCC	GCAGCAGCCC	120
	GCAGATAGCT	TCGATGACCG	CGGGGTGCGTA	CACGGTCACC	GACTTGTAAGT	ACCCGGGGAA	180
	GAGCGGCCGG	TTGCTCATCG	GTAGCACCAT	CAGCTCCTCG	TACTTGCGCG	GCACCTCGCC	240
	CTCGCTCGGC	GGGTTTCGAC	GGCCCGCGCC	GCCCGCCGAA	GACGCCGAAC	CGCCGCTGCC	300
50	CCGCGAAGAA	CTAGCCTCCG	ACGACCGATT	CGCCTGCTCT	TCCCGTGGCT	GCCGCTCCGC	360
	CTCCTCGTCG	CGCACCCTTT	CCTCGTCGCG	CCCCTCCTCC	GCGCGCGGCG	GCACCTTTTT	420
	GTCGTCGCTC	TGGTCCGGCT	CCCCGGTCTT	GCTTCAGTAT	GCAACTGCCC	GCCGCGTGTA	480
	TCCCCGACTG	GTCGCCAAG	GCCACTCTTT	TTGGGGGGGG	GGGGGGNNNG	NNNNCCCCNC	540
	CCCCCGCCGG	GCGGCGTTGN	CCGCCGCGCG	CCGTTTGTGC	TNTTCAGGCC	GCGCCTTTGG	600

CCATCCCCCC CTNNTTTTTC CT

## 1283RP

	GATCAGGAAA	TCGACGGGAC	TGGCTGATTG	TCTTTATAGT	CAAGCATATT	AAACACACGT	60
	GACTTAAACT	AGATTTACAC	GTGACATGCA	ATTGTGTCGT	TTCTTTTTTA	TTTGAAAAAC	120
5	CTGCATCGAG	CTATTAGATG	CTCATCGACA	CTAGTGTA	AACCAGTCAA	GGCTTAAAAG	180
	CTCTGCAGCA	TGGACCACTC	GAATAAGGAG	CATCGTCCTA	AAAAGGAGAA	GGCGACAGCT	240
	AAAAAGAAGC	TGCACTCCCA	GGGCCACAAT	GCGAAGGCAT	TCGCGGTGGC	CGCTCCGGGA	300
	AAGATGGCCA	AGCAGATGCA	GCGCAGCAGC	GATAAGCGGG	AGCGCGCGCT	GCACGTTCCG	360
	ATGGTGGACC	GGACGCCGGA	CGACGACCCG	CCGCCACTCA	TTGTTGCCGT	TGTAGGTCCC	420
	CCGGGGACGG	GTAAGACAAC	NCTGATCAAT	CGCTGGTGCG	GCGGTTGACC	AAGACGACCC	480
10	TCGGCGAGAT	TAACGGTCCG	ATCACGGTCG	TCTCCGGCAA	GCGCCGCCGT	CTGACGTTCA	540
	TTGAGACGCC	CGCGGACGAT	CTGAACCTCG	ATGTGGACAT	TGCGAAGGTT	GCAGATTG	600
	TGCTGCTGCT	GATGGACGGT	ACTTTGGTTC	GAGATGAGAC	ATGAGTTCCC	TGACCTGGCN	660
	CACNCCACGG	ATNCCCTTTT	NCTGGATTAC	AANCNCCAT	TTTTCATTNC	NAGGCCNCTC	720
	CNGCTCNAAA	ACTTTTNACC	TCGTTCTGAC	NATTTTNCCN	GGGGNNCUNT	CCCCTTCTGN	780
	TTTTTTATGN	NGNNCCNT					

## 1283UP

	GATCCGCTGG	CCCATCGCCG	AGAGCTATGT	GCATCGCCTC	ATAGTGGCCT	TGATACGTGT	60
	CTCAACCAAG	ATTGTGGAAG	ACACCGTGCA	CTCCACGAG	TATTTTCAGCA	AGGTCTGCGG	120
20	CATATCGAAG	AAGCTCTTGA	TGCGCCTCGA	GCTAGCCCTC	ATACTCGTCC	TCCGCGGCGA	180
	GGGTTTGATG	GTCACGGCTG	CAGCTCTAAA	CGCTGCCTCA	AACGCACGTG	CTCGGCTTCG	240
	CGAGCAGTCT	GCGCTGCCAG	CCGCTGCTGC	TCAGTGATAA	TCGCCACTTC	TAGGCCACCA	300
	ATTTCGGTTAT	TTAATAAGCA	ATAAATACTC	CAACACTAAT	AGTATACACC	GTTTTCGAGA	360
	GTAAGCACGC	AGCAGGAGGT	GGCAGCTTTT	CTGGTACCAC	CTCAAGCCCC	TTGCCATTGC	420
25	TGCCTATCTG	GTTTAGGCAT	GAGCAACCTT	AGTCAGTTTC	GAACCCGTGA	TATATGTTTC	480
	GAACACGTTA	CCTTTTCGGT	GAAAAGAAAA	AGCCTAAAGG	CGAAATGTTT	TCCATGTTAA	540
	CACAGCAGAT	TAGAGGTACC	TTGTACTGGA	TATTCTGTAG	GATCACGGGC	TACGAGCATT	600
	CATCCAGAAG	CTTTGAACCT	ANGGTGTTTC	NGGATGGCAG	TTNGGGACTT	ATNCCGTG	660
	TNTAAANAAA	TACTTCGTCC	TAGTCTTTGG	AACAAACNTG	CATTTGTTGT	TCTTNGTTTG	720
	GANNATCGGN	AAGACANCCT	TTGCCCTGCT	AANAAGACNG	TTGGGAACNG	NNGCCNNTGN	780
30	CCCNCCTCCG	GNCNNGAACN	GGCCCCNTTN	CNNTTCNNCN	GGGGNNNNC		

## 1284RP

	GATCGATCTG	GTCAGGTCTA	TTTGTGGCAC	CGATGACAAA	AACATTTTTTC	TTTGCAATTCA	60
	TACCATCCAT	TTCAGTTAAC	AATTGGTTAA	CGACTCTATC	AGAGGCGCCA	CCAGCATCAC	120
35	CCATTGAGCC	ACCTCTAGCC	TTTGCAATGG	AATCTAGTTC	ATCCAAAAAG	ACAACGGTTG	180
	GCGCTGCGGC	TCTAGCTTTA	TCAAAAATAT	CACGAATGTT	GGACTCAGAC	TCACCATACC	240
	ACATGCTTAG	CAACTCTGGA	CCCTTCACAG	AAATGAAATT	AGCAGATACT	TCAGTTGCGA	300
	CTGCCTTTGC	CAACAACGTC	TTACCAGTAC	CTGGAGGACC	GTAAAACAAC	ACACCTTTTC	360
	ATGGCGATAG	ACCAAACCTA	ATGTATTGGT	CAGGATGCAA	GACGGGATAC	TCAACGGTTT	420
40	CCTTCAACTC	CCGCTTTATG	TCATCCAACC	CACCAACATC	GTCCCAAGTA	ACGTTAACCG	480
	ATTCAACCAC	GGTTTACGTC	AGCGCGGATG	GATTGGAGTT	CCCAAGTGCG	AATCTAAAGT	540
	TATCCATTGT	AACTCCTAAG	GAATCCAAGC	ACTTCAGCGT	CGATTTTCATC	CCTCGTCCCA	600
	ATCAATTAGA	CTCATCTTCT	CTCTAATCTG	TTGCATTGCA	GCCTCTGAAC	ACAAAGAGGC	660
	ATATCAGCAC	CCACATACCA	TGGTTTCAGC	AGCTAGCACT	TCCAATCACG	TCATCAGCCA	720
	TCTCANTTCT	TGNTGTGGAT	GTTTAAATTC	CCACCTTCCA	GTGCTCTGGA	NACCANTTTA	780
45	TTNNNGTCAA	TTTACCAACT	TTTAGNCGGN	TNNATGG			

## 1284UP

	GATCAAGCTG	ATATGTATTTC	TCGGGCTACT	GGTCGTATCC	GTGGTAATCT	TCCTCGGCGG	60
	CGCTCCCAAC	CACGACCGTA	CTGGCTTCCG	CTACTGGAAG	AACCCGGGGC	CCTTTGCGAT	120
50	GAGCCTCGCG	CCAGGAAGCA	CGGGCCGTTT	CTTGGACGTG	TGGCGCGCCG	TGATCAAGTC	180
	GGCCTTCGCC	TTTATCCTAT	CACCAGAACT	TATAGGCATT	GCATGCGTCG	AGGCGCAGGA	240
	CACCCGGCGG	AACACTGAGA	AGGCATCGAG	ACGTTTCATA	TACCGTATTA	TCCTTTTCTA	300
	TGTGAGCTGC	GCGCTCATGA	TCGGCGTCAT	CTTATCAAGA	ACTGATCCGA	AACTCATAGA	360
55	GGCGCTGGAG	ACAGGCGCGC	CAGGCGCTGC	CTCTTCTCCG	TTCTGTGCAGG	GGATTGCCAA	420

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	CGCAGGGATT	CCCGTGCTCG	ACCACGTCAT	CAACGTCGCG	ATCTTGTCCTT	CTGCGTGGTC	480
	GGCAGGCAAC	TCCTTCATGT	ATGCATCCAC	GCGCATGGTG	CTAGCGCTTG	CGCGCGAGGG	540
	AAATGCGCCA	AAGTTCTCTCA	CCAAGATCAA	CAGATATGTG	TGCCCTACAA	CGCGGTCATC	600
	GTCTGCACGC	TCGTGCGCTG	TCTTGCCTAC	CTGAACGTCA	AGACGACTCC	GCAATGTGTT	660
5	CCAGTGGCTG	TCGAACATAT	GCACCATCTC	CGCTTCATCC	GCTTGTTTCGC	CATGGCTCCC	720
	TTATATCCGT	TCCCNNGCGT	TCTTTTCACA	CTCCNANCCN	TNCCCTNCCA	GTTCCCTGCA	780
	CCNTTTCNCC	ACTATTCCNT	TNTAATGTNT	CTTTTTCGAC	AATGTTCCCT	C	

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## 1285RP

5 GATCCGGGTC CGCCACAAGC TGCTGGTCCA CATCGTGCTG CTGCGCGGCC CCCCCGACGC 60  
 GCCCGGAAAG AAAACCGAAA TCAAGGCCAG CATTCGGGTT ATGCTCTACA TATCGCCGCT 120  
 CGTACCTGTG CAGGGCCGCA CCGTCCTGGT TGATAACGCT GGCCGCTTCC ACATCCGTCC 180  
 CGGCGTGCTG ACAGACCTAT TCCGGACGCG GAGCGCGGAC TCACTTCCGA GCTGGGACGC 240  
 GCCGCCGTCC TACGAGTCGC GCGTGCACGA TCGGCTGTAC GATGGCGACG TAGGCTCGCT 300  
 TGCTTCCGGC AGGGGGGGCC CGCCCGATTG GGCGGCGCCC CGCCCCCCTG GCAGGGTCCC 360  
 GCCACTGGGT CTCCTTCCGC CCCTTCACGC CTTGTCTGTG GATGATCTAA CCCCAGATTG 420  
 CACGTACCAA CAGCAGCACG ATGGACACTC CCTGCCATTG CATCACCTCT CCCCAGCGTA 480  
 10 TGCCGCCACC GCGCCACCNG CCGGGGGGCA ACAGCGACN TGACAATCAC TTNTGCGGTC 540  
 CGTCGCGGCC CCCCAGACCC CCTTGCGCCC TTATTCTGCC CCCCCCAAAC CNACNTGCN 600  
 CCAATAGGG TCAAACCGCG GNGTTGGNAA TTINCTTGNT CNGNNNNCNG NNCNGGTTTT 660  
 GGGCCCCCCC GGTNNCCCC CNNTNTNGC CCAANCGGAA NCCGGGGAGG GTTNNNGTGN 720  
 NNCNGTAAAA ACTTNTACCC CCCCNCCTTG GGTNCCNGGC CGGNGGGTTT TTTTTTTCCC 780  
 CCGGNGCCCC CCCCNNNGG ACCNTTNGGG NACNATT

## 1285UP

20 GATCTTCTTC ATGACGCTAC TGTAGACAGT TTCACAACCG ATAGCCTGAA GACACAGTAC 60  
 AACCAGAGCA AAAGATATCA ACTGTTTCGG ATTCCGTATT CGGAGCATTG CAGCTTTAAG 120  
 GACCTAAGTA TTTTCGCAAC CACGATCCAG ATGAACGCCA TTCGATCTAC AGTGAACCTG 180  
 GCCTCTTTGG AGATGCATCG CATGTGGTTC GACACTTGGT CTCGTATTAG AAACGAAAAA 240  
 TACCTGCGTA AATTATGATT ACATGTTATA TATAGTAAAA GATAACACGC CACTCAGTGT 300  
 TAAATGGTCC ATCATGCCTC TAGGACTCGT TGTCGTGTCT CGACAGAACT GCAGTCCCCA 360  
 TTTGCCTGGT AGGTTTTTGT GAGGCTTTTT TCTAATTGTC TAATTTAAAG TCCTGAATAT 420  
 25 TATCTCCCAA TTGTGGAATG AAAGACACAT GTACCACTAG AGGTTTCAGCC CGATGGCTGC 480  
 AAAACGGCAT ATTTGTATC CAAATCATGC CGCTGGTCCA ACAGTTTAAT AATGTCTCTG 540  
 GAACTTCGAC TACGTCCGGA ACTCGTCTAT CATCTGGAAT ACCNCCTCCT GTTATGCNTT 600  
 ACCATANTCC CCTCCCTTGG TGGCCNAATT CTTAANCAAT TTTTGNNTAA ATNCCCCCNT 660  
 GCTTNNCTAA GGTNAATTCC NNTTGGCCCC CCCCCTCGGG TTTNTCCGTT CTTTGGGAATG 720  
 GAGGAAGCCC AGGCTTGNCC CCCAATACNC GCCCTCCGGG AAGNGTCCTC CTINGCCTTN 780  
 30 CCCANTGGGN TNCTTGGGTT NGNNGCAAAN CNACNNCNGG CCTCTCTNCN C

## 1286RP

35 GATCGCACCT ATAATGAAGA CCGGTTTTTT TTTATGAGAA ATAGCAGCCC TCCAGGGGTT 60  
 ACTTATTAAA TAGCTACAGT AAGATTAGGT TATTCGTTTG CAAATTCATT GGTAGATCAA 120  
 CTTGTACACT TCAAATAATG CTTGCTGGC ACCGTCATAA AACATGTTAT GCCCGGTGTT 180  
 GACAACACT CTGAAGCTAT AGTCAGGTA GTGCGTGGCA TTAGCTGGAC ACACCTTATC 240  
 TTCACTGCCG ACCAAGACAT GCCCTGTGCA CCCCCTGTGC AGCAAAGGTG GCGCGTTAAT 300  
 TAGGTCTTGC CAGCCTAGAA GATACTCAGT GATGGATTG GTCGAAACTG CTACACCGTC 360  
 GTAGAAGTGA TTTAGCTTCC TGTACTTGTT CCCCATGTTG GAGAAAAAGA ACTTAATTCC 420  
 40 GGAGCTGTTT AACCCTTCAT CTGGTTCGAA TTGGTCTTGA TGAATTTGAG AAGCATGATC 480  
 AAGAAGGGCT TGAAGAATGT TAGTGAAAGG TTTAGATATG GCTCGACGAT ATCCAACCTT 540  
 GATTTGAGAG TTCTAGGTGG CCGCGGCGCC AATAGAATGA TCTTTCTGCG TTCAATTGTT 600  
 GACGCCGTAT CCTGAAGGCT AATGCCAAGC CAAATGCACC CCATCNATTG CCCAAAACTC 660  
 CCACNGACAT TATTATGGTT GGCNCGTAGA CCATGAATCT AAACCCCTTA TCACNCACCC 720  
 CCCCACANG GTTACCATCG CCCATGTCCC TTCCCCANCC TGAGNTCNAC CCCATTNTCC 780  
 45 CCCTATTTNC CACATATCNT CC

## 1286UP

50 GATCTTCGCA GCCAGCGCGT AGTCCACCGG CGTCAGTCCC TCGCAGAACG CCCCAGCGTG 60  
 CACGTACAGC ACCACCGGGT CGTCTGGGTG CCGCTTGTGCG GGCCGCGACA CATACACCGC 120  
 GCGCGCAGTC CGCTCCGCGG CCGCAGCCGC CCGCCCCCGG AGCTCGAACA GGTGCGTATC 180  
 CTGCACAACG TACGTCTCCT CCAGCACCTC CCGCCCGCGC TCGAACGACC GCGCGCGGTG 240  
 CCACACGGC AGCCACGTCC CGACCGACGC CCGCAGCGCG GCCGCGCGCG CCGGGTCCGC 300  
 GTGCCGCGCG GCCTCTACGC CCAGCAGTCC CAGCAGCGTG CGCCGCCCCG CCGCGCGCAC 360  
 55 CACCGAGTAT ACCAGGCGCG CCAGCGCTGC CGGCACGCCC AACCATAGA ACTTCAGCAG 420

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	AAACGCGAGT	ACGCTCCACG	TTTGTGTTGG	AGATCCCATG	ATGCCGGCCC	GAGGGACGTC	480
	GACGCCCCGCC	ACCTGACGGG	GCGGCTACTT	ATACACCACA	AGATTCTATA	GAAAAGGAAT	540
	GCGACCAACG	ACGAACGGTG	TATCGTTTGG	GAAAAAAAGG	AGTCCCCCAA	CTAAAGCTTG	600
5	CTTGCTGGCT	ACGAGTTTGT	GTTTCAGGTT	TCTTCATAGC	ATCCCAGTTG	TTTTGTTTGT	660
	TTGGCAAATC	GCAATATGAAC	CATAAANAT	CAAANNTTGT	ACAATTGCTG	CCGACCGTTG	720
	CCCCATCCNC	CGGCGAAANA	TCCAGAAATC	GAGANAATTT	CAGACGCCGG	GTTTGCCAAA	780
	NTCCCGAAAC	CCCAAANTCC	CAACATTCT	GNCACATTG	ATTCTGNNNC	NNNCA	
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## 1287RP

	GATCCCACTG	GTATTAGGTG	TCTGAACACG	GCCAAATAAA	ATACGCAAAA	TGAAGGGCAT	60
	TAATAATCTT	TCATCAGTGT	TGACAATAAC	CCTTGACTCA	TTCTGAGCAA	ATAACTTTGT	120
5	TACTTCGTCG	TTGAATAACG	TGTCATCTAA	TAAGTTCTTC	AGATTGTCCC	TATATTTTAC	180
	AGCTACTGGA	TCCTTGTATG	CTAACAACGC	ATCTAGGGCC	AGTTTCTGCA	CTTCCAGCGT	240
	TCGACTACCC	AATAATTCCA	TCAACCTTTG	GCGGACATCT	TCGGATTGTG	AAATAGCTTT	300
	GATATTCTTG	AACTTGCCCC	ATAATTTCAA	AATTAGATTG	CTATCCGTCT	CAGACCATGT	360
	ATCCGCAGAG	TGCACTGCTA	ACTCACCAG	ATGGTCTTCA	TCTTGGTTGG	CATCGAATTG	420
	ATCATTGCGT	TTTAAGACAA	AAGGTACAAT	GAATCTGCTA	TTTTGCTCCC	GCGAGCTGTN	480
10	GCAGCGCGAT	TAATATCTTC	AATGCTTGTT	TCTAATCATA	CCGGATATCC	GAGTGAACCG	540
	CGANCCCCCT	TAAGGTTTTT	CAACCAAGGA	TTTTTCGAAA	NCAACATNCN	TTTNGAACNT	600
	TCCNAANNCA	AATAATTNAT	CCTAAAAAAT	TTNTGCCNA	NTCCAAAAAN	TCCCCNAGGG	660
	GTNNAAAGAG	TGGCCCCAAA	TTCNAAATNA	GNNTTTTTTN	GGGNTTTNCC	NAAAAAAAAT	720
	CCCNCCCNAC	CNCGNNTTTA	ANAATTTTTG	GGAANCCCAT	TCCCCCCCCA	AGGGGAAAAA	780
15	AGNGTGNCC	CNATTTTTNA					

## 1287UP

	GATCAGGTGG	TGTTGGCCGA	TACCGTGACG	GAAATGGATG	TCCTGGCCAT	GCCCGAGATA	60
	GATTTCTCTG	ACACAACGTC	CTCCTCGAAG	GGCCTGATGC	GGCGAGAGCG	CTCAATGGAG	120
20	AGGCACGTAC	AGGGCGCGAA	CACGGTCACA	GACCCATGGG	ACATGTCTTT	GGAAGTGGGG	180
	AGAAGATACG	CCCCTGACGA	CGACCTGGAG	CAACAGACGT	CGCTACTGGA	CCTCAACTTT	240
	GAACCTCAGTG	ACATGCAGAA	CTCCAAATCT	TGGGGTGAAG	GGACGCACAA	TTCCGAAGAG	300
	ATCAGTGCCA	ATGTGCTTGC	AGAGTCGCAA	CGCCAGGAGC	TGCCCCGGAA	CGAGGGCATT	360
	GAGCGTGAAG	AGGATCTTGA	TTGGAATCTG	GGATTACCGG	AACCAGCAAT	TGTAGTCCCT	420
25	TCAAGCGATT	TTGAACACGA	TAACAGCATA	GAAGTGGGCC	GGAGAGCAGT	CCCCGAATGC	480
	GGACCTTCAG	GAAACTGTGG	ATTTGGGATT	CGACTTGGAT	ATTGCCAGGG	TTGACATTGA	540
	GGCTACAGCC	GGCGAGCAGA	TGCTGGCAGT	TTGCATCTGA	GCTTTCCGGA	AGTATAGTAC	600
	GTCTTCTGG	AACACTGTNC	ACANCCAAAA	CAAGAAAGGC	ACCTGGTTAT	CAATTCTACA	660
	TTCACCCCCA	CCGATTACT	GAAAGGTGNT	CNAAAACCCC	CCCNACANTG	CTCCNTGANT	720
	ACCCATCCCN	NCCCCATTCT	NCCCNAAAAC	GGNTNTCGAC	CCTTTNAAAT	GATCCTNCAA	780
30	TTTTGCNTGA	CATCCTGCTC	NTTCCAACG	AGNCCCA			

## 1289RP

	GATCGGGATT	GACCGTAATA	TTTCAGCTTT	TTGATGTGAA	TTGCCAAGAG	GACCAGCGAT	60
	TTGAATCTCG	CTGACTCTGT	TGTGAGTAAT	TAGTACAAGA	ACCTGTGGCC	TGTCACAATT	120
35	AAGCCCTGGG	AATAGGACTT	CAACTTCAGA	AGCCACGAT	CGTCAAGCGA	TGATACAAGT	180
	GCCTACCAAC	ATTGACTTAA	CATGAAAATT	GATAGCATT	TTATAACAAT	GGAAGCAAAAG	240
	GACTAAGTCC	TTACAGTGGT	CGCCAAATGA	GCCTGTTAGC	AGGTTTCGGC	ATATTCTCTG	300
	AAGATGTCAA	CCTTCCAAAA	ATATTCTCTCA	GAGCATTAA	TATCATTACA	CAAGCCCTTG	360
	GTGTGAGACA	GAATCTTGAG	AGGTGCTGCG	ATAAACTCA	AAATCGCAGT	GCTTGGATTA	420
40	TAGGGCTTAT	ATACTGATTT	AAGTGGTGGT	GGTTATCTAT	TCAGGGTTGT	ATAAAATTAAA	480
	ATATCACAGT	CGGTATACTC	TTACACACTA	ATTATAATCA	CGTGATATTT	GACTATTTAT	540
	TACACCAGGA	CACCTCGCTA	TGAAAATAGC	AACAGGCTGA	TGGTATTAA	ATCTGAAGAT	600
	ATCGCCAACA	TTAGAACACA	CTACTGACAC	AACGGCCAGC	CATTTCGAGC	TATGGCTCGT	660
	ACTACTGCAN	TACTGTTCATG	CTTATCTGAC	NCTGACCNC	TGATTGTTGC	GGAAATCCNT	720
	TTGATCNGCA	AAATCATNTC	GNTGACCNCA	ANTTCTACTN	TATTAACCCC	CCCACCGCCA	780
45	ACCTTTG						

## 1289UP

	GATCCCAAGG	TGCCCCAGGA	TGACGGAAAG	TTGCATGTTT	TTTTCGGCGC	TACAGGCTCG	60
	CTTTCCGTAC	TGAAGATTAA	ATCGATGATC	AAAAAACTCG	AAGAGATTTA	TGGTTGGGAC	120
50	CATATATCCA	TTCAAGTCAT	ATTAACCTAA	GCCGCTGCGC	AATCTTTTGC	TAATAAAAAAC	180
	CCCAAGAAAG	AGAACTTTTA	CGTGTCTAGC	GAAACAAACT	CATTCTCAAA	CTCCGTGGCT	240
	CACCAGGGGA	AACTTGCAAC	AGAACAACCT	AGACGCATCC	TACACTGCGG	TAAATAGCGT	300
	CTCCAATACC	CCTGCACTTG	GGGGGCGCAC	ACCAACGCCA	GCGATCTTTC	TCCAGGGCGC	360
	AGCGCCGCAA	GGCGCGGGCT	CCGGTCTAAG	CCAGGGCGCA	GCTGCGGCGA	AGATTGAGCT	420
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5	CCCTCCACAC	ATACAAGTCT	GGACGGATCA	AGACGAGTGG	GACGTGTGGA	AGCAAAGAAC	480
	AGATCCGTAC	TGCATATTGA	ATTACGCAGG	TGGGCGATAT	CCTTGTCTGC	GCGCCACTTA	540
	CGCGAATACA	CTTCCAAATT	GCCCTGGGCC	TTGTTAAAAC	CCGCGAACAT	GTTCTNCGGG	600
	NNTGNAACCA	NTTTTCCAAT	TCNTNCNCCA	NCCGNGTTTN	GNGNTNTTNA	ACCCCCCCCC	660
	TACCCCCCNA	AAAANAANAA	NAAAAACCCC	GTNTNCNGTG	TTTCACCNCC	CANAAAAANAG	720
	GGTNCCCCGG	GAAAACGAAC	TGGGGGGAGA	GAGAGGNANN	AAATTNCNAN	AATCCTTTTA	780
	NCCCNNGG						
10	1291UP						
	GATCGTGCAC	GGCAAGACGT	CGGAGCTGCG	TCACGACGGG	CGCGGGCTCT	TCCAGGGGGT	60
	ACCCCAGGCC	GTGGCAGTGA	CACGGTACCA	CTCGCTGGCT	GGACTGGCGT	CAACGTTGCC	120
	GGCGGAGCTG	GAGGTGACGG	CGCGCACGGA	GACAGGCGTG	GTTATGGGCG	TGCGGCACCG	180
15	CAAGTACACC	GTGGAGGGTG	TGCAGTTCCA	CCCAGGATCG	ATTCTGACGG	ACCACGGGCA	240
	GCTAATGGTG	CGCAACATGC	TAGCGCTGGA	AGGCGGTACG	TGGGCTGAGA	ACGACAAGCT	300
	CCAGCTGCGG	GCAGGCGCGG	GCTCTGTGCT	GAGCGAGATA	TACGCTCAAC	GACAGGAGGA	360
	CATGGCAGCG	CAGATGGCTA	TGCCGGGAAC	TGGTATGGCG	GACCTGGAGG	CGAGCTTTCG	420
	ATTGGGGGTT	CTGCCGGGCG	TGGTGGACTT	CCATGAGCGG	CTGGCGCGGG	ACGCCCGCGG	480
	CTGGCTGTGG	TAGCCGAGAT	AAAAGTGCCT	CTCCGTCGCG	TGGCAATATT	AGCGAGGCGC	540
20	TTGGCNCCAN	AANANGCGCT	TNCNINTTGC	CGAAGGCGGA	ATTTTCCGCC	ATCTCCGGTG	600
	CTTTACCGAA	CCCACTGTTT	TAAAGGGACC	CGCNAGANCN	NAATTATTNC	CCGACCCNCC	660
	CTTTGANAAA	AACNANACTG	CCCAANANCC	GCCGCGTTTG	CTNCTTTANG	ANATCTTTAT	720
	TNTCCNTTCC	AATNTTTTGA	GCCCGNTTNC	GGCCNACAAT	TTCCCTTATT	TTNAAATTTT	780
	NAACCACCCC	CCCCCAGACC	NTTTTNTTN	CCC			
25	1292RP						
	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTTCATTAA	GAATGATTAT	TATCAAAACC	120
	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTAC	TTAATTAAGA	ATTAGGAACT	180
30	TTATCTATTA	GTCTGGGCTG	TTTCCCTTTT	GATTATTAAC	CTTATCGCTA	ATAATCTGAA	240
	ATATTTAATT	TTAGATTAAT	AATATATTCT	GAGATTTAAT	ATTTTTAATA	AAATAAATAA	300
	TTATTCCTTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTCGTAGAAA	ACCAGCTATT	TGCAAATCAG	ATTTGACTTT	CTCTACTTAC	420
	CATTATTTCAT	CAGATAATAT	TGCTACATTA	ACCTGTTCAA	TCGTTTTTAT	ATTTTATTAT	480
	ATTTTAAATA	TAATAAATAT	ATATTTTAAT	CATTTGATAA	TAGTAAGATC	ATCTGCTTTC	540
35	GGTTTAATTA	ATATTAACCTA	AATTTAATTT	ATTTTAATTA	ATTTTACATN	GTAAANATT	600
	TAAATTAATT	TTAAACCAN	TTTTATTTTN	AAATTTTGNC	AAATTAATAC	TGGGGGNCCC	660
40	CTTTCCAAGG	GGCCTNNNTN	NATTTTTTNA	AAAAAATAAA	AAAGGGCNNN	ANAAACCTTT	720
	TAAAANTTCC	CCNNGGCCCC	NNAANANTNA	AANATTTNAC	CCNAAAGGTC	CCN	
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## 1292UP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAT	ATTTGGTTAA	60
	CAATAAAATT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
5	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAAATTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAAAGGGGGT	TAGCGTTAAT	CGTAATGGCT	TAAAGGGTTC	240
	GTAGAATGAT	TATTTAAAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTTATT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
10	AATTAAAGTA	TTCCGCCTGA	TGACTACGTT	TGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTCCGACTTA	AGCAGTGGAA	CATGTTTTTT	AATTCGATAA	CCNCCANAA	ACCTTACCAN	600
	TTTTNGAATA	TTTAATTATA	ATAATTTINTA	ATTATTACGG	NGTGCATATT	NTCTTCCCTC	660
	CGGCCGGCNA	GTTTTTNAAT	TATCNTNAAC	GAACAAACNC	CCATTTTTTT	TTTNANAAAA	720
	ATTATTTATT	TTTTGAATAT	TNAAAAAATA	TAAANATCCT	TTNTCCTTTT	TAATGGNNGA	780
	GTNTTTTTTT	TTNTTCNN					

## 1293RP

	GATCACCGAG	CAGCTGGTTG	GCCTCGGCAT	AAGCGCGCTT	GGTCTCTGCC	CACTGTTCTC	60
	CAAGACCAAG	CTGCTGTGCC	TGGAACAACA	GGTTTGTGAG	CTGACCACCA	GGAATTTTCAT	120
20	GTTTGTACAC	CTCTGGGTCC	GGGCCCTTGA	GGTCCGCTTC	GAAGCATGAG	TACAACAGTC	180
	TCATCTCCGC	CCAGTATGCG	TCTAGTTCCGA	TGCGATGATC	GGGGTCTACA	CCCGTCGCGA	240
	TATCGCCACC	CAATGAGGCC	TGCAAAGCCG	TAATGGAGGG	CTGGGACGTT	AAGCCAGACA	300
	TGAGATTGGT	GGCGACGTCC	ACAACATCGG	CGCCAGAGAT	GGCGCATTGG	ACCATTGATG	360
	CGACACCTGT	GCCTGCGAGAA	TCATGTGTAT	GCACATGAAT	TGGGAGGTCT	GGATACTTTG	420
25	CCCTGATCGA	GCCAATCAGT	AGCTTTGCTG	CACCGGGCTT	CATGGTGCCG	GCCATATCTT	480
	TAATACCCAA	GATATGTGTG	CCCCATGGCA	ACAATCTMTT	CAGTCAATCC	AGTAGTAATC	540
	AAGGTTGTAC	TTCTTGCCCTG	CTGTAGCATA	TCACCTGAGT	TACAGATAGT	GCTCAACCAC	600
	CCTCCCGCTT	TCTTCACGGG	TNNAAACCCA	CTTCACTGTT	CTAGTCNTCA	CCCNTCNAAN	660
	CTCTGAAATN	TCANNCATCC	CCTTGCTGTT	TGACAAATGT	CATCCCNMTT	CCGCNAAAGA	720
	ATTAACACCC	GTGGCCCCAA	CNCCCTGAAN	GATTTTGGCC	NG		

## 1293UP

	GATCTTACAT	CTGACAACAA	TACGCTGGCG	GCAGATGAGC	TGCATTGATG	GAAATTTTAA	60
	CACAGCTCGG	GCAACCAGCT	ACACGGGATA	TATAAACTCA	ATGCACGCCG	CTCTTTACTG	120
35	ACACAGTCCA	TCAGCATCAG	CACCACCCCC	AAAAATGAAG	ACTACACACA	TCCTATCCCT	180
	AGCAACACTT	GCCGCTGCG	CACCTGTTCA	GCCCCGACCT	GTTCAGCCCA	CGGACCTCGC	240
	CGCAGCGGCA	AACGTCCCCG	AGAAAGCTGT	TCTCGGCTTC	TTCCAATGTT	ACAATGTGGG	300
	CGATGTGGAG	CTGCTCCCG	TGGACGACGG	CGCACACTCC	GGGATCCTTT	TCGTGAACCG	360
	CACACTAGCG	GACGTGGACT	ACTCCTCCGA	GCATGTGGTT	CAAAAATGGT	TCCGTCTGTC	420
	TCTCCACCAT	GGGCAAAGTA	TGTAAGGCCG	GACCAGAGAC	AGTTTGCCTT	GAGATATGTA	480
40	AGTTTACTTG	GTGTCCTACA	CCATGCATTA	TGACACGGGC	TTACGTACCT	GCTTCTATAA	540
	GCTAGTTTAA	ATGTTTTCTA	TGCGTATTAT	ATGGTTTACC	CGCGCCGATA	GTTCGCAGAG	600
	GCTGCTGTNT	TAAGGCCNAA	CTTTATTCCCT	AANANGGTGG	ATTACCCGGT	NGAAANAATG	660
	AATCTGAATT	GGCGAAATTC	CCGCTGGNCT	ATTANCTCCC	CNNCCCGTCC	NAATAAATGG	720
	AANATGGTGG	GGTTTAATAC	AAAANGGNCC	GNTGCCGCA	ATGNACTGGA	TTAATTTCAA	780
	AAACCTCCAA	NTACCCCCAA	NTGGN				

## 1294RP

	GATCCGGAAT	GTCGCTCAAG	CTCCGCTGCT	TTCGGCTGGC	CTCGCTGTTT	TCTGTGGAAT	60
	CGTTTCTGGT	GGTCTCCTTC	TCCCATGTTG	ACCTTGGGTT	CAGCGTCTTC	AGCTGGTACA	120
50	CCTCGAGAAG	CTTCGAGTTA	TGGAATGCAA	ATGGGTTTAT	CATCTCGACC	ATATTGCTG	180
	CGCCACCTGC	CTGCCCTTTT	GGCCTTACAT	CGGGAGTCCA	ACTTCAACGT	AATGCTATAG	240
	AAAACGCCAT	TGGCCTCGCC	GTCTTATCAC	GTGACTGTTT	ATTGAGCTCG	ACAGCTACTC	300
	GACTAGCACT	GCTGCTGCTT	TAAGTGGGCT	ATACACTTTA	TATCGTTTCA	TTACTTTCTC	360
	CGTGGTCCGC	GGATGGGTGG	TGCTGGCTTG	TGTGCAGACT	CACTCTTGAA	CAGAGGAGCG	420
55	TTCTTAAACA	TGCTGGGTAC	GACAAAGAAC	CTTACGTGCG	AGCCTCCGCA	CGAATACATG	480

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5	GTCCATATGT	GTCACCTGGC	CGTTCCGTGC	CGTCGCTGTC	ACGTCTCTTA	GCTGGCAGTC	540
	ATGTTGTCCT	CGCTGCCCAC	CAACTTGCCC	CGATAGTTTC	GCCGGTCGTT	ACTCCAGCAN	600
	ACCGTGTNGC	TTNGGCTTCC	TTCACACTTA	CAGGAATCCG	GAANTGCCAG	ATCNTACTTT	660
	TTGGTTTGGC	CGTTTCCNTT	CCTGACANAA	ANTGGTTTAT	ATTTTGCCCG	AAAAGNTTTA	720
	ATTTTACATT	TTCNAAACAA	CATANGTTGC	NTTTTTACNN	AACC		

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## 1294UP

	GATCTGGAAC	TCCAAGTTCC	TGATGTCTCG	CTTACGCTTC	TCTCGCTGCT	CATGAATCGA	60
	CTGCTGCTTC	CACCGAATGA	ACGACCGCTT	GTCCACATTA	GGATGTACCT	CGATGTCCGA	120
5	GTCATCCGAG	ATTTCTATCT	TGTCCCACTT	TGAGTAATCG	ATTGCCATTG	CACTACCTTG	180
	TTTCGTTCTG	GCTTCACTAC	TGTTGTCTTT	AGATCTTCTG	GATCCACCAA	TAAGTATAT	240
	CAAAGATTCA	TATATGCAAA	CGTCCAACCTA	AATAATGTTA	CACATAAGGA	AGGACCAAGG	300
	CAACGCCTGC	CCAGTTCTAG	CAACTTCTGT	GTGTCACTCT	CAACGATAGA	AGTCTGGTCT	360
	CGAGATGTTG	AGACCGTACT	CGGCCACAGC	GCTGCTGAGG	TCGTTGACGG	TCAAGGTGAC	420
	CTTGTTTCGCA	TTGGTCTTTT	CGTTTGTGTTG	GTGCTGCTGC	TGGCTGATCT	GCTGTGTGCC	480
10	GGGCTGCTGC	TGACCGAGCA	TCAGTTGTCTG	GGCGCGGGCC	TGGCCGTGTT	TGGAGTTATG	540
	GACGCGAATG	AGGAGCGGAT	ACGGAATACT	CGTAGGCGTT	CGGCCGCNAT	GTCGCTAACG	600
	AACTCTGGTT	GCCAACGCGA	AGAAGGCCTT	GACCCGANAT	CNGTGCACNC	CGAACCCTCC	660
	TGGTCANTTA	TTATCCATCA	CACNTCGGGA	AAAAGGGGGG	GGTTCTCTCT	AAGTCNAAAA	720
	CNCTTGANGT	CTGTCTCTGC	GGTGAATCGG	ATTTCCAAAA	CTTCTTTTCT	NGGGTTTGCC	780
	CCNGCGGCCC	CCNGGGGNGA					

## 1295RP

	GATCTTTCTT	TCAAATTGGG	ACGAGGTGCT	TAAGTCATCC	TGATCCTGCA	CAATCACGTC	60
	CATATTGGCG	GAGATCAGTG	CCGGTTTGGC	ACCAGAATCG	CTGCCCCGCC	AGGTGACTAG	120
20	CAATCCGAGC	TCGTGACAG	TTTCCACCTT	TAGCTTACAC	CAAACCAGAG	GAAAGTCCCG	180
	CGACAGCTGC	TCGTGCAACC	GTTTGAACCTG	CTTGATATGTC	TCCGTGTCGG	ACTTCACCGC	240
	TGTGCAGCAG	TCCGCTGCAT	CCACCACCCA	TGCCGAGGGG	ATCTGCACTG	CACGCTGTAG	300
	CTTCTCGACA	GTGAGATTGC	TGAGCGTCTGA	GTTGTGTCAGA	ATTTGCTGGA	GGTGGTCTCC	360
	AAAGCCCCCC	TGAGGTTTGG	ACACGTCCCA	GCACGATGGC	AGTGACGCCC	CAGTCACCTC	420
25	CGAAGAAACA	ACAGCACTCC	GCGCTGTCTG	AGCAGAAAAG	CAGGCCAGCA	ACGCCAGCGC	480
	CGTTGCAAAAG	GATATCGGTT	GCCCCAAAGG	CCAAGCTGCA	AACATCATTC	TGGTGGTCAG	540
	CGACTGCTTT	TCCCACGAGA	TCCGTGGGGA	CCATGCGCCA	GATGGCGCCC	TTAATATAAG	600
	CCCCTCCTCG	CCAGCATGAC	TTCTGCCAAC	TCCCAGAACAT	TCTAAATGGC	CAGCTGCTGC	660
	TTTGATGGTA	CCTNCCGCNG	CTNGCGCCAA	AATTNATATA	CCATAATCCC	CNTCCTAAAT	720
	ATNCTTACAT	ACCACGCCCC	AAAGCGCTCC	CCGNAGCNCN	CCCAGCCCCC	CACCTTCNCC	780
30	NNAAGNANCC	GNTGNG					

## 1295UP

	GATCAACTTC	AGTTCTGCGC	GTTTGTGCGCA	TGGAGGCCCG	CCAACGGCAG	ATAGCTTCTC	60
	AACTGTGGCG	GTACCCTGCA	CGGGCTCCAC	GACCGCTGTG	CAGTGGAAC	GCTCGTAATT	120
35	GTTCTTGGTG	TAGTGCTTGA	AGTACTCCAA	AGACCACACG	AATGCGAGGC	CTGCGAGGAT	180
	ATAGAAAACC	AGCGTCCCGT	ACCTACCGAT	TGCCATGGTT	GAAGCAAGGA	TTCCACTGCC	240
	GTAAGTACTC	AATTATTGAG	TGCTAGCAAG	CTGATGTTGA	TTGTGTGATA	TCAACGGTAA	300
	TCGGTTCGTTA	AGGAACCTTT	TCAAGAAACG	CAAAAGAAAT	GCGTGCCTAG	GTCGAGCAGG	360
	TGACAACCTC	ATATTACTCA	TAACAGTTAT	CTATCTAAGA	AGCGGCACTA	TCGATATACT	420
40	ATCAGCTTCG	TATACACATA	TATATCGGAG	GTTTATAATC	GCAAGTTAGC	TATAATTGCC	480
	ATCGAGGTGT	AATACATCGA	AGATTGTCTA	CGAAACTACT	CTGTCAACCA	CACATCAGCG	540
	TATGAACAAT	AACAGCAATA	TTATGACAGG	CAATTGCATA	AAAGTATTCA	AAGAGGGTTA	600
	AACAGTTAAA	TTCCGTAAAG	GTTTCAGNGAN	TATTCCTGTA	CACCCCATAC	CGAATCGCCC	660
	TGCACCAATT	GTTACATGTT	TCANAGATTC	TCCGGGACTT	CATATGNACC	ATGTTGCCCG	720
	CCCNAACTCN	CATTATGTNA	ATGCTTGTNT	TCCTGACTCC	CCCGCTTGTC	CCAAATGCCA	780
45	TCCCAGGGTG	ANAGGTGCTC	GTGATCTC				

## 1296RP

	GATCCATTGT	GCGTTTGGAG	GTCACGCCAC	GGACGTGGAC	ATGTACGTGA	TGAGCTTCTGA	60
50	CGGGCAGCTC	TTCATTCTGT	CGGCACGCAA	GAAGCTTGAG	TTCCCGACGT	CTCCGCGGGA	120
	GAGTTGGGCG	TACCTTTCGT	ATTACAGCGG	ATACAAATTC	GAGCGCATGG	CGCTCCTGGA	180
	CCGTCCGGTG	CCGGAACTC	CGCGCGAGGT	TCTGGAGAGC	CGCGGCAAAC	AGGTCTGTCCG	240
	CAACGGTCCG	CAATACAGGA	CTGTGATGAG	AACCGGCGTC	GGGGAGCACA	AGCTGGTGTCT	300
	CGGAGCTGAG	ATCGACGGCA	TCATTGACTT	CCGCGAGCCT	ACGGGCGACA	ACCTGAAGCA	360
55	CTACGTGGAG	CTGAAGGTGT	GTGAGAAGAA	CCGGAACCTC	TCAGAGAAAC	TTTTCTCTTC	420

	TTGGCTGCAA	TGCTTTCTGG	TGGGCATAAA	CAGGGTTATT	ATTGGATTCC	GGGATGAGAA	480
	ATTCCTCCTG	AAGAGCGTCG	AGGAGTTCAG	TACGTCAGAG	ATCCACACCC	TGTTTAAAGG	540
	GCACGGAATA	TTCCATGTAT	GTGTGTGACG	CCATAGATTG	TATGGTGCTC	CTTACAAATT	600
	GCTATNTGAC	TCCCCCGGGC	CCTGAAAAANA	NTTCAACTGT	TACAGTCTCC	TGCNNCATGG	660
5	TGCTTACTTT	TGCCCCACTG	CCCAACAAAA	ACCCCCAATG	GGANAAATTN	TCCCTNGTTG	720
	GTCCCCAATT	GGNGNGNCCC	CCANATANAA	AATTCCGNAT	TATTCCCTTG	TTTCCTTAN	

## 1296UP

10	GATCGTACGG	TTGCTGCTG	CGGTTTACCG	ATATGGATCG	GTGTGTTGCA	GTTGGCGAGA	60
	GCACGGTGGT	CGGTGTCTCT	GGCGACGTCT	CGGACATGCA	ATACCTACAG	CGCCTGCTCC	120
	AGGACATGGA	GATCGAGAAC	AACTACGACA	ACAGCCACGC	AGACGGCGCG	GAAGCGCTCA	180
	AGCCGAGCTA	TATTTTTGAG	TACCTTGCTT	CGCTCATGTA	CCAGCGCCGC	TCAAAGCTGA	240
	ACCCGCTCTG	GAACGCCATC	ATCGTCGCCG	GCGTCGAGGA	CGGCCAGGCC	TTCTGCGTTT	300
15	ATGTGGACCT	CAAGGGCGTG	AAGTACTCCG	CCCCAAGCTT	GGCTACTGGC	TTTGGCGCCC	360
	ATATGGCCAT	TCCTCTCATG	CGTAAAGTCG	CAGATGCCGA	AAAAGACTCG	CCGGCGTCTGA	420
	CCTCTCAATT	GCGCGAGCGA	CTATCCTGGA	GTCCATGAAG	GTGTTATTCT	ACCGCGATGC	480
	GCGTAGTTCC	CGTCGCTTCT	CGCTTGCCAT	CATCGACAAT	GATGCCGGTG	TTTACGATGG	540
	AGCAACTGGA	AGTGGAAAAC	ATGACCTGGG	GTTCGCCCCA	AGGATATTCC	GGGCTATGGC	600
	NCCCAAATNT	TTTGAATTAC	CNNGGCCGCA	ACGCCGCACC	CTGTTTACTA	TCTTGTTCGC	660
20	GGNTGTCNCC	CAACCGCTNG	GNTATCCCAT	ACNTTCAAAA	NGCNTAATCA	TCTGCCCTGA	720
	ACCCCNCTGT	TTTNGTNGAN	ACCTTCNCCC	CTTTTCNCGA	TTTCCCGGAT	TGNCAAAAAC	780
	CCTTTGAAAA	AACATTNCCC	NTTGGNAAAT	CGATG			

## 1297RP

25	GATCTCCTCG	ACGCTGGTGA	CCTTGCCGGC	CTTCACAAGA	CGGCCCAACT	TGGTCACTGG	60
	CACCCAGCCC	TTCTCCTCGA	CCTCTCTTCT	GCCCTTGCGG	CCCTGACGGC	CCTTGTTTCT	120
	GGCGCCGAAG	CCGCCCTTTC	TTTGTTCGGG	AGCTGACATC	TTGCTATCGT	CGGAATGGAA	180
	CACGGAAAGC	TGGGGGAGTA	ACTTTCGATC	GACGCTGCTG	ATGTAGTTAC	GATACAGCTC	240
	CGGCCGCGCG	CTTGCGTGCT	GAAAACCTGC	CCACGGTCTG	CGTCACCAGA	AAGGAGGTCT	300
30	GGGTGCTACC	GCTGTTTCCG	GCCTCACGAC	GTGTCTGGGT	TTTCACTGTA	AACCCACACA	360
	TCAGACAAAC	GCAGTCCCGG	ACGGCTCGAA	AGCAAAACCC	GCGTGAAGGA	GCAACGCGGA	420
	AGCTGCGGCG	TCCGTGCCGA	ATCTCGTCAA	AAACAGGGGT	CACAAAGGGA	TTGGCGCTGG	480
	CGCCAGGACT	GCTACGGGGG	CATTGGCCCC	GGCGGCAGCC	CCGAGCAATG	GAGCAACCCC	540
	CTTCGCGAGG	TACGGCTCAC	ACTGCGGTAT	AAAGGCGGGC	AGAGCGGTGG	AAGCAGACAG	600
	TGACACACAG	GAGAGGACAG	ATGTCCGACN	NCAAAATGAC	AATCCTATCA	ANAGGNGCGT	660
35	CGGGGCCAAA	CTATCAANAG	NTTCGAAGTT	CCAAACTNGC	CAGATCAAAA	GGCCCCAAAG	720
	GGAAAAAACT	TCCCCCCCCAC	GACCCTTTGN	CATTTTAAAC	CGCCNG		

## 1297UP

40	GATCCAAAAA	CAATGAACTG	TTTACAATGT	GGAAGCCGTG	ACACAAGTGA	ATGGCGCTCA	60
	GGACCGCTAG	GAAGGAAGTC	TATGTGCAAT	GCATGCGGTA	TCTGGTACAT	GAAATTAAGG	120
	CAGCGGTTTG	GGGAGGAGGA	TGCTGCGGTG	ATTATGGAAT	ACCGGAGATT	AACTAATAGG	180
	CACGATGATC	GCAGGGTGCC	CAAGAAATTT	GAGGTCCCAT	TGCCTGAGGT	CGAAAAAGTG	240
	AAGAGAGCCA	TAAGAGCTCG	TGTTGTGGAG	TATTTGAATG	ATGTTGAAAT	CCCGGTTTAA	300
	ACGAGGAGGC	GGGCGTTATT	ACATAAAGGC	AAGCCGGGCA	GTGCGTTAAA	AACAGAGATG	360
45	AAAACCCCTG	CCGCATGAAG	CACTGGAAGG	ATGAAACCAG	TTTGTACAGC	GGAAAGGACAA	420
	TACCGGCGGG	TAGGAAGGTA	GAGACTATGC	TGTGGCATGT	AAGGAACGTA	CTTTTATTTA	480
	TCTAACATAA	CTAGGGTTCT	TTTGACCTGN	TACCTTTGTA	TTATCCTTTG	AANAACGTAA	540
	CCCCCNCCCT	TTAAAAANTT	TTTNNNTTGN	AAATAAATCC	CCTTTTAAAG	ACCCCCCCCN	600
	NAANCAAACC	CTTNTNCCCT	TNGCCCAAAC	CCACCCAGAA	ATTTTCCCN	CNTTNCNGAN	660
	ACANCNGTTN	CGAGATTCCC	CCNTTTNCGC	CNAAAAAANC	TCCCCCCGAN	TNTNTNCCAN	720
50	AGNGCCCTTT	TNCNCTCCCC	NCCNANAATC	CCCAAATTAG	AAGGGGTNTT	CNCCCNNGCT	780
	CCCCGAGATC	CAAAA					

## 1299RP

	GATCTCCCAC	ATTGAGACGG	TAGCAGCCCA	CATATTGCGC	TTGAACGCCA	TTAAACGGCG	60
	CCATTGCTCC	CATAGAGCTT	TCAGATTTCC	TGTTAGGCTC	CAACTCAACG	TCATACTGGA	120
5	GTTTAAATCG	AGTGGGTGCT	GTTGATATCC	AACTTGGAGG	CGTTCTTTT	GTCCTCGTAT	180
	CGCTTGAATA	GCCGCCCAGG	TCCCGTGGCG	AAAATCCATA	TATATCCATA	TTGGCCACCC	240
	AGCTTGTAC	ACATAGAGGC	AATAGTGCCA	GTAATGCCTC	GAGCCGAAAC	CATGCAGCTC	300
	CCC GCGAGG	AGGCGCCCCG	CAGCGTCGCG	TTCCATAGAC	GGCAAGCCCG	GCGAGTGC GG	360
	CGCACGCTCA	GCACGCAGTT	CCTCCCTGTC	ACGGTATGTC	CCCAGCCGGC	GGTGCGCACA	420
	CCCAGATACT	AACACAGCAC	AGACGCTGTA	TCAGCTGATT	GTCCAACCGG	CGTACTATTT	480
10	CACGTTTCTG	GCGAATGTGC	TAGTGACGCG	GTTGCGCGAG	GGCGCGGCAG	TGCCCATAGC	540
	AGTGGCGTTC	TGGATGTGCA	CGGTGGGCCT	GGGCATTCCC	GCCC GCGCTG	CCATTGTGTC	600
	TGCCGCGACG	GGTGTGGCAG	GGTGTGCTGG	TGGGTGCGGT	GTGCTGCCCG	AACTACCACC	660
	TGGAGTACAT	GGAGACCTAC	ATTGCCGAGCC	TGCTCGTGAC	GGGAGAGGGG	GAGTCCCTGTT	720
	TTCNCCGATG	GGCTCCCGGC	GGTGGGCGGT	TCC			

## 1299UP

	ACGCTTTTGG	TTTTCGGCGT	GATGGTGGGT	GGTGGTATAG	ACGATGTGAT	CTCCGGCTGC	60
	AATTGTAAGC	CTTCTCCTCC	GGAGATATCC	CGCACGGAGA	AGTCGTCTAA	ATTTAACATT	120
20	ACGTTTCATGT	AATCACAGGG	CACCTTTTCA	AAGACACAGA	CGATCATGCC	ATTCTTACGC	180
	TTTGCCACACA	TGGACGCCCA	AATGAATTTT	TGTGTATGCG	AGGATGCTGA	CGATGCAGCT	240
	GAAGCAGGAG	ACGACAGCGA	TGTGACGCCCT	GGTTGTATGA	CGCTACTAT	TTACCTGTG	300
	AATACTTGTT	CTTGGCCCTC	TGTAGACATA	ATCTTGTATA	GGACAAAGCT	CCTGCTGTCTG	360
	GTGTGTATCA	GGTCAAGTAA	AGTAAGCGCC	TTAAATGCCA	ATTGGAGAT	ACCGAAGATT	420
	AAGCATGCCN	AATCGTTAGC	CGCCCTAAAC	TGCCATGGGT	GATGCTGGGA	ACAGGTAAAT	480
25	ATGGCCTGAG	GTGCTGTGTA	CTTACCTGAT	ATAAAAGTAT	GCAGTATGCG	GGGCGCTTCG	540
	TACGTTCTGTC	TGTAGTCTAT	CGGATCCTGG	ATAGATGTTA	GTTTCATCGGT	AAATGGTTGG	600
	AGATAATTTT	CGTCTGCGA	GGCCTGTATA	TGTGTAATAT	TCATGAAATG		660
	GTTGGGCTAA	GCTTTCAAGC	AGCTGCTTCT	TTAGTTCTTG	CTCATTACTG	ACTTCTCTCG	720
	CAGGATCTAC	GCCATCCGCG	TTGGTGCTGA	C			

## 1300RP

	GATCTCTCTG	CGCGGTGCAC	AAATGACGCA	GAAACAGGCA	TTACGGAAT	TGAAGAGGCC	60
	TCAACTGCCG	CCGATCGCTA	CAGGCGCAGT	GGGACGACAT	CCTTTCTTTG	GTGCGTATGA	120
35	GGATACCTAA	ATAAGCACAT	ACAAAACGTT	AAATATGCAT	AAGGAGATAT	ATGCGAAAGT	180
	TAAAGTGTTT	TTAGTGGCCC	TGGGCCACAG	TTGCGTGTIT	CAGCGATAAT	GGGAGACCAG	240
	CCCGGCACGT	GATCAGATAC	GGTTGTAGTG	GCCATACGGG	CTTGCGGACG	AATCTACGGG	300
	GTATGGTGCC	TGACGCTGCG	CCGGCGGCGT	CTTACGCTGA	GTTCCCCACA	GCCGTTCTCTC	360
	GTA CTGGTTG	ACGTCTTCGT	CGTGCAACGC	CCCTCGTTTG	CCGTAGCGGC	CCCGACTGCC	420
	CCCCGCCCTC	TGCGCCTCGA	GATCGTAAGA	CTCGTTGCTG	CTGCTCGAAA	AGCCCTTCTT	480
	GCGCTCGCTG	TAGTACTCGT	CCTTGCCGTA	GTACCGCGCG	GCCTCCGGCG	TTACTACGGG	540
40	CTGGTATACC	ACTTGTGGCG	CGGAGCATAT	ACTTGTGCAC	GCTGCTTCTC	CTCGCGCCCG	600
	CCGCTGGCGG	TGCCGTCTAT	AGCAGCAGCA	CGGCCAGCAC	AAGAGTCGCA	GATTCCNCTC	660
	ACCCCCCAT	AAACNCCGAN	TTACACCCCC	TATCCNATAC	CCAATTGACG	CTACNCATCC	720
	CNCTATACCC	CATCNTTGCA	CNCGGTACCT	ACTTTTCCCN	AANTGACCCC	CACNTNC	

## 1300UP

	GATCGAGGAG	TTTCCACTGG	AGGTGGCGCG	CTACATGACG	CTGCTGCGCG	AGATAGACGC	60
	CAAGTGCGTG	CACACGGTGC	CGGAGCTTAA	CGCGCAGATA	GGGCGCTTCC	TGGCTGGCTC	120
	GCGGCAGCCG	GGAAGCCCGC	AGCTGCAGAC	CATCAACCGG	CTCTTCCAGG	ACCTGATGCC	180
50	GTCGCTGGAG	GAGAAGATGC	ACGTCTCGTC	CATTGCGTTC	GAGACGCTCG	ACCGGCTCGT	240
	CGCGCGCGTC	GAGCTCGCGT	ACGAGGTGCG	GCTCAAGAAC	CAGGAGATCC	CCGACAAGCT	300
	GCGCCTGGGG	AACGACAACC	ACCTTGCCAT	GCACCTGCAC	CACGAGCTTA	TGAAGAAGAT	360
	CGAGTCCAAG	CAGCAGAGCA	AGTCGCAGCA	GGCGCTGCGC	TCCGAGTCCC	GCCGCGAGGC	420
	GATGGCGGGC	AAGAAAATGC	ACGTGGACCC	GCCGCGCGCG	CGCCTGCTCT	CAAAGGCCCC	480
	CGCTCCCGNT	GGCCCCCGGG	CGCCCCCTGG	CCGCCAAGCG	CCCGCGCAAA	CTTTCCCCCC	540
55	CGCCCCCGGC	GCNAGCGCAA	GAAGCCCAGG	AACAANTACT	CCGCCCGCCC	CCNAAACAAC	600

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AATTTGGGA	AGGCCTCTTA	CTGCTACTGC	AACCATTTCNC	CCTACGGGAA	AATGTCGGTT	660
GCGAANGGGA	AAAATGCCNC	TCNATGGTCC	CTCCCCTGGA	TCACTCNAAA	CCTTACCGAN	720
GGGAAATGTT	CTGCAANAAT	GCAAAAAAAC	CCTACATACA	GNCCGGTTAC	TANNTCCCCC	780
CCNCCTNCN	TGCCTTNCAA	TGGGTTCNC	NT			

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## 1301RP

	GATCCGCGAG	ATTTCATCGTG	GACCCGCCAC	AGGCAATTAC	TATAACAACA	TCCTGCGGTG	60
	TTAAAGGACC	TAACTCACGC	TCAAGTATTT	CAGGATGATA	TCCTAGATGA	AGAGCTGCGC	120
5	CACACGCTGG	TTCCGTTTACA	ATATTGCTCT	CTTCCGCAAA	ATTTAAACAT	GTCTGTACTA	180
	CAGCGAGCTG	GTCAAGCACA	ACAGATTTTG	TCCTGTATTT	TTGGGCGTAA	CTCAGAGTAA	240
	GATCCGTCAC	GAAAGATGTG	CATAAAGAAG	TAGCAACGCT	TTTAGGATTTC	ATCGAAACGT	300
	TCCTGCCCCAG	CAGCAAAGAT	CTGTGCAAAA	CCTCGCACCC	CTCTGTTTTCC	ACTGCTACAA	360
	CAGGGATAGA	GTCTGCCAAA	CCATGTTTCT	CCAGCCCATTA	TACAATCCCA	TTATATAACC	420
	CCCCGCCACC	TACGCTGCAG	ACGATACCTT	TCACGCTCTC	CAATTGCACG	CCTTGGAGAT	480
10	GCAGTGCTTC	TACTACTTCA	TCTACCATTG	TTGCATGCCC	TTCCAGATG	AGTGGTTGTC	540
	GAATGGATGT	GCATATATCG	GAGCGACTTT	TTCTAATTCA	CATTCCCCAT	CAACTCCGGA	600
	CCGTAAGTTA	TCATCGCTCT	CTTTCAATAC	ACTTCCCATT	GANATCACAT	CNGCCCCCGT	660
	TGANCGGTTT	CGCTCTACCT	CCNCCGCCAA	TTNTTTCNGN	CCTACNCGGG	CAGGTNTCCT	720
	NTTNNCGTGA	CCCGTGGTGC	TGCACCCNTG	CNTGCNCCGA	CTCCCNAAAC	NTTTGGNTGC	780
	GNGAAG						

## 1301UP

	GATCATCTGC	GTGCGATACT	GGCAAAAAAT	GAGAGACAGC	ATGATGAAAA	TATAGTTAAT	60
	AAGATATTGC	ATGATATAAG	CACAGGCGGG	TTTCGTGCGA	GAGGAAAGGG	TGCACTTGAT	120
20	CTGGAAATGA	GTGAAAAATGA	AGACCAAGAG	TTACAACAGT	TTAGACAGAA	AAGACGAGAA	180
	CTTTTGAAC	AAAAGATATT	GGAAAAATGGT	GATACTAGCA	AGCTCGTATC	TAACCCCAAG	240
	TCATACGCCT	TTTTTCAGAC	GATGGTGGAC	GATGTTACTG	AAGCATCATT	TGGAAATACA	300
	TTTGATGCCA	ATATAGATGA	AAAAACAGAT	CCATCTGCTG	CAGGTGCGAA	AATTGTCTATA	360
	TCAGAACAAT	TTGTAAAGGA	AACCCGTGCA	TTCTTGTCGA	GCAAGAGTGG	CGACTCAGAA	420
	ATCCCTGCAG	AAACTAAATC	TATTTTCATCC	AGCACAGTTG	AACGTGAAGA	AATTCAAGAC	480
25	TTCATACATT	GAAGCAAAAT	AGTAACATTA	ACATTTGAAA	GGAGTCTAGA	CTTCCTGCTC	540
	AGATGGCTGA	CTCAGCAGTG	AGATAGAGGT	GATTACNGCT	TTCTTTANAT	ANATTCCNCN	600
	GCCGCNAAAT	TTTTATATGA	ACTACTTCAC	AANANTTTTA	AAGTTGGCCC	CAGGGGGGCN	660
	ATCTTAAGGG	AATAAANATN	GCGTCCAAGC	CCAATACTTT	TNTNGGAAAN	NGTNGNGGTC	720
	CCCCCNAAAG	GATTTAAATT	CNACCAACTT	NTCCNCCANN	ACCCCCCCCC	TTNTTTTCNG	780
	NG						

## 1302RP

	GATCGAAGAG	CTTCTCGCTG	ACTTCGAACG	GCACAAGGTA	CCCAAGCTCC	TGTAAAGAGT	60
	TATGAAACTC	CGTAGCGGAA	AGCGTGAACG	AACCGTTAAT	ATCATTTGTC	ACATATATCA	120
35	TGCGCCACTT	CTTCACGCGC	TTGTATAACG	AAGTAACTC	AGACAAGTTT	ACGGTACCAA	180
	AGCGCGTCGC	GCCAAACAGG	CTAATTAGCG	CGTCCACCGA	ACTCATGCAG	AACTGCCGAAT	240
	TGTCATCATT	CTGTAGCAGA	TGCTGTAGCT	CCTCTGCTGT	GAGACGCTCC	ATCTTCCGGA	300
	CGTCGTGATT	CATGAATAAT	TTCTTTGCTG	TTATAGCATC	GGGGTCTTCA	TTAGGAACGG	360
	TGGCGGGCTT	GGCTTGGGTA	TGGTTCCGGT	GAGGCTGCTG	AGCTGGCTGC	GGCCTTGCGAG	420
	GCAAATTATA	GCTCTGTGCG	CTCGGTGGTA	TTGGCTTCCC	GTGGCCCCGGC	AGGCCAGGCG	480
40	GGCCTGTGGA	ACGCGAGGAG	GATTTCCCTG	AAGCTGCCCA	ACGCCATGCG	CAGGCAACTA	540
	CTATGTGTAC	AAAAATTGCC	GTGNTCCTGC	AAAACCTTTG	GTCTGTACAG	AACCCANCCC	600
	ATGGCCCATG	GAACGGNNTG	GNTTTTTGCC	CCAAATTAAN	CCCTGGANAA	NTGGGNAATT	660
	TTTGGCCATN	TTTTCCNATT	AAAAANGGNG	GGGTNNAAGT	GCNAGGGNGC	CCATNTNGGG	720
	GGGNAAANTC	CGCGCCTTTT	TNTTTTNCAT	AANGGNCCNC	NTTGANNNCC	GCCCCNNNNC	780
	CCCAC						

## 1302UP

	GATCAACAAC	ATACTTCTAA	AGACATCAAT	ATACGCCCGC	ATGTCTCCGG	ATGAAAAACA	60
	TGAATTGGTT	GAGAGGTTGC	AGTCCATTGG	ATACCAGGTT	GGCTTCTGCG	GCGATGGTGC	120
50	GAATGACTGT	GGTGCCCTTA	AAGCGGCCGA	CATTGGTATA	TCTCTATCCG	AAGCGGAGGC	180
	ATCTGTGTCT	GCGCCATTTA	CATCCCGCTT	GTTTGAAATC	AGCTGTGTTT	TGGACGTAAT	240
	GAAAGAAGGC	CGTGCCGCGT	TGGTCACGTC	CTTCGCCTGT	TTCCAATACA	TGAGCTTATA	300
	TTCTGCCACA	CAGTTTGTTA	CAATATTGAT	CTTGACAGC	CGTGGATCTA	ACTTAGGGGA	360
	CTTCCAGTTT	TTGTACATCG	ACCTCTTCTT	GATCGTGCCG	CTAGCGGTGT	TCATGTCTCT	420



5  
 GTCGAAGCCC TATGAAGTAT TGGCCAAAAA GCGGCCAACG CCAATTTGGT TTCTCCGAAG 480  
 ATATTGATTC CTTTGCTCGT GCACATCGTG ATTTGTTCGT GTTTCAGCTT GTCCCGTGGC 540  
 TCGCAGTCCA GCATATGAAG TGGTACCGGC AGCCAGTCGT CGCGACGACG AACATGTTGC 600  
 TTCCCANGAN NACNCAACCC TTCTTNGTC TCCACTTCCA TAAACCCCTGG TCCCAATCNT 660  
 GCTTCCGGTN GTCCNCCCN NCCNCAACC NAANTTCGAA AATTTTGGT TATGGCANTT 720  
 CCCCCTTCCC TGNCCCTCCC GGTGGANNAT TTCCCCCCCC CGAAACAAC TGGCNNTTT 780  
 CNCTCCCGAA GTTNTCTCCAT NTC

## 10 1303RP

15  
 GATCAGGTGG CCTTTATGGC CATACTTGTT GGACTCATAG TATATCTCGG CGACTGCACT 60  
 ATTACTGGAC TGCTTGTCAA GATCTTGCGC ACCCATCACG CCGACTATAC TACATGTCTC 120  
 GTTGGGCTTT GCGTCGCTAA CCGGCAGAAA AGATACTTTT ATACTTTATA ATACCAGTGA 180  
 GGCGGCCATA CCACGTAATC CATCTTTGTT GCCAAATAAT TACAATATC CTTTATAGCTA 240  
 CTGGAATTGG GCTTATCCTT ACAGTGTAC ATCAATTTTC TATCGTAATT CGCTATCTCC 300  
 GCTCGCAATC ACTGCACTGC AAACCATTAT CGTCCTGATA GATAAAGATT ATAGGGTAGC 360  
 GATCAATAGT ACCGGTAAAG GCGTGACCAA TATTCTGCTG GGCGTGTTTA GATGGCCGAG 420  
 ACGCTAGAAT GTGGGAGCAT GCTGGTTTAG CGATATGGGA AGCCTTCACT AGAACCCCTGC 480  
 CACTAGTAGA GCACAGAACG TTGAGACTTA CAGCTGTTCG AAGTATAAGT TGTAAATTTTC 540  
 CAAGGGTGGC AAGTAATATC AATTGATTCTN AAATGACTTA CCCCTACGTT GAACTGCTTA 600  
 CTTTAANTTG GGTGCGGGCCC ATCAAGCCCT GACACTCTTG ACTTTCCCCC ATGAAAAAAC 660  
 TCCCGGGTGG GTTCNANCCC CATTNCCCAA ATACANTCCA TANGTCCTGG CCTTAACCA 720  
 CTTGNTCCGG AGGATTTTTT TNCCAANAAG ANNNNACTTT TNAATTTNGC CAC

## 25 1303UP

30  
 GATCTAAGTC CTCTCCCCCA AGCGGTGACG CAAGTGGACT GTCTGTGCTT CGGTAAATAA 60  
 AGTTATCGAG ATGGTCCACA AGCTCATCCA CCTCGGATAT ATGTGCGCTG TGAGTAGGCG 120  
 CAGAGTCACG TGCGGTGTG AACTGACAT CAGACTTTTCG GGACGGGCTT CCTAGCTCAG 180  
 GGTCCAAATC AATGGACACC TTTTCCAGCT CTGCCAGCGA GCGCAAGAAC TTTTGTCTA 240  
 ATATATAGTC GTTAGTTTGG ACCACGCAAG AAACCGGTCG TTCTGTGGCTT CCTGACGCTC 300  
 TCCCGTGATC CTCGGCTGCG CTGATGACTT TGCCAGTGGA TGGGTGAGCG CTCTTGGAGA 360  
 TGACTTGATC GGGCGACTGC CACTTTGCCA ATCGAGGATC GTCTACAGTT GTAAACGGGC 420  
 GCACCTTCTT TTCTGTAGGT GCTCGCGCTG CTGGTACTGG ACTCCTCCTG GACTGTCTGG 480  
 GCGTTACTGG ACCTGTCTGT GCTGCTGTTA CTGGAACCGA AAAAGAAAAA TGACTTTCCC 540  
 TCTTTTCATA TGACATTCCC NGTTGTGANA CNTACTATTG GCCCCNAGAA AATAANTTAG 600  
 GGNAAATAC ACTCNCTATG TTTGCCATATA TTTCCNTAC CATATACAGC CTGCTGATT 660  
 CCAGTTTTAN AANTTTAAGT GCGTTACCTT ATATGTTGAA NCCCGTTATA TGAAGAATAA 720  
 CCCCCAANT TTGCAANGAA CCCCGNAGGC ATTGNCTCCT TCANCANNAT TAAGNACATT 780  
 TTGTCTTTTC AAGNACTTTA TAAGNCC

## 40 1304RP

45  
 GATCAATGAG CGTGGCTACT ACTGATGCTT ACTGCAGTGC TGTGTCAATA TTACATATCG 60  
 GTGGATAGCT AGATAAAAAAT GCTATACATA TATCTGTGCG CATTGTGCCA ATCTATATCT 120  
 ATTTGTGCCG ACGTTGCGGA CCAGTAGGAG GTTGTGTTCC GCGCGGTGCG CAAATTCCGC 180  
 TGAGATCAAG CCATTGCTG TGCTCTTGCC CTCCCCTAGA TGGTAGGTGC CACTTGTAAT 240  
 AAAACCGACG AGATCTTGTA CGCGCGGCAG AGGCTGATCG GCGTCATGGG TCCGTTTGCC 300  
 CGCAGCATTG TATTTCTCTG AAGCGACTGC CTGCCAATGG GCGAGATGCT TGACAGGCAC 360  
 TGCATACAAG CGGGCATGT CCCTGAAATG GCCGCGTTTCG AGGGCTGTAC AGACAACGGC 420  
 GATCACGGGA AGTTGGGTGG TCACAACAGC CAGTTGGACG GGCAAGCCTG TGTCCATAGG 480  
 AGGTTTGGGA AAAAGAGACA ACTGGCTTAT TGTNAAGTTC CCGGGGANCT NCNAAAANAA 540  
 TCTTGGTGGC AATACCAACN CCTAAGGATT TCANCGNGTT CCCCAACTTN ATTNNTTTN 600  
 TNGCNCCGT TTCAAAATCA TATNGGTGGG TTGCNGGCGN GAATNTTCTT TTCNATTTCA 660  
 AACCAACNG GGGNGCCNT TTGAGATTTG GANACNCCC TCNAAANANA NTTGTCCCCT 720  
 TTCNCCNNA AACAATAATN NGGAGGAAGA GGTTTTANCC CNNTATATNC CCCCNCN

## 1305RP

	GATCAATGTA	TCCATTATAC	CCAGCTTTTCG	CAGCGACATA	ATATATTGAC	TTGATTTTAA	60
	AGCGGTAGAA	CTTTACGGGG	CTAGGGCCGC	TAGGTATCCA	AGGTTTAGCA	TCAGGATGCA	120
5	CGTCTGCAAA	GCACTTCTGC	AAGGCTGGAA	TGGGCTGGAG	TACTTCGAGC	TCACCCGCGA	180
	AGTTTGACAG	AGGTGCTTTC	ATGGGGTCTT	CAATCGATAT	AGACGCAACT	GAGAAAAGACA	240
	CGTTGTTATT	GTTTTTAGCG	TTTACTTGTT	GTAGTGTCTG	GTCGACCATC	AAAAAATGG	300
	GCTGGCCGTC	ATGCTCTACT	CCCTCACATC	TGTCGGGAGA	AATATAGTAC	ATTCTAATAC	360
	CATATGGAGT	ACCGTTTTGA	TTGATTGTTG	TCAACTGGAA	AGAACTTTTCG	TCTTTAATTA	420
	ATTTCTGAG	TTGCACTGCT	GCTTGTGTT	CCTCCTGCGA	CGCTTGCGCG	AAAGCCGAAG	480
10	TAAC TAGTGC	CAAAAAACAT	GTAAC TAATG	AAAAAATCGA	CTTCATTGTT	GCTATTGAGT	540
	GCCAATAGGC	GAGACTCATC	CATATGTNAT	GAAAGCGTTT	ATANATCNTT	GTINTGGCTT	600
	GAAAGAAATTA	TTATACTTTT	CCNGCGGGT	ACATTATCTT	CCAACCAAAT	TGTTTCCTTT	660
	TNGANAGGNA	ATCCCCAAAA	TTTTTNAAT	TAATTNGTCN	NCGCANCGGT	TTTTTCCCCG	720
	GNGGGGAAAA	NAAAGCNGGN	NACCCGCCAA	ANCCGAATAA	AGGATTTCCTA	TNAAAACCCA	780
	ATTNTCCNAA	AC					

## 1305UP

	GATCCCCAAG	AAGAACATCA	AGATCCACGG	GTTCTAGGCG	CTATGTACTT	TGTGTAACCTC	60
	AATACATATC	CTCCTCCTCC	TCCACCACCA	CCACCTCCTC	CTCCACGTCC	CTCTGCGCCT	120
20	CCGCATAGTA	CCTCACACAG	TACGGGAACA	GCCTCTCGT	GAACAGCCTG	GCCAGCTCGT	180
	CGCCGTTGGC	AAACTCCTCG	CCCGGCCGCT	CGCCTGTCCA	CCGGAACCCAC	GCAAAGAACC	240
	TCCCGTCGTA	GCGCTTCGGC	CACTCCATCT	CCACCGCCGC	GCTCCGCACT	TCCCGTCTCT	300
	CCCCCACCCT	GAAGTCTTTC	CTCAGCTCT	GCGCCCGCAG	CCCTGCCCTCC	ACCTCCCCGA	360
	ACTCCACCCT	GATCGCAAAAG	TCCCACGCC	CGGCCCCGCG	CCACTCCACC	TCCACCCGCC	420
	GGATCGCCTC	CAGTACCCGC	CAGTCCGCG	CCCGCACGTA	GTTCCGCGAA	ATCCCCGCTG	480
25	TGCGTCAGCA	CGAATCCCCC	AGAAACCCGC	GATCCCTCG	ATCGCCTTGC	TGCGCCGCGC	540
	GTATACCGGC	CCCAGCGCCG	CTGCCGCTCC	ACCTCCAGCG	CCCGGTCTCT	CCGCTCCCGC	600
	NCCGCTNGGA	NTCCGGAAGN	GCTCCACGNG	CGGGCCTGCN	CCCGTTAGTC	CCCTGCCCGC	660
	CATTTAGGNG	GGGNNCGGCC	TTNNITGTTT	NNNGAAGGNA	GNGTCCCGNT	TCCNGGGCCG	720
	GNTNNGTTTT	TGGGNNGGAG	NACGGNGTTT	TTGGANCNCC	CANTCNCGGA	NTCCTGGNGC	780
30	GAANGGNNGT	TNCCNCCNNN	TTGAGCCCCC	CT			

## 1306RP

	GATCTGATAT	TGGGTAATTG	CAACCTTTGC	ACCGCTTTGA	AAAGTACTTT	AGGAAGTGGT	60
	ATTTGCAATA	TAGTTTCATCA	TTGTAGTGGA	AGCACGAGGA	TACCTTACAC	TTGGTACCGC	120
35	AAACCGTGCA	GCAGAAGTGT	TCCTCGTCAAT	ATAGCTTACC	AAATGTATTG	TAATACACGC	180
	CGCTCAGTGG	CTTATTGCAC	ACATAACACA	ATAGCTTGTT	CCGCGTGAAA	TAATCCTGCT	240
	GGCATAGCAG	TACCACTTCA	GACGTATGCG	GGAGCTCATA	AGGGAAGAAC	TTCCGGGCGAC	300
	ACAAAGCTCC	ACAATCGTGA	CAAACCAGAC	AGTTTTTCATG	GTAGTAATCA	CCAAGCGCCT	360
	TCAGGGAGTT	CTGCGTGATA	ACCCCTTTGC	ATTGTTTACA	GATTTTGGCC	GTTTTTTGAG	420
	ATGAGGTGGC	GGTTTATGCT	CCGCAGACGT	TCGCATTACT	TGCTCCGACG	CACTGTGTCT	480
40	ATGGTTGATA	TGGTCACTAT	ACGTCCAGCA	ATAGCTGTGC	TTCTGTATAT	TAGTCATGAA	540
	AAACAGTAGC	ACTCCCTATC	TTACCCCTTGC	NGATCGTATT	GGTACCGCCA	AATNGTTAAC	600
	CCATTTTCCA	AGAACATTCTN	ACCNCTTCCG	TTTTTGCCCCA	AAGAGAGGTN	TGCTATATTT	660
	GCCAACAAAA	GCCCAACTGA	AATTNAANAA	ACCCTTTTTT	CCCCCTTTTN	TTCTCCCCGA	720
	GGAACCTTTT	CGGCAANTTT	CNCCCTAAAT	TGTTNTGGGG	NTGANANCCN	AGAAAANC	

## 1306UP

	GATCATTTCA	GTGGATGGCG	ACATTTCATAT	GGATATCAGT	TCGACTTTTG	TTTCCAGTCT	60
	TATTCCACTG	ATTTTCAGGT	TACAAGAATT	GGGAAGGGGT	CTCCATTTTG	TAGGGACGAA	120
50	CAATTGTAAG	ATGCTCAGG	AATTCAAGAC	TCAGGTTGAA	ACGAAAACTA	TTATCTTATC	180
	CCTTCCGTGA	GGGGACGATA	CCCTACAGAT	GATTATCCAA	CCCCTCTCTT	ACGAACTGTC	240
	ACTACATACA	GTTTTCACTG	ATTTTATTTT	CATATCTAAG	GTACAAAGCT	CGGAACTAG	300
	GGATATCGCA	ATTATTGGGG	AAATTAANAAT	TGGATATCAA	ACAGCCAATT	TTCAAGTGAA	360
	ATCGTACAAC	TTGAAATTGT	CGGAGACGCT	GCTAACATCA	AAGCTACGGG	GGAGTTGTTT	420
55	TCGAGCCGTT	GAACCTTTAT	GTTCTGATAG	TGACATCAAG	TTGCTTTTTG	ACGAATGTCC	480

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5	CCCCCCCCGA	AATGAATACC	CGCNATNTNC	ATTCTTNAAC	CGAATTCCCA	AAACCCNTTN	540
	TNAANTAATC	CCTTTAAAAA	TTNATTTTTT	CCNAAGNTTT	ACNCCCGCNA	ATTTTTTTTCC	600
	CAAATGGGCC	CCTTANATGA	AAAAANACTN	CACCCCCCN	NCGAAAANAA	ATTTCTNCTTT	660
	GGAAANTNNN	AAACGAATTA	TTCTNCNCCCT	TTNTCCCCC	CCCGAAANAC	ANTNTTTCCT	720
	CCCCCCTTT	AGGAAAANTG	TTTTCCCCNA	TTTNANANTN	TCCNCCCNCC	CCCNNAACNA	780
	AAATNTTAAA	NCACCCCNNTN	TTNTNG				

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## 1307RP

	GATCCCTTTA	TCTCATATTA	TAGTCCATAG	TACCCCGTGG	ATGCCCTACCA	CACAGAGGTC	60
	CCTCTTCTGG	ACCTGAGACC	TAGATATCTT	GCGATATCAT	TGAAAATATC	GTTCAATTGC	120
5	TCCTCCGTGA	GCCCGTTAAC	TTCCGCCTCG	ATATCAGCAT	CGGGTGTTTC	CGAGATGTGG	180
	AAGTTCTCAA	CTTTGCCCTC	CAAAAACTCC	TCAAACCTCT	CTTGTTCTCT	CAGTGTCCGT	240
	GGCAACAAC	CATAAAATTT	CGCAAGCTTA	TACAGCTTCA	CATTGTCTAG	ACTTTCGAAG	300
	TCGCCCAACG	TGAGAGGGAA	TACGCCGTCC	TTACAGTCCG	GAATCTCACC	GTCCGCGTTC	360
	GGCAATGGAG	CCAAGAAGTC	CTTCTCCTCC	GACTTCGTCC	AATTCACTAA	GCGCCGCACC	420
	GACCGCTCTT	CCATCGTGTG	AAGCTGGCCC	TGAAGCTCCC	CCACTAGCTG	CACTAAGTCC	480
10	TCATTCTGTG	CGAAATCCGT	TGTATCAAAC	TTGCCGGCGC	CCCCTTTAGG	AAGGAACTTT	540
	TCGTCTAAGT	TTGCCATGTC	ATGCTTTTGC	TTGCTGACCT	GTAGCTCCAG	CACCGACTGT	600
	CCTGTCTTGG	TGATTAGGAC	GCTCTGCCGT	TTAACTAGCG	CCTGTAGCTC	CTCAACTGTT	660
	TCTTCAATGC	CTCGTCTGAC	ATAACGCACT	TCAAATTTAG	TAGAACGCTT	CTGAATATTC	720
	CTACACCAAA	CGCCGCAGAG	AGAATGGTAA	AGA			

## 1307UP

	GATCCACCAA	AGGGTATTTT	ACTATATGGG	CCTCCGGGGA	CAGGTAAGAC	ACTTTGTGCC	60
	CGTGCCGTGG	CCAACAGGAC	CGATGCTACA	TTTATCAGAG	TCATTGGCTC	CGAATTAGTA	120
20	CAGAAGTACG	TCGGTGAAGG	TGCTAGAATG	GTTAGAGAGT	TGTTTGAAAT	GGCCAGAACA	180
	AAAAAGGCAT	GTATTATTTT	CTTCGACGAA	GTGGACGCAA	TTGGCGGTGC	TCGTTTTGAC	240
	GATGGAGCGG	GTGGTGACAA	TGAGGTCCAA	AGAACTATGT	TGGAACCTAT	TACGCAACTA	300
	GACGGATTCTG	ATCCACGTGG	TAATATCAAG	GTGATGTTTG	CTACCAATAG	GCCGAACACC	360
	TTAGACCCAG	CATTGTTGAG	ACCCGGTAGA	ATAGACCGTA	AGGTTAGAA	TCTCTCTCC	420
	GGATTGGGAA	GGCCGTGCCA	ATATTTTCCC	GCATTACAC	AAAGTCCATG	AGTGTGAGC	480
25	TGTTGATTAG	ATGGAATTGA	TTCCCAGTTG	GTGTCCAAC	CCACCGGCGC	TGACTANATC	540
	TNGTTTGGCC	CGAGGCTGGC	ATTTTGTCAA	TCCAATTCCC	GACCCAGGTT	ACCTACAGAA	600
	ANGACTTCCT	TAAACCNGTG	GATAGGTCTT	CCACGGCTAT	AAAAATTAC	NCCCCTTCCC	660
	CGTTTTNTGC	AAACCCNAAN	CNNTCNCCCC	CCTTGNGGCG	TTTTTTTAAA	GGNTTATTTA	720
	TCCCAAANNG	TNTTCTTTTT	ACNATACTAN	TGTTCCAATT	TCTATNAAAT	NTTNTCCCCC	780
	CCGTGAAANNC	CTNCCCCGTT	NGCACCCCTA	T			

## 1308RP

	GATCTGTCTG	CTGGTACACC	GATGAACGAA	ATAATTGTGA	CCGTCACGGA	CTTCGAGAAT	60
	GCACTTCGGA	AGATAAAGCC	TTCCGTTCAG	GATAAAGATA	GAATGAAATA	CAATAAGCTA	120
35	AACAAAAA	TGGGCTGGAA	TGACGAAGCA	GGCGTGCAAG	TCGAAGAAGA	AGCATAGAGC	180
	AGCAAGTTAA	ATAGGCACAG	CTATGTACAA	ATAACCAATT	TCAACTTGTT	CAAAGTCGTC	240
	CGCGTCTTAC	AGATTTTACA	CATGGAGACG	GCGGAATTTA	CTTGTTATAA	TGCCCTCTCC	300
	TGCGAACGTT	TTTTTGAATC	TTCCAGACAT	ATTCCGTATT	TCTTCTTTT	CGAGAAAGAA	360
	ACATATGGTA	TTTCTCTATT	CCTGTAACCT	GAGCTTAGCA	ATTTCTGTGG	ATATAGTTCC	420
	GCAAAGAGGT	AGATCCGTGG	CACCTCTGAC	AAGAACGAAG	TTATTCTTCA	GAGAAATGAAC	480
40	ACGGCCGGAT	ACATGCCCAG	AATGTATATG	TTCATAAACT	TGCGCTCCAA	CATCAATGGA	540
	ATGGATAAGA	GCCAGCGTAA	CAAGTCCCAT	ACTAGTATAG	TCCAGCGGAA	TGCTTCAACA	600
	TTGGAATACC	CGCACATGTC	ATATCCGGAG	CTCTTTGATT	GATATAACAA	CCCCCNCCCT	660
	NTTNTGCCNC	AAAATTCCCC	CTGATGGTAC	CCCTAANGGT	TCTTGCAAAA	GCGGAACCCCT	720
	ATCCCCCTGGG	AGCCNAAACC	CTTTACGAGN	AACNNATTAT	GGCCCGGTNT	TTNACGTCCC	780
	TNNCCTGTCTN	N					

## 1308UP

	GATCACGTGG	GCCGTAAAGTC	GCAGAGAAAC	TTGCAACTGA	ACTGCCACTG	GGGCTCATGC	60
	ACCACCAAGA	CGGTAAAGCG	CGACCATATC	ACCTCCCACC	TGCGTGTGCA	TGTTCCCCTG	120
50	AAACCCCTTCA	GCTGCTCCAC	ATGCAGCCGT	AAGTTTAAAC	GCCCCGAAGA	CTTGAAGAAA	180
	CACCTGAAAG	TGCACATGGA	GGACACCATG	AAAGAGCGTT	CGCGTGCGGC	GCCGGGCTCG	240
	CGTGGTGTTC	GCAAGACAGG	CGTTAACAAG	GGCTCTGCGC	TACAAGAGAA	GGCGGCTACG	300
	TTACCCAACC	TGACTGTGGA	GAGCTTTGTC	AGCCAGGAGA	TGCAAAATTA	CTACCCCTAC	360
	TACAAAAGCA	GACAGCACCT	AGACGAAACA	CTGTGCGACA	TTATTCTCCC	GCCCCCAGC	420
55	CGCTCTAGGT	TGGTACTTTG	GCGTCCGAAC	CGCCAAGCTA	CACACGGAAA	GCAGTGTCTT	480

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5	CTTCACGACG	CTGTCGCAGG	ACATGTCTCG	TCGCTTGCCT	TCTCTTGCTC	CTTGCAACAG	540
	CCCCCGGCCT	GCGGTTAAGA	TGGTAATGCT	TCCCCCGCCC	CAGAACAGCA	ATATGCACGC	600
	CGTGCCCTAG	ATATCCCAGC	GATGCCCAGG	CTCCCTCCCT	TTGGTGAATC	TCCNGGAGCG	660
	AATCCCANCC	TTTGCCCGAG	ANACACTTCC	GACCCNCTCC	ATATCCCTGC	TCTANCTGCC	720
	CNCCTCACCG	CTTCTCATA	AAATCGCATT	GTTGCCCGCAN	CCTATCCTCA	TCAAGCCCCC	780
	TGATANACCC	TGNAAGAGAC	TGANTCCCCC	CCAAACC			

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## 1309RP

	GATCAATTAT	TAGAGGCAAT	ATCAAAGAAG	TCCCATATTA	CTGAGGAGAA	CAGGGAACAG	60
	CCTGGAGAAA	GAATGCCGCA	GACGTACAGA	TACACGCTGG	AAAATCAGCT	TGCCCAGTGA	120
5	GTGCTCGAAC	AGCCGATAAG	AGTATTGACA	GTGGTAGCGT	GCAAGAGTCA	ACGACAAAAT	180
	GAACAGAACA	TCATACTTCG	GGCGCGAGAT	GTTGAAGCTC	GACTTGGTCC	GCCCCGTGGAC	240
	CTTTTTTTGAA	GAAGTTGCGC	CAGGATCCCA	CGGCGGCCCT	GCGCGACGCA	GCAGGGACTG	300
	GTCTCCAGCG	CGCCAGCAGC	AGGGAGCTTG	TCACCACGCT	CACAGAGCTC	ATCGCCATAC	360
	CCGCGGCGGC	AGCCATGGGC	GGCAATTGTA	TGCCCCACGG	AATGAGGACG	CCCATGCTGA	420
10	CTTGGGAGCC	ATGAGAGAAAT	TGTACAGGAC	TGCCCCAGAA	ATGTTTCACT	TGACGCGGTT	480
	AACGTGGCGC	GCGCGAGATT	CGATGGCATA	CAGAAATGCG	TTTAGCGGCG	GCGCCCCGAGG	540
	AATGTCCCAA	ACCACGATTC	CCGCGCGTTC	CGCACGAAGT	CACTGTTGCC	GGACAGCGAA	600
	ATACCGAGTT	CNCTTTTACA	ATTGCCACAA	TTTCTTTTGAN	GCCGTCTCCC	GATAAGGCAC	660
	ATATNGTTN	TTTTTGCCGC	ACTGCCGCAA	NGTNCCACTT	GCCCCCTGG	TACTTTCCCT	720
	GAACATTTTG	ACGGATNCCC	AANCGTGCAA	ACTCTCCNC	CCCGTGTNN	CCCATACCAT	780
15	CCANTTTTTC	GCCNC					

## 1309UP

	GATCAGGACC	GCGGTCNCTG	ATTCGATTGG	CCATGAGTTT	AAGTATGACC	CAGAGGGCCG	60
20	CCCTGGTGTA	TCTAATCTGA	TTAACATCGT	AGCTGGCATC	CAGAAGAAGA	CTATCGCGGC	120
	GGTGGAGGCA	GATATTGCTG	GATTTAAGGA	CCACGCAACT	TTTAAAAACT	ATGTTACAGA	180
	CATCCTAGTA	GCTGAGCTGA	GGGGGCCAG	AGAGGAGTTT	GCCCCGTATA	TGAATGATAA	240
	ATCATAcata	TACGAGGTTG	AGCGCAATGG	GGCTGAGCGA	GCAGGTGCCA	TAGCTGCTAA	300
	AACCCCTGGCA	GAAGTCAGAG	CGATAATGGG	TTATTAGTTA	TATTTCAGATT	CCAACCTTGT	360
25	CTATAGACTA	GCAATAATTA	TAAAGATACA	TCAAGAAGAC	CAAGAGCAGA	TGCGTAACTG	420
	GTTGTCACTC	TTTGGACCTG	CCGGATATCA	GCACATGCAA	CCAATATCTG	CTTCAGCAGT	480
	CCTCCCGCTT	CTCGTTAGCT	ATTGTGCCAC	CTTGATTCTT	CCATCCGTTA	TACAGCCAGC	540
	TCAGCACATC	ATCCATCTAT	TTTGTGCCN	TTCTGCTAGG	CTGATGCAAT	AGACTTCCAT	600
	ATTTGGTAAT	CATTGTCCCN	TTATTTTTTA	GGNTACCACC	ATCTNTTTTC	CNATGAAAN	660
	CGTGACAATC	CNCCNGTTTT	TCNACCCTCC	CTCCATNAAA	TNTCTTTCAT	CGTGGGTTTC	720
30	GGATCAANCC	CTNNGGNTCN	TCCCCTNCGC	CTCCATCCNG	GNATTTACAC	CCNTTNTTTT	780
	CTCCCCCCTC	ATNAANC					

## 1310UP

	GATCCAAAAA	AATTTTAATA	CTGAAAAAGA	AATGCCACAA	CTAAGCTCAG	CTACCTTAAA	60
35	GAATCGGGAC	CAAAGCTGTA	AGGCAACAGC	TCCTCCAATG	TTGCTGCAG	AACCTTGGAC	120
	CCGTGCGCGT	TCATCATAAT	CACCGTGAGC	TTCTTCGGAT	CAACGAACTC	GCGCAGGACC	180
	TGCCGGCAAA	TCCCACACGG	GGTCACGAGC	TCGGACGAGT	CCCCACTCAA	TGCGATGCAG	240
	ACCCAATTTC	TATGCCCCGC	TGTTACCGCC	TTTACGACCG	CTGTGCGTTC	CGCGCAAATA	300
	CCGGCTGGGT	AATGCGCATT	CTCGACGTTA	GCGCCGACAA	TATACTCGCC	TGACGCTGTC	360
40	AAGATGCAGC	AGCCACGCG	GAACCTGGAG	TTATGGGCTG	TACGAGAGCT	CCTTCGCGGC	420
	TAGTGCTCGA	GCAACCGCGC	CCTGATATGG	CTCTCCCTGT	GTGCTTGGCA	TTGGCTTCCG	480
	TGGCGTCGCC	TCCTAGGTAT	TGGGGTTCCC	CTAAGTACTG	GCTGCGAACC	CTTATGTTTT	540
	TTGCAGGGA	ACGAATTGCG	CCCGAACCGG	GTGAATCCCG	GGAACATNCA	ANTACCCNCT	600
	TTTGGNTNNC	GGGNAAAGGG	NNANNTCCN	NNCTINGCNC	CGGCNGGAAN	AAANAATGTT	660
	AACCATGTGG	ANTAAACCTT	TAANATGANN	CCTATGGCCN	GTTTAACTTT	ATCCCCCNC	720
45	CCCCCCTTTT	AAANGTNNNA	NCCCCGCNT	TNTACCTCTA	NNCCNGCGGG	GGNGCANNANC	780
	CCACAAATNN	TNTGTTGNGC	GCNGNGCGTN	NCTAATATGG	AGCCTNGGGN		

## 1311RP

	GATCTTATCG	TTCAGCGTAC	CGTCTGCAAG	AATCTGAGAC	ATAAACTTGC	GCTGCGACGA	60
50	GTTCTTGGTA	AATTCCTCGT	AGTACTGTGC	GTGTGCGCT	TCCAACGCTT	CCTTCCCCCG	120
	CTTGACAGC	AGCTCCACCT	TTTCCGTGGA	GAGCGGCTCT	TGCTCGCGAG	AAGCCTCCCG	180
	GTCTAGCGGC	ACCTCGTGCC	AGGGCATGTC	CGCAGGCACC	AGAAGGTTGC	CGCTGCGAAC	240
	CGAGCGCAGG	TCATCGACCA	TGCCGCGCGC	AGGTTCTCTC	CCGGCGGACT	CGGCATCGAA	300
	CCCCGCATCG	GACTCGCCCC	CCTCTCCGCG	GGACTCGGCG	GCACTCGCTGT	CCTCTCTCGG	360
55	TTGCTCTTCG	GCTTGCTCCT	CGGCTTGCTC	CTCGGCTTGC	TCCTCTGCTT	GCTCTCTCGG	420

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5	TTGCTCCTCC	AGCGAATCCT	CCGGCTCGCT	GCTCTCTGCT	GCTGCCGCTG	CCGCTGCTGC	480
	CGCCGGCAGC	CCATGTTGCG	AGCAGCCCGC	TGACGTCGTT	CTGCAGCCCG	GCATCGCCGT	540
	CTCCTTCGTC	GCCGCTGAAT	GCCTGTTGCG	TGAGCTCGTC	TGCGTTCGCT	CAGCCCTTCC	600
	ACAGCGCCAA	GTTGTCTTT	CTNAACCCCG	CANNGCCAAT	NGTTCNCGG	CNTCATCCCC	660
	CNTTNTTCC	CTGGTTTCCC	CTTTGGTNGN	CCCCNGGNAN	ACTTTTTCCT	TGGCTTNCNN	720
	CAATTCCTTT	TTCATTGGT	TTTCCCCCA	AAATTTTNAN	ANNGGGTTAN	CTNNTCANNN	780
	NGGCNGNNNA	GAGAAACCT					

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## 1311UP

	GATCTTCTGA	TGCATATTTT	CGCTCTCACC	TTGCGCGTTA	AGTTTTTTCCA	TGTAGATAGC	60
	TCAAAGTCAT	CATCCCCGTC	ATCTTTTTTCA	GTGTATAGAT	TCTGTGATAC	TTCTCCTTCT	120
5	TCCTCTTCCT	CTTCTTCCTC	TTCTTCCTCG	TCTATATGAT	CTTCGCCTGT	CAGTTCATTG	180
	TCTATTCCAT	AATTGGGTTT	AACTTTTCGGC	TTGGGCTCCT	TTTGCTGGCT	ATGATCTTCC	240
	TGGATACGTT	TCTGTCCATC	TGCCAATCCC	GTTTTCTCAT	CAGTAGCTTG	CGAACCGGGC	300
	ACAGTATGGA	TTTGTTTTGA	GCTAATTGCA	TTACTACCGT	CACGATCTTC	AAGAGGTCCT	360
	TTGCCAGCAT	GACTTTCCGA	AGATTTCGAG	CGTTTACCTG	CAGGCGCACT	CTTACCCCGT	420
	TTATCTGCAG	GAATGTAGTC	CTCATCGTCT	TCATCTTCCT	GTATCGTCTG	TATGCCTCTC	480
10	CTCACCATGC	CGCCCTTACG	CTGTCCCTAC	ACTCTTCATC	ATCCTCCTCC	TCATATCTAC	540
	CTCTTTTCCA	GTCTTCTCCA	CTCATACTAT	CTCTACCACA	TATCAGGATA	ACGTATAATG	600
	TGTGTGACTTT	TTTGGATAGC	ATCNCTGGCC	CTAGGAANGC	TNGGGTTCGG	AATATAATTT	660
	AACATCTTCC	CAATCACAAA	TINCTCAGTA	ACNGTGGTAA	ATTNAAACGN	AANTTTTTTAA	720
	CTTTCCATAC	GGTTTANGNC	CCATGGCTCT	TGAAANCGGA	AAAATCCGGG	GCCCCCTTN	780
	GAACCTTGTTT						

## 1312RP

	GATCATTCTC	ACCAGTACAA	ATGTATATTT	ATATGTAATT	GTCTCTCTCT	GCTTTTGCCA	60
	TATTTTTTTA	TTTTTTGTGG	TGACAGCGTG	CACTGACGCT	GACGCGCAAG	CCGAGGCGC	120
20	GATTCTTCGC	AACTTTTCGT	CAACGCGCGA	CAGACAGTCA	GAAAGTAATA	GGAAACAATT	180
	AAATACGTTG	TTATGTTATA	TGAAGTTATA	CATAAGTGGC	TGCCATCAGG	TTATATATTG	240
	CTTTAAATAA	CCCATTTCGT	TGGAAACCTC	CTCTGTGAAT	GCCTCGCTCA	AACCGGGATG	300
	GTTCTGTTCG	ATCTCGGGCA	AATATTACTG	ATAATTGATC	TACAGCGTCT	TTTGTCTCTT	360
	GAGTCCGTGC	TCTATCACGG	ACGCGTTCGT	ACTGTAGCGG	ATAACATGTT	TAAAGAAGTT	420
	TAGTTCCCTC	TGTGAAGGAG	CAGCAGCTTT	GAGTGCCTTT	TCATCATAAT	ATTGTTCAAG	480
25	TAGGAGAGG	AGGTAATGTT	TGTCTCTGGG	TTCTTTGAAG	GGCTGGATAA	TAATGACTTG	540
	ATTGTGACTC	CTGGTGATGG	TACATTTAAC	ATGCCAATCC	CAGTTCCTCA	GTTAGATTCT	600
	TACCGGTTTT	GTTATACCTT	GTTTINATAAG	GGTTACTTTG	CNCCCNACT	TGCCAAGAAA	660
	TCATCTTATC	CCTTTGANAG	GTCACCTGTC	CCTTAATTGT	AAACCTACNC	CCTTTACAAT	720
	CTATGCTTAT	ACCCNGCCAT	TGTCCCTGAA	GGATTTTNTT	ATTAACCCCTG	CNCACATCCC	780
	TTGGCTGG						

## 1312UP

	GATCAGGCAA	AGGATTTCTA	CTCGTATGTT	GGCAAGAACC	TGTCACAGAA	ATCCGACAGC	60
	AAGTTGCTTC	CTCGGAGGAT	TCAATTTGAA	CTTCAGAGGT	TTGACTATTT	TCACTCTCTA	120
35	CTCCAGTATG	TTGTAGGATG	TAAAGCTCGT	GATTTTGCTG	TGTCACCTTG	GAGGTTTCAA	180
	TCTTCGATCG	ACCCTAATAA	TAAAAATACA	AACATGCACC	TCGTGAAGAA	GTATCGTTCC	240
	CATTTCTTAC	CATTTAACAA	GATAAAGAGC	CAACAGCGCA	TAAGGCTTTC	TAAAGTGTC	300
	AACATATTCTG	ACTTGAATGA	CTTCTACCAA	CTTGCATCAG	CTACCTCAGA	ACCAAATAAG	360
	CCCCTCAAAG	AAGGACTCTT	ATGGTCTTAC	AGGAATAATG	GATGGCATAA	ACAGTGGGTG	420
	GTACTACAAG	GATCACAGCT	CTCAGAATAT	TCCGATTGGA	AGACGAAAGC	TAAGGTGCTC	480
40	AGCCGACCGG	CCATTAATTT	GACGTTTGTT	TGTGTTAAAC	GTTCCGAGAA	AAAGCCTAAC	540
	GGATTTGATA	TCATAACTAC	CGACGGCGAG	GCTCGTTCTT	TCCAAGCAGA	GTCAGAGGAT	600
	GAAATGAAGC	AGTGGCTGTA	TGCGCTTCAC	TCTGCTGTCTG	GGATAATAGC	CATTGAGGAG	660
	ACAGATGAGA	ACAAAGATCC	ATTGTCTATT	GTCCGTAATG	CGGATCCGTC	AAATAGTGCA	720
	TGCTGTGACT	GTCGGAGCGA	TAAGCAAGTG	AATGGATATC	TCTGAATAT		

## 1313RP

	GATCGTGTCT	TGCTGACTTG	CATGTCTAGC	TCAGTTCTTT	ATTACCCGCC	TCATGTTGAA	60
	ATTTTCCAGG	AACCATCGCA	CCAAATGTAT	CGATGATATA	GATTACATCT	ACCCTTCCGC	120
	AAGCCTGGAA	GGAAAGCTAGA	CCTCTAATCT	AGTAGCTTGC	CATGTACATC	CCGCCATCCG	180
50	ACCCGCGAAG	ACCAGCCAAG	GTGACGGCCG	GCCAGCTCTG	CGAGCTGTGC	CACGCGCGCA	240
	AGGCGCTGGT	AAAGCGCCCC	AAGAAGTTGC	AGAAAGTCTG	TAAACTGTGC	TTCTTCCATG	300
	TATTGGAAC	CGAAATCCAC	AATACCATTA	TGGAGAACAA	GCTATTCCAG	CGCGGGGAGC	360
	GGGTGGCAGT	TGCGCGCTCC	GGTGGGAAAG	ACTCCACGGT	GCTTGCCTAC	ATATTGAAGC	420
	TGCTCAACGA	AAGACACGAC	TATGGTCTCG	AGATTGTGCT	TCCTGAGCAT	CGACGAAGGG	480



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5	CATGTGGCT	ACCGAGACGA	TTCCGCTAGC	TACTGTGAAG	CGCAACCCAG	AGCAATACGG	540
	TTTGCCCCCTG	AGATTGTGTT	CCTACAGGAC	CTCTACGAAC	TGGACGAATG	ACGAATAGTG	600
	CCTGCGCCCN	GGAATGCNCA	ACACTGCNCC	TTACTGCGGG	TTTTTTCGAC	CCAGCGCCTG	660
	ATTCCGGGGG	GGNAATGCTT	GAATCCACCN	NTTTGTTAAN	GGCCATACCC	GAAAAAATGC	720
	CNAAAGNGCC	CANAAATCCT	GGCCGGGAAA	TTTGGCNAAT	CNAAATAACN	CTTTTCCCCA	780
	AANAGGTCCC	GNTAANNNTT					

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## 1313UP

	GATCAAAAAA	GATACGGATG	TTATGCTTGT	TAAAAATATTA	TATGCTATAG	TACAACGTAT	60
	CGCGTCAAAAC	ATAACGCATG	AGGACTATAT	TTTTAATTCA	CTAACTTCGG	CGAAGCATCT	120
5	CCGGAAGAAA	TAGCCTCCTG	TATGGGGCTA	AGTCCATAGG	CGTCGGTTCCG	GCTCATCTCT	180
	GGAGACTTTA	AAGAATTAAG	TCCGAAGGCT	AGGCTCCCAT	ACCCCAAAGG	CGAGTGGGCA	240
	CTTTGTTTCA	GAGATCCTTC	TGACATAGCC	TTTCTTAGTG	ACAGTGGCGG	AACATGGGCG	300
	CGGGAAGGAA	TACTTTGTCC	GTGCAATGAA	CCCTCGGATA	AAGGCCTACT	TAGCCCGTTT	360
	TTGAAAAATG	TGACAGTCTT	GTTCTTGATA	TCTAGCTTGT	ACCTCGTTGG	AGTGGGTTC	420
	TTTGCAAGAC	CAGTGGGTTT	TTCCGAAAAG	CTTCGCGTCT	TCCCGGAATG	AATTCTGAGT	480
10	CCTGGTAGGG	AACATCCGAG	ACTTCCCAAA	AACCNITTCN	CTNTCCATTT	TCNAAAAAAT	540
	GGAAATCNNC	CCGGCCATTA	TNGATCTCTT	CCCAAATTAC	NNCNCNCCC	TCACCTTGNG	600
	ACTTGGGNAT	ANAGANCCCC	NTCNAACCCC	TCCAAANAAA	AAAAATTCTC	NTNGTGCCCC	660
	NTNATPCCCC	CCCGGGGCCN	NNTTTTAATT	CNGGGGAATT	AAATTTTGTA	TCCNNGCNGG	720
	TNGAAGCANG	TTATNGCCCC	CCCTTGACCC	ATNTTTNACT	TNTTAATTTT	TCCCNNNNCG	780
	GNTGGAAACT	TTGCCNAAAG	GCANGCTTTT	TGAACCACT			

## 1314RP

	GATCCATAAA	CTATCTTCTC	ACTCGCCGGA	TGCAAAGTAT	CAAGGAATAG	GCGACAATCG	60
	GTAATGATTG	GCTCGAGCTC	ACGCAGATAT	TGGCGCACTT	CTGATATCCG	TGGGTGTGTC	120
20	GATGCATGAT	GCACATGAAT	AAAAGGAAGA	AGCTTCGAAA	GAGGTACACG	GCCCGGGTAG	180
	CGTGTGATGA	GAGCTGTTAG	TTCCGGCTTCA	ACATCAGCAA	GTTTCTCTAT	AGGGGACGCA	240
	GGGTGCTCAA	CATCATTTAT	TAGACACTCC	AGCAGTTTGT	CTGAAAAAAA	GGTGTGCATG	300
	GACAAGTGCA	CCTCATCTTT	TGAGATGCCG	CGGATAACGT	CCCTCAGCGA	CGCCAGTCTC	360
	ATCGTGCAAC	TCCGTGCAAA	AACTCTTGAT	TGATAGCGTA	ATGCAGTCAG	AAGAAGTCGT	420
	TAAAAGCACT	TTCCGATGCCC	CAGTGAAACC	TAATCCTCGT	CCGATATAAA	ATCGAACGTC	480
25	TTAGCAACAA	TCTTCCATAT	CCGGAAAGTG	TTTTACAAGC	TTCTTACGAT	TTTCCACTCC	540
	TCGATTGAAT	ACTCCGGCCN	AATTCTTTTA	CCATATACAC	CCNNTNCNGG	GCTTTTGCAC	600
	GAATTCNTTA	TTTGTGTAAG	AACTGGACAC	TTTGAAACTT	TGCACATTGC	NGANTCCGAA	660
	ACNCTTTTCN	CNCCGAACCTA	ATNTNAACCC	CAATCCTGAC	CCAATACACT	CCCCCCCCAA	720
	CATGACCCCG	CACANGATTN	TTTTTTCCCN	AGAATTTNTT	NAACTNTTTG	CCCCCTNANA	780
	CATTNTAAAT	C					

## 1314UP

	GATCTTGCTG	CAGACAGATG	CCGCGGAGCT	ACCCTTTTCA	ATCCTTATAT	AAACCCTTTT	60
	CCAGCTGTAC	CGCAGTAAAC	TCCCCTTGCT	TCAGGAGCTC	CAGGCTGCCA	CGCACACTCG	120
35	AGGCCTACAC	GCGTGACTGC	ATTGGCTTCT	GTGCGCACAC	GGAAGTCTTA	AACGAACCTC	180
	AATCCCATCC	AACCAGTTCT	GCTAACGTAG	CTACTTCTGG	CCAATCGCTC	AGCCCCATAC	240
	CGTCGAGGCA	ATCTTTCCAA	GCCACATAAA	CGAAACCTAC	ACAGTTACTG	CGCAAGGCAA	300
	GTGCCAAAAG	ACCACAGGTT	CCGCAGTACC	AGAGCAAAAA	GCTTACCTGT	CAACACTTCG	360
	AACATTCGCG	TGGCCTTAAC	CATATGCCAC	ATGAAGCAAT	AGACCCCTAA	AATAGAAAGC	420
	GATTGGCGCG	GAACAGACAT	TCCTGGTGTT	GTACTTGGAA	CTCACATAGG	GGCTGCACAC	480
40	GTGCTTAAGT	CCTCGCTTGC	AGCTGAGGCC	ATGTGCCCCC	CATTAGTGAC	CCACGTTGAT	540
	CTCGAGCCCG	CAAATGATCG	TCAGCGTGCA	TCCGACTTGG	CATTGCAAGG	GATGTTGATC	600
	CCCTGANGGG	AGGCTTGCAA	CAGCGCCNCC	CTTGTTTCNC	ATCCATAGGC	TGTGAGGCC	660
	GGAATGATCC	NCTCTCCAGG	GGAACNCCCT	CCCCAACGCC	CCATAGGGCC	CNCCCTGGGN	720
	TNTTGCCCGG	ANACTCCNAA	NCNNGGTTTA	AANNTTTTTT	TTAAANGNCC	CAGTGGTNTC	780
	AAGGCCCCCN	NGCCTTTTTT	CANCCCGCAN	TTNCTNAATT	TTTGNCNGCG	GNA	

## 1315RP

	GCGGCCGCTC	NNCCAACCTAG	TGGATCTTCA	TTTGTGGCCC	GGCCGACAGG	TTACCACCGC	60
	TTTTCTCTCC	CGTCAGCATC	TCAACTAGCT	GCTGTAGCTG	GTACTCCCTG	TCGCCGCGGA	120
50	ACACGTTGCA	CTTGCTTATT	GCTGTGCATG	AAAGATCGTG	CAGCTGAAC	ACATTACCGT	180
	AAGTGATCAG	CCCAACAAGC	GCGTTGGGGG	GCAGCAACGA	CAGAGAGGTG	ATGATCGAAT	240
	CCTTCAGCGC	CTGGAGGTTT	TCCTCCTCCG	CGGTTACGTC	CACGACGTAG	AAGAAGATCG	300
	GCGCCACCTG	CACCGGCCGA	TTTGTGATGT	ACTCAACCGT	CGTGGAGTTC	AGTTCCGCGG	360
	GCATCGCCTC	CTGAGACATG	TTCCGATAGT	GCTGCGGAAG	ATGGTTCCGC	GTCCCCGCAC	420

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	AGAGGGCAGG	CCCACACGTT	CGACCGCACG	TCGATCTCGC	AGTACGGGTT	CAGCACCCGC	480
	CTTACAGTGT	TGGCCCCACC	CACACACCAC	CCGGTTTGTT	ACGAAAACCA	CCGCCCAGCT	540
	CCCTCCAATC	TCCTTCCACC	GCGTTGTTAC	AGCATCCCCN	CCGGCNCAC	GTTCCCTGT	600
	CNCGTTCCCG	TCCGGGAAGC	CCGGGAAAAC	ATTCCCACGA	NAACCGCACC	CCNTTTAGTT	660
5	CTTCCTTCCT	NTTTCGAANC	CACCCTTGAA	CCGNGANCCA	CTTTTANNCC	CCTTTACCCC	720
	CTTTGATCCC	CNCCGAACCC	CCNAAATGGA	ACCAANNAGC	CCNTAACNNN	TGCNAAAACC	780
	GANTTGCCCN	TTTCAAGGTC	CCATCCTTTG	CCCCCGNGA	ANAAAAANTNC	NCCGCCCNA	

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## 1315UP

	GATCTTGCGG	AATATCGGCT	CCCAATCCGT	ACCCATCCAC	TTCGACACTA	CCGACTGCAC	60
	CGCCAGCGTG	TTCATCGGCA	CAAGCTGCTC	TCCTAGGCTC	AGCACC GGCG	GCACCACAAA	120
5	GTAGAACC GC	CGCGTGGTCT	CCAGCTGCTC	CCGCTCGTTG	CGGAACGACA	CGTAGTAGCA	180
	ATACGAGCCC	GGTACGTACA	CATCCACATC	CACGCAGCTG	TCCTCCAAGA	AACCTGCGCT	240
	CAGCAGATGC	TTGTAAAAC T	TGTTCCGCTG	GAACTTCGTA	TTCTTTTCCG	GCGGGCAGTT	300
	GGTCCACACT	AGCCCCGTCC	GTGTACACAG	CGATCCGGCG	GCTACCACCA	ACCGCACCCG	360
	CAGCCCCGCT	TCCTCCCCAG	CGTCTCGGCC	AACAGGTAA	CATGGCAACG	TGAGCACACC	420
	CTTTCCAACC	TCTCCTCTCA	CCGGCTCCCC	GTTGTCTGCT	AATCTCAACA	GCACGGTTTT	480
10	CATCGCTGTT	TGCGCCCTTT	GCTGCGATCT	AAAGGAAGCT	TCGCTTGTC	TGCAGCTGCT	540
	AGCCTTGGGA	ACTGCCATAG	TCCTTTGACC	TTGACGCCGT	GTTAAATAGT	GCATTTTCAGT	600
	ATACACAATT	TGACTTACGN	NCTCCNCNG	TGCTAACTGA	GGGANATTAC	CCNAAACCCG	660
	GANGGANA	TAAACNGNTNA	NAATTTNCCC	GGTNGCACNC	NTGCCNTATG	NTTCCNTTTT	720
	TGGAAANAAA	CCCTNNGGNN	GGTNGGTTGN	NAAAAATTGA	AAACCCNGGN	TNAATACTNC	780
	NTTNACNTTN	TCGGAAAACA	AAANTNCGGC	CCCCCCGN			

## 1316RP

	GATCCAATAT	ATGCGATGGT	CTGAAGGGTT	GTCCACGTGA	GTAGCTTAGC	GAATACTTTG	60
	CCAAGGCGTC	TGCGACATCA	AGAAGAGTCT	CAAGATAATA	ATAGTCCTTT	TTGGGCAGTA	120
20	AGCGAAGATT	GTTCTCGCC	TTTGTCAATT	CTGGCCGGTC	CCTGGACCCA	TTTGGTGCGC	180
	TGTTGAAAAA	GCGCCAAAAG	TACTTCAAAA	TGACCGATTT	TTGACCTGG	AAACCTGCCT	240
	GGAGAGAGAA	GTCGTGCAGC	AACGTAAATT	CACTGAGAGA	CAGCAGTGTT	TCGATAATTG	300
	CAGATTCTTG	ATTCTCCTTC	GTTAATTTTG	GGTACAATTT	AGATGAGCTT	AATAAAAAAT	360
	GTAGTGTCTG	GACAGATGGC	GATTCAGCCA	ATAAATAATG	GCTGATGGAT	TAAATGATGC	420
	CAGCTGCGCC	AACCTCATCTG	CATTCGCTAA	GGAACGCATT	GATTTTCAGAC	TATAGTTATT	480
25	GGCAGCATCC	ATGTACTTTG	TTGTACTCGA	TCAGGTCCTT	CACTGAGACA	CCGTCAGAAA	540
	CGCTCACCGT	CTCGTCAATG	AGTTAGAGCC	ATCCATAGAT	TTCCCCGAGG	CAGTTCCCGC	600
	CATGAATTTT	CACCCACTTC	CCCCCCGGTC	CATACCGCAA	TTTGAACATT	CCCGGTCAAT	660
	ACCTTCTTCC	TCCCCCGGNT	NTTCCNCAAN	AGGGAAGTTA	NATTCCTGNC	CTTTTTTTTN	720
	AAAACCCAAT	TCNCACCTTT	TCNNGGAANT	TTTCCGGGTT	GAGNAAAANT	CCNACNCCCG	780
	GTNGCCGGTT	TAATTNCC					

## 1316UP

	GATCAACACT	CGTACAAACG	AATATAGTCA	CATGACCAGA	TAATCGTCGT	GACTGGCACC	60
	CATACATCGG	CACCCATGCA	CCCACATGAT	GGTTTTCTTG	GCGGGTGGGC	CGTGCTGGGC	120
35	GGGCTCCCCG	GTCTACGCTG	GGCGGTGTAG	GCGGCCGGCT	GGGCGGCCAG	GCGGAGCAAT	180
	GGGCGGAGGA	ACAGCGAGCG	CGCCAGCAGC	GGTGCGCAGC	TGGAGCGTCC	GGCATGTGTG	240
	GAAAAATTGT	AGAATATAGC	ACTGTTATAC	TGAACAGTAT	ATAGAAAGAG	CACTTCCTGT	300
	AGGTTTGAAC	ATACTATACA	AGCTCCCAAT	CATCGACGAT	GGCTGTTGGT	AAGAACAAGA	360
	GATTGTCAAA	GGGCAAGAAG	GGTTTGAAGA	AGAAGGTCGT	TGACCCATTC	ACCAGAAAGG	420
	AATGGTACGA	CATTAAGGCC	CATCCACCTT	CGAGAACAGA	AACGTCGGTA	AGACCTTGTC	480
40	AACAGTCCAC	CGTTTGAAGA	ACGCAGCTNA	CTTCTTGGA	GGGCNNTTTC	TTCAAGGTNT	540
	NGCNTTGGCC	AACCANCGG	TTCNTAGGAT	TNNCNCCTCC	NAAAGGTTC	ATTANAAATT	600
	TACAGGTCCC	NGGGCAAAAC	CCTTTNGACA	CCTTCCCGG	TTTGGGATTC	CCCCCCCCNA	660
	CATTTTAATT	CAAAGGNCCA	AAATTTGGCN	ACCTTAATTA	NGGNATNTCC	TNTTNAAAAC	720
	NGNAAAAANN	TNTNTAATTN	TTTNNCCTTG	CNTNCCCAA	AAAATTTNCC	CATTTNAAAA	780
	ACNTTTTNNC	CNTCCCCTCN	NTTNAACNCC	NAAGGTTTTN			

## 1317RP

	GATCTTTATC	TTTCGATGAT	ATCTTTCTCTG	AAGAATCGAC	AAACACCTGG	TCCAGCAAAT	60
	TGGAAGCTAA	GTCTCTCCAA	TCGGATGCCA	AATAGTTGAC	ATACCGCGCA	TTTAACTTCA	120
50	CTAACCGGGC	GGCACCAATA	TCCTCCAGAA	CTGTATTTAT	TTGCTACGC	TGAACGATTT	180
	GTTCAATCAG	CGTAATATT	GTCAATACAA	AGAACCAAT	TCTCTGCATC	TGAGGTATCC	240
	TTTATGTGG	AGCTCCGACT	TCGGGCTCTA	AGTTTGGATT	TAGAATCTTT	TGGGCCTTGC	300
	GCTCTAGAGA	TATGGTTAAG	TAATCTATAG	CATCGCTGAA	GAAGCAAGAG	AGCAATTGCT	360
	GTGCATTCTT	CGGTGTCATA	GATATCGTCC	AAACATTTT	TGATTCATTG	GGCAGCCATG	420

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	ATTGCGGAGT	CATCGATTGT	ATAGTAGCAA	GGCAACCAGA	CTTGTATTCA	CTAAACTTGC	480
	GTAGTCTGGA	CATAACATCA	ACTGTGGCCT	CCAGTTACAC	CATTATCAGT	GGTAACTGAG	540
	CCCAGAGAAG	CGGTTTTTGA	CCGATGTACT	TGTNTCNATC	TTTTTGAACA	NGGACNCGGA	600
	AATTTTCATTT	CANGTCNGGC	TNCNCNCTCC	CAAAACNGTT	CCNTGGTTCT	NGTAAAGGTT	660
5	TNNCCCTAAA	AATNGGGNTT	CCCNNGTNAG	NTTCCCCCCC	AATTCNAACN	NAANACCCNA	720
	TTTTTNTAAT	TCCCCCNCCA	AAATTCAATT	ATACCCCCCN	TTTTNGGTAT	TNTAAATTTN	780
	GGGGGNCNCN	NTTCCAAAAA	GGNGCNG				
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## 1317UP

	GATCGTTCTT	ATATTTGTTA	AAGAAGAGTT	TTCTTCAAGC	ACTTTGAGCT	GAATAATCTT	60
	GTCAAACATA	TTGTCAGGGC	TCCGCTGGTC	GTTAAACCGC	CGAAACCTCT	TGAGGAACCC	120
5	ATCTAAGATC	ATAATTGCCT	TTTCTGGCTC	CGATAAAGCT	TTAATAGATT	GATGGTTGTC	180
	GCCTCTTTCT	GCAACGCGGG	ATTTAGTTAT	TTCTCTAACG	GATTCCACAT	CCTTGTAAGT	240
	CAAAAATGAT	AAACACACGA	CTTTGACTGC	ACTGTTGTAC	GGAATATAAT	TCTCCTTCAT	300
	CTTTTCCAAC	CATTGCAAAA	GTTGTTTCCG	CTCGAACGGC	ATATGATTGT	TTCTGTCCAC	360
	AATTACAGCT	CTTGAAGTAT	CCPTTTGTAG	AAACTCTAGC	GCGTCACGCA	TCAATTTGCT	420
	CTTATCCTTA	GTAACAATAT	TATCATTCTG	TATGTGGCCC	CAGGACTCTC	CAAAAATATT	480
10	CTTCAATGCC	AGCGCGACTG	TCGTCTTTCC	ACAACCAACC	GTGGCCACAG	GGAATGAAAA	540
	TGAACTTGGT	ATCTCGTCCT	ACCTTATCGA	GCTCCAGATG	CATACTGGTC	CCCCCNAGCT	600
	CCTTTATATC	CTCCGAATTT	CCATAATATC	CAATCCCAAA	ATCCCCAAAT	CNTTCTTAGG	660
	AAATTTTCC	NNNACTNGAA	ATCCCCTTAC	CTTGTTNTATA	CCCCCTGNAA	ATTINGGATN	720
	TTGATTCCNG	CCAGGGANTA	CNATTTCCNA	TTTTTNTTTG	TGANNAACAA	NGCTTTTGAA	780
	TTTTTGTCCC	CNCCCNCTGT	GNANTACCCN	CCCTCCTCCC	CCCCTNTTTN	TTACN	

## 1318RP

	GATCGCCTCG	TCGTTCGCCC	GGCTCGTCAG	GCTCTGCGCA	AGGAACTGCC	CGAACCGACC	60
	AACCAAACT	GGCATGTCTT	TCGCGTAGAT	GAAACCTGCT	TGCTTGCTGT	CCACCGCATC	120
20	CCACACGTTG	TTCAGAATAC	CCTCTGCCTC	CGTCATGACT	CCTGAGCCGT	GAGTGCAGTT	180
	CCCAAGGCTT	TTGTTGTGCT	TGGCAGTTGA	AACGACGCTC	GCAGCGGCAA	AACAACACCG	240
	GCCCCGCGCC	AATTGCTCAC	GTGCCTCCTC	GCGCCACATA	AGCACGCACA	CCCTGACCCG	300
	ACACGCACCC	TGCAAAAGTAG	GTCATCACCA	AAGGGGCACC	CCGCCTGACC	GTTGCCTGCG	360
	TCGAGCAGCC	GCCCCGCCACG	CGCCAACGGC	CACCAGCATG	CGCGTTCTCC	GTAGCCGCGG	420
	GCGCCGTTGG	CCATCGCCGA	AAATACCTCG	GTTTGGCCCC	CTGATGCCGT	CTGCCGTCCG	480
25	CCGCGCCCGC	CCGGCGCCCA	GGCACCAGTG	CCTGGTCAAG	GCGCCCGGGC	GGGCGGGGTC	540
	GGTCACGTGT	GCGGTTACCC	GGGCGTCGTT	TAGATCGAAG	GTTCTAGGTC	TGTGCCGTGC	600
	TGCCCCTTGT	TGTGCTACCG	CCAACAGTGG	GCGCGCGGTA	CGCGGCAGGC	ACCACGTGGC	660
	AGTGGCTATC	ACGTGAAAAG	AGGGCGGGTA	ACGGTGGTTC	GCCGCTGAGA	CACATCGCAA	720
	CTATTTACAG	GGCACTTAGG	NGTTGACC				

## 1318UP

	GCAAAAAATG	AGGTCCGCCA	TGCGCGGCGG	CTCGCGCCCG	TCCGCGACCA	AGCTCCGCGG	60
	CCCGTCCGCG	CCCCACAGGC	ACCAGCTCGC	GCCTGCGCGG	TAGCTCGCGC	CCATCGCGCA	120
35	GTCGCGCACC	GCGCCCGCGC	GCCGCAACGT	CCACATGTCG	CGCACCACCT	TCTCGTCCAG	180
	CACACCGCCC	CCGCACGTGG	CCGGCGCTGG	CGCCGCCCGC	GGCACCTGGC	GCTCGTCCGC	240
	AGCCAACCTC	CCTGTCTATG	ACAACGCTGT	AGGAATGCCC	ATCTTTGCCC	TTTCCGCTCG	300
	CTGCCGCTGT	GTGTGTGCTA	TACGCTGCCT	TATATACCTG	CCAGGAGAAA	TGTCTGCTAC	360
	TATCCCCGCG	AAAATATCCA	TCCGATGCGA	ACGGCGGAAC	TCGCCGGAAA	CCTGGAGCCC	420
	CGCCTCTGTC	GATCGTATGG	AGAAACAGCT	AAAATCGCTC	AGCTACTCAT	CTCTGGCGCT	480
	GTGGTTACCG	GTCGCCGCAA	TGCGGCGCAT	GCCCAAGTCC	GTTTTTTCTC	TGTGGCGGGG	540
40	CCAGGGAGAG	CGGGGCGCAG	ACGGCCAGAT	TTTGTGCACG	GCAGACCGCG	TTGGCTGTGG	600
	TAACGCGTAT	GAAATACGGG	GAAGCGGCGA	TTACCAGTGG	GTTTCGCTGT	CAGGGGTGCC	660
	TGGGGCGCGG	GAACGCGGTT	ATGGTCTATA	TTACAGAATG	TGTACAAAGG	AGTCACGTGG	720
	GGGGGGTCGC	GGGCNGGACA	GCTGCCTCTG	TTTCTTCC			

## 1319RP

	GATCTTCCTG	CCTTTTGACC	TCTTCATTAA	TCTTCTCCTT	TAACCTCTTT	TCCGTGTCAA	60
	GAATGTCTGT	TAGCAGTTCC	TCTTCTCTGT	TCGGTTTCTT	CCTGTTCTCT	CTGCCAAGAT	120
	GCAGCATCGA	GTTTGTGCTG	ATGGGCAAGA	AATTAGAATT	GATATCGCCG	ATCCCTACGA	180
50	AGAAATCGTA	CGGCACAACC	TTAATGAGAT	TCTCGCACCA	GTTCCAGACA	TCACCTCTAT	240
	CGTCAATGAC	TACGACCATC	GACTGGTCCA	TCGGGAACAG	ACGCTCGAGT	GATTTTTGCG	300
	TCAGCGAACC	GTTTTTCATC	CGTGACAAAA	TTCTATCGCC	AAAGAGCTTC	CCATCCGGGT	360
	CAATTATCTT	GGCAATCTCT	AGCGCATAGG	CTCGAGTAGC	CATGGTGTAT	ATATGCAGCT	420
	CGAAATGCGG	GCGGATCTTC	GCAAAGAATT	CCTTCAGGCC	TGGCCGTAAT	TTCACGTTAG	480
	TACCAACACT	TGCGCCGTTG	GTTGGCTTTT	GGCCCCCATA	TAGAACGGCG	GCAGCACAGC	540

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	TCCTCCATCC	GANAGANAAA	AACTGCNCAT	CCTTAGCGCC	CCGTATTCCG	GTTTGTTTNG	600
	GTTCCCTTTG	ACCACTCCCC	CATGGTGGGT	TCACACCCGC	NATNGATTN	CCGTCTGGTT	660
	CAATTTTACC	CCCAGCATNG	CTTGCGCNCN	TCCNNNCAAC	TTTGACTION	CCNCTGACCA	720
5	AAATCCAAC	TGCNTTGGAC	CCGATTGT	TTTTNTTTG	AAACGNNANT	TCCTNGTCNN	780
	CTTGGGNCCC	CNCTTTCCCN	A				

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## 1319UP

	GATCATCGGC	ATGCTGGAGA	ACCCAATTTT	CCAGTCTCAG	ATGAACGAAA	TGCTCAACAA	60
	CCCGCAGATG	ATCGACTTCT	TGATACAGCA	GCACCCGCAC	CTGCAGGCAA	TGGGCCCGGC	120
5	GGCGCGCGAA	ATGCTCCAGA	GCCCCTTTTT	CCGCCAGATG	CTCACCAACC	CCGACATCAT	180
	TCGCCAGATG	TCTCGCCTGC	AGATGGGCAT	GGCGGGTGCG	GGCGCCGAGC	AGGGCACCAG	240
	CTTTCCAGCC	CCCGGCTCCG	CCGCCACACC	CGACGCCGCC	GCCCCCTGCG	CGAACCCGTT	300
	GGCTGCCATC	CTAGGCTTGC	AGCCCCGGCG	TGCTAACCCG	CTGGGCGCTG	CGCCCCGAGA	360
	CCGCGGCCTT	GCAATGCCCC	CTCTAGACCC	GGCTATGCTC	TCTTCCCTCT	TCGGCGCTGG	420
	GCGCTGCCAG	CCCTGCGCCC	GCCGAATAAC	AGGGCTNCCC	AAGNANGNGN	TANCAAAACA	480
10	ANATTCGCCC	ANGCTNAATN	AATTNNGGCN	TCTCCAACCT	GAANAAANAT	TTCCGGGCTT	540
	NAAGCGCNCG	AAGATGTTCT	NTCNNGGGCG	CCCTTNTATT	CTTTNTNTAA	GGNAAANTTN	600
	TAGGTGNNGA	NTTNTCTGCT	NCNNGGGGCG	NCGTGCGCGT	TTTTNTTTAT	TCCCCNTTNT	660
	TTGTNTTCTC	CNTNCTGNIT	TGCNACCCCA	CNCAATTTT	TTTNGGTGGG	GGCTNCCNTN	720
	TTTTCATNNN	TTCNANNNAC	GNCGNFAATT	ATANTTGTNT	ATCACGTCCT	NTTTNTTTTT	780
15	NNCCNACNGN	TTGGGTTGCC	CCTTTNANNT	GAGGNTGGTG	TAGGGAAGAA	AAAT	

## 1320RP

	GATCTTTTCA	AGAAGTTTAA	CAATGACTTT	AAAGCTAGCA	TTGATAAAGT	ACTCAAGAAA	60
	CCTAACAGAG	CGGAGATGTA	TGATGCTCTT	TTGTCAATTA	ACGTCCATTC	TAACAATATC	120
20	ACCTCGGGAT	TGAATAGAGC	TATCTCCACT	GGTAATTGGT	CGTTAAAGAG	ATTAAAGATG	180
	GAACGTGCTG	GTGTTACCCA	TGTCTTGAGT	AGGCTTTCTT	ATATTTCTGC	TCTGGGTATG	240
	ATGACAAGAA	TTTCTTCGCA	GTTTCGAAAA	TCTAGAAAGG	TTTCTGGTCC	TAGAGCTTTG	300
	CAACCCTCGC	AGTTCGGTAT	GTTGTGTACA	TCCGATACGC	CGGAAGGTGA	GGCCTGTGGT	360
	TGGTTAAGAA	CTTAGCATTT	ATGACACATA	TTACCACGGA	TGATGAAGAG	GAGCCCAATA	420
25	AGAATCTTTG	CTACTTACTG	GGCGTTGGAG	AACATTACAT	TGGCTAAANA	ANGGCNCCCT	480
	TCCTTTTAAA	TNNNGGGGGT	TTTATTTGGA	AAGGGTACTA	CCCCCGGTNC	ACAAAATCCC	540
	CCCCGNGTTT	TTGTTCCCCC	TTTTAAACTN	TANAAAAAAC	GNGTAAATTT	CCNNATTTCT	600
	TTTCCCNNTN	TCCCAANNNC	CTCAAAACTT	NTTCTTTTGC	AAGGAGGGGG	GAAATTTNTN	660
	ACCCCTTTNT	TTTNTNGGAA	GAGAATTTTT	GTCCCGGNGG	CCCCCAAAAA	TTTTTAAGGG	720
	GAANTCNTTA	NATTCCCNAN	NGGGGNTNNT	AATTTTGTGN	TTTTTANAAAA	AAANCCCCCC	780
30	CCNCCGNNA	A					

## 1320UP

	GATCATGAGG	GAATCCTTGG	AAGAGGATGA	CAAGAAGTCC	GACGATGAAG	GTGACCTGTC	60
	TATTCAGAT	GCGCCTTCCT	CTGAGGAGGA	TTAGGCATAT	AATGGGTCGT	TTATATGTAC	120
35	ATTAATTAA	ATTCCGCTTT	AGCTTTTPTA	CTCTTATCCT	TACGGTAGCT	CACCCATATC	180
	TGTAGCCCTG	CTCAGTTATC	ACTAAAACGA	GTGCCAGGCC	CTAGTACTAT	ATAATCCCCA	240
	GTTTCGAGCT	AGAAACAATG	TCTGATTCGG	CTGGTTTGCA	TGGGAGTACC	GCGATGCAAG	300
	ATCCAGATAG	CACTTTATGC	GAGGAAAGGT	TGGCGGCTAC	GCCAAAAGTT	ATCAACAAGG	360
	TCAGCAAGAA	AGGTTCAAGC	CCCCTTTCAG	TGTTTAAAGT	TAAAGAGGGG	AGCCTATCCT	420
40	GCCNAAANTG	CGCCAGGGTN	CNTGAATTTN	GGAGAAAAAA	NTGCGTTTTT	TCCGGAAAAAG	480
	CGCCCCNTGA	NNCCAAAATT	TATTNNGGGAC	CCNCNACACC	NCGAGAAATT	TNNTTNAAGN	540
	GCGCCCTTTA	AAATNCCCAA	TNTCTTCNAA	ANNATTTGAG	GNGGAAAGAC	ANTTTNTPTN	600
	AATTNCGCGG	GGGGTNTTTT	TTGCCGCCCC	GGNGNTCNTC	CCNCCTCCAC	NANTTTNAAA	660
	NATAGGAGGA	ANGGGNGGNG	GCCANATTTT	CACCTTTTCNN	AGTTNGANNG	CCNGNAAANA	720
45	GNNTGGATGN	CCACCAATNC	GGGTGNTNGA	AAANANTNCN	NACTGCTTGT	ACACAAATTT	780
	TTTTGTGCCG	CNGGTGACAG	AAAAAAAGAN	GGATTTTTTN	ACAACCNNAA	AAANAAAAAA	840
	AAAA						

## 1321RP

	GATCACGTCG	TTCTTGGAAT	TTCTATCGTC	GACGGTGCTG	TTCTTCAGCC	GGGAGGCGAT	60
	ACGGCTGGCG	ACGCTGCGCA	TCAAGACGGG	CGGGGACGGC	GGGCGCGGCG	GCGAGATGTC	120
	TGCGGAGCTG	CAGACGGCGG	TGAATTTTGC	AAACATACCG	ATGTGCATCG	GGGCGCCGCT	180
	GGCGGTGGTG	CTGGCGGTGT	GGCAGTACTC	GAACCTCAAC	AGCTACTTCA	CGCAGCTGCC	240
	GTCTTCTCG	TGGTCGATCT	ACCTTGTGCT	GCTGTCGATC	CTGGCGGAGC	TCGCGAGCGA	300
55	GCCGCTGTAC	GTGGTGAACC	AGTTCATGCT	GAACATACCG	AAGCGGTGCG	AGTTCGAGGG	360



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	TGCGGCGGTA	GCAGCGTCCT	GCC TGGTGAA	CTTCGCGGTG	ATCTACTGGT	ACGAGAAGTG	420
	GTTGAATGGG	CGCGGCAGAC	GTGCACGACA	GCTACAGCCA	GGAGGCATCG	CGGTGCTTGC	480
	TTTTNCCCCG	GGGAAGGTTG	CCCCCNCCAA	AAC TTTNCCT	GGCCCGNTCT	ACTTGAANAA	540
5	CTTGCGNCTC	TGGGCCCCCA	AAAACTTTTT	TCCCTTTTNT	TNACAAGTTC	CTTTTCCGGN	600
	NATTTTTTAC	GGGNTTNTTC	CNCCCGNAAT	TTNTTGCCCC	TTCCNAAGGT	TTTTTCCCCC	660
	TNTTTNTTTA	NCCCNCC TTN	NCAAGGGGGA	AANNTTTTTN	CTTCCCCCNC	CCCGGGAGAA	720
	ANNGGGGANT	TTCTTTTTTT	TTAAAANGGN	NCCCCCCC GN	ANGNNTTTNN	CCCCCNAGAA	780
	NATTTTTT						

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## 1321UP

	GATCGAATTC	GATTTCCTTT	CGGTGCAAGG	AAACAGAGCC	TTCGTAAAG	TGGGATACGA	60
	AGACCGTGCC	CAATTTTCGT	CGGCCCTTTC	TACATACATC	TCAAGCGAGG	AACTTATCGG	120
5	CGTGCCATTA	GTGGTCCATA	TATTGCAAGA	ATGTACAAAG	TTAGAGAGGA	TGAAGGTTGG	180
	GGAGGACGAT	GAGCTATGGT	TCAAAAGGAG	TTTGGAGGAA	NAAGTANCGG	ATTCCAGTTG	240
	TAATTAGCTA	CAAAAGCGGA	ACGGGTGACA	CTAAAATTCC	ATGCGCTAAC	TTTTCCACTG	300
	AAAGAAGCCA	CATGAAGCTT	TTATATCTTC	TGGGGCTCCT	CTGGGACGCT	TACACGTCCA	360
	GAAGTGTTC	CCAAAATTCC	TCGACGTTTT	CGAGGTTTTA	AGAACCAGATC	GGTCTCCGTG	420
	CTTGACAGAGA	GGTGCATTTG	ATGGGGCGAA	AAATGGTTTT	TCAACCGCCG	AGGGTCGGTTG	480
10	TTCAGGAGCT	TTGTTAGTTC	GAAGTTGGAG	CGCCATTCCA	TTGATTGCC	CTTGCTCTTC	540
	CTCCCTNGCA	CTTGCCGCTT	GCTGCTATGT	TTACTTACTA	NAAGCACCGA	NCCACACTTA	600
	TCTGGTTTTT	TTTTCTATC	CTGANACTCC	CTTGAATTAT	TGCCCTCCTT	TGACTTTCCC	660
	CCTGTTCCAC	GTTNGTTACA	CNTTTGCTTT	GAATATCTTT	CCTTTCCGAA	GCACCCATNT	720
	TTATAATTAG	TCCTATTGAC	CCCCCCCACC	TGGTTTTTGT	TTTCCTCCCA	ACANGTTCTC	780
15	TTCTCCACTN	AGNTTTGTAT	ACNGAATGTC	NACCC			

## 1322RP

	GATCCAGGAA	ATAGTACAAC	GCCCTTGGAT	AATGCCAGGG	ATTCTGACT	CCTAACGAAA	60
20	AGCCTCTCCT	CTTCTAATTT	CTTATTAAAG	TAGTTAGCTG	CAAACTGTAA	CAAATCCCCC	120
	GGCGCTCTTT	GCTCCACTTC	TTTCTGGAAT	GCGTCCAGTA	GGTCACGGTG	TTCTGTGAT	180
	AAAACCATCG	AGTAGTTTGT	TGTGTGATGC	AGAAAACCTG	CCTATAGCGG	AACCAAAATG	240
	CTCTAGTAGT	GTGACGGCAC	CGTTTTATCC	AGTTTGCTAA	GCAGCTGCCC	TAGGTTAGGG	300
	AGAGTAGAAA	GTGTCAATGG	ACCCGAATTT	CCTTCTGCGC	GCGGCGAACG	ACGTTAAATG	360
	TGATTACCGT	GATCACGCTA	CTGGGGCTAA	CTACCAATTG	AGACAGGCTA	GTTGTGCAAG	420
25	CCTGAGGAGG	TCTCCGAAAA	GCTTGATGTG	AGGATACTCG	TGTTCAAGTA	TCTTGATATG	480
	CTGTATTGAT	CTGTCCGTGA	GACCTCGAGC	TCTTCGTCCG	TCAATGCCCC	GCGCCTAGAG	540
	AGCTAGGTTG	ACTCCGAGTT	CTACAAAATT	TCNAAACNCC	TTGAAAAATC	NCAACATTGT	600
	TNTGGACCAT	CNANTTCCCC	NCCTTCGGAA	NNAAGCCCTC	CANCCTTTTT	TNACGTTGCT	660
	NACTTNCCCN	CTGAAAAAAC	GTTCTNATTTA	CCCNTNTNTA	CNCGGCAGGA	AACCCCCCAN	720
30	TTCTTTTTTC	ATNAACCGGT	ANCTNAAAGA	ATTTTCNNGC	CATGNGGTTT	ANG	

## 1322UP

	GATCTTCACA	ATCGACGCCA	CGTCCATCGC	GATGTTCCGC	CGCACTGCCG	TCACTGTGAG	60
35	ATATTCTGTAC	GGAGAGAGCC	GGTACGTGTT	GATCATGAAG	TTGCGCACAT	CCTTGTACGC	120
	TTTGGCCGTC	TTGAACCGCA	CCGAGTCGTT	GAAAAAGTCG	GGCAACGCGC	GACGCTCCAG	180
	CTCATGGATC	TCGTTGAACT	GGAACCACGA	GGCAAACGAC	GGCAGCATCA	CCGGGTGCGC	240
	CTGCTTCGCT	AAGAAGCGCG	CCGCCTTGTC	CTCCAATTTT	TGCGCCTCCT	GCTCGTAATC	300
	GATCTTGGGT	TGTTCTTGCT	GCTGCTGCTG	CTGTTGCAGA	TGTGGCAGCA	CAGGTACAGA	360
	TGGATTACAG	GTCGCCGTGT	TGCCCGACGA	AAGCGTTCCA	TCGCCAGCGT	TGTCAATATT	420
40	GCCATCTGG	ACATCCATTG	GCTCGCTCAT	CGTTATAAAG	AGTATGCCAC	GCTACTTTCC	480
	CCGTTTAATA	GCTTTCAAAC	GCGTCTTCGC	TCTGCTACCC	CGCTTAANTC	CACACTGGTT	540
	TNTGTTTTTC	NCCATACCCA	AANTTTTAAA	ACCCATTTTT	CCACATCAGC	CCCATATCCT	600
	CCGTTTGGTN	GNGGAAATTT	GAAACCCANC	CCTCGCCTGG	CGGAAANNC	TNCTTATGGA	660
	CCCCCTTCCC	NTCTTTCAAT	CGGTCCCCTT	NACCAAGNNT	TTAGCCCCCC	GGNANANGAC	720
	CAATTNGGTC	CTTCCGTCNC	TTTCCCTTNT	TAAATTGAAA	AAGGTTNCCC	TTTGAAAAAT	780
45	AACCCNGCCC	NCNTCCCCCC	GANAAATGGT	TTTTTTGT			

## 1323RP

	GATCAGTTTG	CAGGGACCAT	GAGCAGGGCG	GGCGACGAAA	GCAGCTCTCC	TTCGTACACC	60
50	TCCGTGACAG	GGCTCAACAC	GCCCTCGCAG	GCGGACGACG	ACGAGGAAGA	GGAGATGCG	120
	GCACCGTTTT	ACATCCATCC	AGATTTGAGG	ACATCACAGC	TCTACTTTGA	GAAAGATGATC	180
	GATGAAGAGC	CCCTCCCGGC	GCCTGTTAAG	CGGGTGTTC	ACATTAAATC	GTATGGAGAG	240
	GAAATTTTCC	CTGTGCGGAA	CTCTCGGTCT	ATCCACCAGC	TGAAGCGATG	CGATATGCTT	300
	GTGTATTCCA	TCGGGTCTCT	AATTACCACC	TATTGCCATG	GTGATCCTCC	GGTACTTGCG	360
	AGGTGGTCGT	CCAAGGGAAG	ATGAAAAAAT	GCTACTGGTC	NCNCCAATCA	ATTNNCNAACC	420
55	TCCGATTAGG	GGGGGGGGNT	TNTTTTTTTT	ATTTTAACCC	CCCTTTGGGG	TGACCCGNNC	480

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	NAAAAAAAG	GGGGCTTTGN	NNNTTTTTTT	TNGNCCCCGC	CNCCTNTTCG	GNAGNTTTTT	540
	TTTTCTGGNG	GGGGGGCCCC	CCNNNCGGAA	AATNTTNINC	AAAAGGAAGN	ATTNCCCCN	600
	NANGGGGANT	TTTTTTNTTA	NNAAATNNAA	AAAAAATTNN	TTCCATTCCC	MNAATTTNNN	660
5	NTTTTTNNNN	CTNTTNCGGN	TTTGNAANTT	NACCCCCCNC	NANAANTTTN	NTTTTTTCCC	720
	CCCCCCCCC	CCCGGGNNNN	TNCNTTTTTT	TTNNNGATN			
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## 1323UP

	GATCCGTTTT	TCCAATATTT	CACCGTCTCG	TAAATCAACA	GTTGAAAAAC	AATGGCGTGC	60
	TTAATCGACG	AACGCAGCAC	AACCAGCAAT	AGGCTTCGAA	GCCGTTCCAG	AGGTGATATC	120
5	GCAAAGTTGC	TCGAGCACTA	GAACGGACTG	GGTCATTATA	TAGGTGGTAG	TAAGAAGTGG	180
	GTAGAAGGAA	GGGGACTATG	GTACAGCGCG	GGCGTGGAGG	CAGGGACGCC	GCAGTGGGTG	240
	CCGCTCATGG	GCATGGGCAT	ATGCGGCAGT	TGTACGAGTT	GGTTTACAAC	CGGGGGGCGG	300
	TGGGGACGTA	GACGTTTACT	GCCGGACCTG	CCGCGGCACG	GGACGCTTGA	CCCGAGCAAT	360
	GTTGTGTGCA	CGCTAGTGGA	GCTGTACCAC	TCGATTCCGG	GCGACATCCC	GCTGATTAAAG	420
	ACGCATTCTNA	TCGCCCGGTGG	GTGTNTCTGA	NCNAAGTTGG	ACCCNGGAAC	CTGATTGTTT	480
10	TGTGGCNAGA	ACACATNCCC	TTGTTGGTGG	ACCCACCCGA	NAATTAAACC	GCCCCNCCAA	540
	GACNAGCCGC	CCTCCCCCN	GNGCGTTTGG	GTNNNGCCA	TTNGTCCGGA	CNTCCAAGAA	600
	NTTTACTNGC	ACCGNCGGNG	GCACCGCCGN	CGGGGCACCT	NTTTCAACNC	CNTTCCCCCC	660
	CNTGGGGGGG	NCCCCCCTT	TGAAAAANNG	TGGGGGGGAC	CGGTTCCGGT	CCCNTTCCCC	720
	CCATTCTNATT	TTTNTTTANA	NANNAACCAAC	CCGCCTCCCT	TNNCCCCACN	CAAANNNTNGT	780
	TNGTTAANCT	NCCCCNTTAT	TCTNCCCCCC	CGNCNCNTAT	TCCNACCCGN	CNGT	

## 1324RP

	GATCCTACCG	GGATGCACGA	CGCATACAAG	TATATCAGGG	ACCTTGCCGA	GGAAATGGGA	60
	CATAAAATTG	AAGGACCAGA	TCACAAATTGG	TCGTTTCCTTA	TCATAGCCAA	GATATATATA	120
20	TATATCTGGG	ATAATTACAG	CGCTTGGTAT	GTATACCTCC	TACATACAAA	TACTTACATA	180
	CACATAAATA	TAATACAGCT	ACTTGTAAAG	CGAGAAAGGT	TACTTCTGGA	GAGCCATTAG	240
	AGACGCAACG	AATGTCAAAA	TCAACCTCGG	GCGGACTTCA	TTGATATCTT	CAGGAACCAA	300
	CCAGATTAAA	GCACCAAGTT	TTCTCGCGAT	AGAAATTGCC	AAATTAGCGT	TTGCATACTT	360
	CTCTTCCTCT	GTTACGGCCG	GGAGTAACCA	AGTCATAATC	CACATATCCT	GGAGCTAATC	420
	CGTTCAATAC	ATCCAATAGG	AAATGGGCAT	TGCTCAACGA	AGCATCCCTG	GAAAGACATA	480
25	TCCTGCTCGA	TTTGCCACCC	TTGGCACTTG	CCTTGCGCCC	ACTTTAGATC	TGACATCTGA	540
	ATNCTCTACC	AAACAAACTN	TGAGGANATN	TGTTTGACAA	GTTTTCTGCN	CCTCACTGCC	600
	AAACTAAACT	AAGGTCACAC	CTNTTTGCNT	CCCCAATTCC	AACCCCTTNN	GCCCCCCCCA	660
	AAAACTTNA	ATTCCCAAAT	TCANNCCCTN	TTTGGTTTCC	CCCCCAATNA	NCNTNAATTT	720
	CNNCCNTNN	CTGGNCCCGG	NNGAAACCCN	TGAAATAAAC	CCCCGAATAC	CTNCNTTGCC	780
30	CGAAC						

## 1324UP

	GATCTTAAAG	AGGCTCAGTA	TGCAGAGGCA	GTTTCCAGAA	GAAGACAGGC	TGGGCTTCGA	60
	AATCCCTCAG	CTCCCGCCGT	GGAAGAGTCC	GCAGATGAAG	CAACACACAC	AACAGGGCCA	120
35	GCAAACGCCG	CTGCGGCGGC	CGCGCTGCAT	CCTCGGTGCC	CCTTATGAAC	CGAGCAGGGC	180
	GTCGTCCACT	GGTGACGGCC	AAAAGCGCGA	CTACGACTAC	TCCGTGTTCA	ATGAGAGCAG	240
	GCTCTTCACT	GAGAGCAAGA	TAGACCAGTA	CTTGAAGAGC	GAGGCCGCAA	CGCACAAACG	300
	CGTATTCCAC	CGCGACCGTC	CCCACGACGA	CAGCTACCGC	CCCGACTTGC	AGCCGCTCTG	360
	CTGCGACAGC	TCGGACGAAG	GAAGGGAGAG	CCCCGGCGCG	CGCAGAGCGC	GCCGTTGAGA	420
	ACGCCCCGTT	TGGTGGGTCTN	AGCATCCCCC	GGANATNCNT	CCCAGAAAAA	ANTNTTTTCGA	480
40	ACACGCCGCC	CGCCCGCCCC	CCNCAGAAC	TCCCNTTAGC	GAACNTTNNA	AGAAGAATNT	540
	TNCCANTTTG	CGNCCCTNCT	TGGANAATGG	TGGGCCNGCT	TNACNAAACG	CTAGGTTGNC	600
	GCGCCGAAAA	NCACTTTGCT	TNACCGCATN	CTCCCCNGAA	AGANAGANAG	NTCCCCNCAC	660
	TTTTNCGCAA	TTTTNTCCCC	CGCGANAAAG	GTTCCCGTTN	ANCCGANGGG	NGGCGCANNA	720
	ANAAACCTAC	NCANTTTNAA	CATTCCCCCC	CNTTTTTTNC	AAAAAAGANA	ATGNNTTTTT	780
45	CACCNTGACA	ANTGATNNCT	TTTNTGAAGG	GNGGNAGTAC	CCCCCGCTTG	CCTNTCCTCC	840
	CCTTAGANCT	NCNATTTTGT	TTTTNT				

## 1325RP

	GATCAATGCG	GGAGTGGCAA	AAAGCGACTC	AAGGTGAACG	TGTTTCAGCA	CTGTTTCATGA	60
	TGGGGGGGTGG	TCATTTTGCC	GCAGCCATCG	TATCTCACCA	ACGCATAGAT	ATCAGTGGCA	120
50	ATGCCAAGAG	GCATGGAGAA	TCGTTACAGG	AACAGGCCGT	GCACTTTCTT	GAGCACAAAA	180
	CGTTTTCACG	ATACACCACG	AGGCGGAAAC	AAGGAGGTTT	ACAATCGGTT	ATGGATAACG	240
	CCAAGGGGAA	AGCAAATTCC	GCAGGCTCTA	CGCTACGTAG	ATACAATGAG	GCGGCATTAC	300
	GGAATGACGT	TCAGGACCTG	TTAAAGAAAT	GGAGGCCATA	CTTGGAACGC	TGCGAACACA	360
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5	TATTTATTAG	GGCCAAAAAT	GTTGCGGACA	GGAGCGTATT	CTTTACGGAA	AATACCCCAT	420
	TGACCAAGGT	TAGACCCGAG	GATTTCGGACA	TTCCCATTTCA	CAACCCGTAG	ACCTACCACA	480
	AATGAGCTAA	GGCGAGCATG	GTGCGAGATA	ACATACTTGA	AGAAGACATT	GAAGCCCAGC	540
	CATCACATCG	GAGCGGCATA	CTCCTAAAGC	GACAATGATC	CACTGCCAAT	AAGCGACGTT	600
	GTACGCAACT	TAACCCCGNG	GNAAACCTTA	NCAGGAACGG	CTTCTTTCTT	TGGATTCNAG	660
	GCCCCNNNT	ATTCCCTNIT	CNAAAANCNT	NTTTCCCCAA	CCTCTTTTFA	AACCCCGGA	720
	AAAAANNNTTN	AAACCCNCNC	CCCCCCCCA				

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1325UP

	GATCGTGCCA	TGTCTGATGT	GGTATTTTCGA	TGCGGGGCCG	GGTGGGAGTG	CCAGCTGGAC	60
	TACGAAATCA	AGGACGAACG	TGAATTTTCA	GCCGCCCTAG	ATACTGTCAA	GGGTGCGCTA	120
5	GCCCCCGAAA	AGAAGTCGCC	CTGCCGCACG	ACCGTGCAGC	CTGGGCCTGG	AGCAGGCGGG	180
	AACAACACGC	CGACACGCGT	ACCTCTGTCC	AAGCTCTTTG	TAGGTGCGAA	AAACACCAAG	240
	TTCAAGCCAG	TGATGCGCTC	TGCGGATGCC	GCTATCGCGG	CAGGCAGTGC	CGCTTCGGGC	300
	CGCCACTGTG	CGCTATTCTGA	TAAGACACAG	ATAGATGACC	CACCTGGTCAT	GAACAAAGCC	360
	GGTGACGACG	AAGTCGAAGT	TGTAGTCGAT	CCTATTTTGT	CAAAAAAGCT	ACGCCAGCAT	420
	CAGAGAACAG	GTGTTGAATT	CATGTATGAC	TGCGTCCGGG	GGCTCGCAAG	GTCCGAGAAG	480
10	GACGATGATA	GAACAGTGAT	GATCTTGGAA	TATGATAGTG	ATGTCAAGGG	TTGTCTGTTG	540
	GCGGACGAGA	TGGGATTAGG	GAAAACATGC	ATGACGATTG	CTCTGATCTG	GACGCTACTG	600
	AAGCAGCATC	CCCAGGCCAT	CGTCTGTTCC	ATGCTCCGCG	AATTGGGGGG	TTTGGTTTGC	660
	AGGGTTTTTT	GCCANAAATT	CTCNTGGTAT	GCCCCGGTGA	CTCTGATTGG	CGACTGGGAA	720
	AANGATTTTCN	CCNATNGGNN	GCCGANGAAT	AAATTGGANC	CTNGAANCCN	ATTGCNAANT	780
	ACCCCCCAAA	ANAAAAAATG	N				

1326RP

	GATCGAATTA	AGTCAGATTT	GATTGCGATG	GCTACTAACG	AACGTGCATT	GTCAGACGGA	60
	CCGAATCAGG	TACACATTGA	AACTCGTGAG	TGGCTAGTGC	AGACAATCAT	AAATGAAAGT	120
20	TGTGGCTGGA	GCAAGGGAAC	TGCGATGCCT	TAACTTTCTC	AAAAACTCA	TGGGTGGTCA	180
	AAAATCAATC	TATTCAGTAT	ATAGTATATC	AAAACATTAA	ACCAAAC TAG	GCGCCAGAA	240
	TATTGCCAAA	ACATPGCACT	GGAGTATTAG	TATGTCAGAG	AGTAGCAATG	GGCGGCTAGC	300
	TGGTTACGTG	GCAATTCACGG	ATGACTTATA	GAAGCCCAT	AATCATCTTT	TAGTGACAGT	360
	AAGATCAGAC	ATTAAATAAC	GTATCGAATT	TTAGGGGAGA	AGTCATCACA	CTTGCATTAG	420
	TATACCGCAA	TAATTCGCGG	ACCACATCAG	TTAATACTGG	GCAATGGTTT	TAAAAAGCGA	480
25	AACTGGGTTT	ACATTCAGTG	TGTTTTGCAA	CATAGATGTC	TCTCCTCATG	CTGCTTCTCG	540
	GTTGAATAAC	CATGCTTCAG	TAGGCACCGT	TCCCAGTATT	TGGTAATTAG	TTGCCAGACT	600
	CCTTTATAAA	GGATGACCCG	AATATGANCT	TCCATTAACA	TTGCCNGGAA	AANANATTTG	660
	GCANCCGTAN	ATATTTTCCT	GCCAATTGAN	ACCGTTCTNT	GAACCCCTNC	TTGGGGNCCN	720
	GCTTCCCAAA	AACGAANTTC	CCCGGTNGNT	NTTTTATAGG	TNCNAAGAAA	AANA	

1326UP

	GATCAACAAG	CGGTTCCGCG	AGCTGCCGGA	GAACCTGCGC	CTCAACGGGG	TGACGCCGAG	60
	CGGCAAGCCG	CGGCTGTTTG	TGTGCCACAC	GTGCACGCGC	GCGTTTGCGC	GGCAGGAGCA	120
35	CCTGATCCGC	CACAAGCGGT	CGCACACGAA	CGAGAAGCCG	TATATCTGCG	GGATCTGCCA	180
	CCGGCGGTTT	AGCCGGCGGG	ACCTGCTGCT	GCGGCACGCG	CACAAGCTGC	ACGGGGGGGAG	240
	CTGCGGGGAC	CGCGTGCTGA	AGAAGGGCTC	GCCGCCGCGG	CAGCGGCTGA	GCCGGGCGGT	300
	GCGGCGGCGC	AAGAGCGCGG	AGGGGCTGCG	GGCGGCGGGC	AAGCCACGGC	GGCGGCTGTC	360
	GTCTCTGCG	CAGTCCGGGG	AGAGCTACGC	GTCGGTGCGG	CCGCGCAGCG	CGGGGGGGGG	420
	CGAAGAAGGT	GCAGTTCTCG	ACGCCGCAGC	TGCTGCCGGT	GGACCTGACG	CAGGAGCCGT	480
	CGACGTTTAC	GGCGCTGGAG	GCGAACGGTG	GTTGCAGGAC	GTGAACAGCC	TGTCCGCGCT	540
40	GGACGGACGC	CGGAGGAGGG	GAGCTGCAGC	CCGCGTCCGC	GCTGTCTGTT	CAGGCCACGC	600
	ACACGCCGTC	GCTGTTTGCC	CACCTTTCCC	NGTTGGCCGT	CCTTACGGGA	ACCTGCTTGN	660
	CGCTTTTGCC	CCGAATTGCA	GGTTCGAAGG	GCTTNCCTCC	CGNNGGCNCN	CCGCCCCCCC	720
	CGCATCCCCC	CCCGTNNCCC	AAAATTTCAA	GTTAACCCAA	NAACATTCCC	TTTCTGCCT	

1327RP

	GATCCAAGCG	TCTGGAGTAT	GCTAAACGAG	CGTCTCATGC	CAGGAACAAC	GTATTATCTC	60
	GTTGAACGCT	GTCCTCGAGC	CTCGAGCCAA	ATCTGACCGT	TTTTTTGCTA	GAGCATACCC	120
50	AAAAAGAAAC	ATCTTGATGC	GCTAAACAAC	ATGACAATGA	TTAGCGCGAG	GATGCTTTTC	180
	ATGTTCTAAA	TTCATGCTTC	GAGGTCCGAG	TCGGTGCCGC	ATGTAGTCCT	GCCGGCCGAT	240
	TATATTGCGG	CGTAGCTGTG	GTGAAACATC	GGCGCTAATT	GACGGATAAG	CAGCTGTGTA	300
	CCTTATTTTC	ACTATTTCTT	TTCACATACC	AACGACTAAG	GTTGATTCCA	AGAGGTACTG	360
	ACTGACCCAG	TGGACAGCGT	AGTTATCGGA	GTAACCTGGC	AATGTCGTAC	GGGTTCTCGG	420
	GGACGGGAGG	AATGGGCTGC	TCAAGGCCGA	CGACGCCGGA	GCTGACGAAG	GAGCTCAACA	480
	TCCCCAAGGA	CGTGCGCAGC	GCCATGAGGA	AGTCGCTGTC	GTACGACTTC	CTTAATGTGC	540

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CTGGCGGGGA	CGAGCAGGCG	AGCCCATCGG	GACGCCGACG	ACAGCGACAG	CTGAGGACGG	600
CGCCGACGGA	ACTGGAAAAC	CAAACCGGCG	AANGGGCCCN	AGGGCNGNGG	ANCAANGNCG	660
GAAAGGGGGA	ANTTTGCCGA	NTACCNCTGT	TGGCCCNCCC	CCGCGGTTC	GANTTTGGGT	720
TGNCAAAATC	CCCTCCTCAC	TTNCAAACCT	NCTGAGTNN	AGT		

5

## 1327UP

10	GATCGGAGGC	GTCGCTGGAG	CGTGCTCTTG	TTCTGTCTCT	GCTTGGCTAC	GCCCGACTTG	60
	GCAGCCGCGG	CGCTCCTGAG	CGTCTCATAC	TTGCTGCCTG	CTACTTGCAT	GGTTTCTATC	120
	GTCACGGTGC	AGCAACTGGG	ACAACAGCAC	CCAGCAACGG	TTGCATTTAT	ATAGTGTCTA	180
	CCTGTACGAT	AGGGGACTGA	TCGCTCTGCG	ATGCGTATCT	ATCTCATTGC	GGAAGGTTCT	240
	CGAAACGAAA	AGCGCCAGTC	GCTGTGAGC	GACAATAGCG	AACCACAATG	ACACAATAGT	300
	GCGCGTCGGC	GACCCGATCC	CTGCATGAAG	ACCGAATGCT	CGAGCAGATT	CTTGTGCGGG	360
	CGTCAGCGGG	TAGCGCGGCT	CGTCGTGTGG	CGGAGCCCGG	ATATGCGATG	GCACCGGATG	420
15	GCGATGTGCT	CGGCGCTCGG	GATTAATCTA	GCTCTTCGGA	GATATGCTTC	TGTAGGAGGA	480
	AGAGGGCGTA	GGGAGAAGGC	CTGGACGCGG	GCTTGGGGAG	CTCTGCAACG	TTGCGGGGGC	540
	GTGCCGCCGT	AGGCGGCGGC	ACACCGGGNA	AATNCNCNGN	GANCCTNGTN	CCCTCCNTTC	600
	CNCCCCCAA	ACTTGCGGGC	NTTNCCCNCC	CGAATNNCAA	GGNNGNCCCC	NAAATCCTNA	660
	ACCCCCCGNA	GGAAAGNNTT	GGCCTNTTGA	NCAAANNACN	CGCGTTNAAA	NTCCCGGGGG	720
	TTTGNGGCCC	CCGAAAANGG	GGATAAACCN	GGCNACNACC	TTTGTAAATC	GCGTTTCNTT	780
20	TTNCCCCCAN	ACNT					

20

## 1328RP

25	GATCTCTTCT	GCAAGTTTCT	TTATCGGAAG	CCCAGGCTCT	GGATTTCCTT	TCTCAACACC	60
	AATGGTATTG	TCTTCGATAT	CAGAGAAGGA	GCGCTTCGAA	TTTTGCGCAC	CACCATATGG	120
	ACTCTCTTCA	TTATTTTCGT	TATTTTCTCC	ATCACTTTTCG	CTTGCCAAAG	AAGAAATCCAT	180
	CGCACCCATT	ACATCGAATT	CTTCATTATC	AGCTTCTCCA	CTGTGTGTAG	TATTTTCGTT	240
	ACCATTTATTA	TCTGTGTGCT	TATTGATTGC	ATCACGGCCC	ACACGGCTCA	TTTGATATCAT	300
	GCTAGATGTA	TATGGGACAT	AATCCACCTT	TTCCAACAGA	GGACCGAATC	GCTCAACCAA	360
	GTATTGATTT	AAAACCCAGGA	AGTTCTTTGT	ACTGACCTCG	GCATATTCCCT	GATCTTGCCC	420
30	GAAACGTGCC	GAAATTACCT	TAAATAAGTC	GAGCACGCAT	GAGTTGGCCA	TGTTATCAAA	480
	GTAAAGATTT	TCTTGTAGCA	GCTGACAAAT	TGGATCAAAA	AGATCTTAGA	TATGAGATAG	540
	TTGTGATAAA	ATTTCGATTT	TACAGCCACG	ATACCCTTGA	TACCCGAAC	GCAGCCAGCC	600
	TTAACTGTAT	AATATGGATG	GTTCCATTAG	TTTCCAATAG	TCAATAGATG	CCATTTTCCA	660
	ATATNAACCC	CCCTTGACAG	CATAATATCA	GTTCCNTGTT	NTNATAATCC	CCCCATTTTA	720
	CCAAACCNCG	NCNGTTGATT	NCCCNCCCTC	CACCCCT			

35

## 1328UP

40	GATCGGAGGT	ACATAAGTGC	TCTACCGACC	AACCCCGCTC	TCCATGCATC	AACCAATGGA	60
	GTTGAAACAG	TTGACTGGCG	AGCAGGCCGC	CGCACTAGAT	GCGGAACCTCA	TGGGCCCAGA	120
	CGTTGGCTAC	TCGCTGCATC	AATTGATGGA	GCTAGCAGGT	CTTGCCGTGG	CGCAAGTCGT	180
	CGTGCGCCAT	TGGGGCGCCG	CACAGGCGAA	GAAAAAGGTG	CTTGTGCTAT	GTGGGCCCTGG	240
	CAATAACGGC	GGCGATGGCT	TGGTTGCTGC	ACGGCACTTG	CGGCTCTTCG	GCTATGACCC	300
	TGTGGTCTAC	TTGCCGCGGC	TGTCGGCCAA	ACAGCCCTTC	TACGCACAGC	TTGCCAAGCA	360
	GCTACACTTC	GTGCTGTCC	CAGTGCTCTC	CGAGGGCGAT	GACTGGCGTG	CGCATCTTGA	420
	GCCACGTGAC	ACGCTCTGCG	TTGTGGATGC	GCTCTTTGGC	TTTTCTTTTC	GTCCGCCGCT	480
45	GCGCGAGCCC	TTGCTAGCA	TTGTCGCAGA	GCTCAAACGC	CATGAGGATG	ACATCCCAAT	540
	TGTCGCTGTC	GACATTCCCA	GTGGTTGGGA	CGTTTGAACG	AGGACGCTCA	CCCCTTTACA	600
	CTTATGCACG	TGTGCTGATN	TCTCNTGAAC	GCCCCCAAAA	AGCTGCTCCC	NCNCACATTG	660
	AAACTGGTTT	TTTACCNCCC	ATTANTTTTCG	GNGNNGTTTC	ATCCCNAAAC	CCCNCCCCGN	720
	CCTCCNTGTT	TTTANTCCNT	CCCCGTATCC	TGNNCCCATC	CANANTGCGT	TTTTGANTTG	780
	CCATTGCNTN	ATCT					

50

55

## 1330RP

	GATCTTGGAT	TTGACATTGT	CAATGGTGTG	AGAGGACTCG	ACCTCAAGCG	TAATAGTTTT	60
	CCCTGTCAAA	GTCTTCACAA	AAATCTGCAT	ACCTCCCCTC	AAGCGCAACA	CCAAGTGCAA	120
5	CGTAGACTCC	TTCTGGATAT	TATAGTCGGA	CAACGTGCGG	CCATCCTCTA	GTTGCTTACC	180
	CGCAAAGATC	AAGCGCTGCT	GGTCTGGGGG	AATGCCCTCC	TTGTCCTGGA	TCTTCGATTT	240
	GACGTTGTCA	ATGGTGTGAG	AGGACTCGAC	CTCAAGCGTA	ATAGTTTTCC	CTGTCAAAGT	300
	CTTCACAAAA	ATCTGCATAC	CTCCCCCTCA	GCGCAACACC	AAGTGCAACG	TAGACTCCTT	360
	CTGGATATTA	TAGTCGGACA	ACGTGCGGCC	ATCCTCTAGT	TGCTTACCTG	CAAAAATCAA	420
	GCGCTGCTGG	TCTGGGGGAA	TGCCCTCCTT	GTCTCTGGATC	TTGGACTTGA	CGTTGTGCGAT	480
10	GGTGTGAGAG	GACTCGACTT	CGAGTGTGAT	TGTCTTTTCC	GTCAAGGTCT	TGACGAAAAT	540
	CTGCATACCA	CCTCTCAAAC	GCAACACCAA	GTGTAAAGTA	GACTCCTTCT	GGATATTATA	600
	GTGCGACACG	TTGCGGCCAT	CCTCANNNTTG	CTTACCCTGC	AAAAATCAAA	CGCTGCTNGT	660
	CCTGGGGGAA	TGCCCTCCNT	GTCCCTGATT	CTTCNANTTT	GACATTGTCTN	ATGGGTNCCN	720
	AAGANTCCNC	TCAATTNTTG	ANTTCTTCC	CCGNCAGGTN	TTGAANN		

## 1330UP

	GATCAGATGT	TTTGTGCTAG	TACGTCGCGA	TAGTACTAAA	ATTACCATAT	GCCCATCAGC	60
	ATTATACTAA	CTAGTGTGTG	TTTGCAAGTAA	GCGGTAAACC	ACCCATTACG	CCTGTTGTAT	120
20	CACCAGAATC	CAAAATGCGTT	TTTGAAAAGA	GGTTAATTGA	GCAGTATATC	GATGAGCATG	180
	GGGTAGACCC	AATCTCCAAG	ACAAGCTTGA	CTAAGGATGC	GCTAATTGTC	ATTGCCCCAGA	240
	CACCCACGCA	GTACGCGCTC	GCAAACGCAG	TTAACTCGGC	TACGCTCAAC	GCCAATTACA	300
	GCATCCCCAA	CCTTCTGTCA	ACACTACAAA	ACGAATGGGA	TGCCGTGATG	CTGGAGACAT	360
	TTGAGCTGCG	GAGTCAGCTG	GATATGTGCA	AAAAGGAGCT	ATCGTCAGCG	CTGTACAAGT	420
	GCGACGCGGC	TATCCGCGTC	GCGGCACGCG	CGAAACAGGA	GAATGATGAA	CTCAGACACA	480
	CGTTGACGGA	GCCTGACGGA	GGCAGTCGGC	GGGCAGGCTG	CCGATGCCCC	GCCCCTTCCA	540
25	GCGGAATTGA	TTACCGCGAT	GGCAGAAACG	CACAAGAATA	TGTGCAGCAA	ACGAAAGAAA	600
	GAAGGAAATG	AAAGCCAGGT	AGTGACGGCA	TTTGCTCCTG	GAACAGCCGG	TCCAAACGGG	660
	NTGCGAGGTC	AACCGGTTTT	TTGGTTACCC	GTTTNNNTTG	TTCCGGAAAA	ANAATTANCT	720
	NNCTTTTTAA	CCCAAAGGCA	GGGCCNTINT	GCTGAACAAA	AAGGGTTTTT	GCTNCTNNAA	780
	AATTNGCCNC	TNAC					

## 1331RP

	GGATCATTCT	CAGGTATTAG	AGATTGCTGA	TGGGCACGCG	CTTTTTCTTC	AAGGAATTCCG	60
	ATCGGAGGCG	CCTCTAGAGT	TGAAACGAGT	TTATTATACT	CAGCCATTGC	TACAAGCATA	120
35	TAATCAATAG	CCGCAGCGCA	ACTCTGAAGA	TGATCTAAAG	AAGGAGCATC	TGCCTTTTCT	180
	CGTAGAACAT	TGAGAGCGGT	TGCCCTCTATA	ACTTCATGCT	TATAAGTGGA	AGCACTCGAA	240
	ATAACATGTG	ATAAAGGTGG	AGAGTTGGCC	AATGTGTTCA	AAGCTTCTAA	TTCTGAAACG	300
	GAAATTAGTG	CATACCCAGC	AGCTGCAGCT	TTATTCTTCA	AATGATCGAG	AGAAGGTGAT	360
	TCGGCTACTG	TTCTCAAATC	CAGAAGAACG	TTTGAATCAA	GGATTTCCTA	GTTTCTTTCA	420
	GATGCATGTT	TCTTGAGGAA	GCCTTCATCT	GGGCTCTCCG	TATATCTGCT	TCAACTCATC	480
	CATAGTAATC	AGCAGAAATG	ACAATCCATA	TATGGTTCTT	GGCTTTCTGT	TGTAGTTAGT	540
	CGATGGCTGG	ATTTTCCCAT	GGTAGAAAGA	AGAATATCGT	GCTCTTTCTT	TTCAAACAAC	600
	AAATATCATA	TGCCCTTGGC	TTTCTCCTGC	CAAAAATCCA	AAATTAGANA	TTTCTNATCC	660
	CCTTTAATAN	TTCCACATGT	TCCCAATTCC	TCCCATNANA	TNACTGTCTA	ACTGTTTGTG	720
	GCNNACCCAA	AAANATTCTT	TCCTNTCCCT	TTTCCCCANA	TGCTCCTTTN	CCAGTC	



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1331UP

	GATCGTGCGC	CTGCTCCACG	AGCGGCTGCC	CAAGGCCACG	CGCTCGGACG	TGGCCTGCAT	60
	CAAGAGCTAC	GTCTACGGCG	ACGGGCTGGA	CGAAACCCCC	TGGTGCGCCT	CCCATGCACG	120
5	CCCCCGGAC	TGCCCCGCGC	AGTCGCAGGA	ACGCCAGGGC	ACGTGCGGGC	CGGGCGACGA	180
	CGAGCTGCGC	ATCTTCACGC	TCTCGCAGCT	GCTGGAGGAC	CAGTCCGCGT	CCGAAGATGT	240
	CATCCCCGAT	AGCATGGATG	CGGGCGACGC	GGTCAGCCTG	GGCTCCCCGC	AGCCCCAGGC	300
	AGGCCTCTCG	CAGCACAGCT	TCTGCCCAGA	TTCCACGCAC	GCGTCGCCCC	TTGGCGCCCG	360
	CCGGTTAACC	CCCTTGACGC	GCGCGCCCGC	CTCCCCACTC	CCCGTCCGCG	TGTACACCGC	420
	GCCCGCCTCC	CCGCTTGACT	ACATTTCCCGA	CAGCAAGGGA	TGAACCCCTA	CGTCCTCCAG	480
	GGCCCCAGCC	AGGCCCCGAG	CCCGCCCTCC	CTGNTTGAAG	GTNNGAANGC	CACCTTNCCA	540
10	AAANTTTAGG	GGTNGNGGCC	CNNGGCCGCT	CAACCGNTTG	GCGTCCGNAA	AANCCNNTGG	600
	CGGCGTNNCC	CCNNCTTTAA	GGCGGCNTCG	AACNCNGCNT	NTTTCGGGNA	GGGTTTCCAN	660
	ACNCAACNG	TNNNNCCCCC	CCTTTTTTCT	TCNAANAAAG	GCCTNTTTGT	GTCNNITCCG	720
	CCNGGNNNGN	AATTTTNTTT	TGTGGGGCTG	NNCCCTNAGA	AAACNCCCNC	NGGGNCNNNG	780
	GGGAAAAAAA	AANTTTTTTT	CCNTNGGT				

1332RP

	GATCTTTTAT	GTTCCTTTAG	AGCAAGGTCA	ATTTTCACAC	CACTTCTATC	ATCTTATATC	60
	CAGAATAATT	TGAACAAGAA	GGTACCGTCT	AGTGAACGAC	GTGATTTTCAT	GCCGGCGTCC	120
20	AAGGTTTCATG	AGTCATTACT	GAAAAATGAAG	CAGCACTATA	TCGAAAATAG	GTTGCTCGAA	180
	CTACAAAAAC	TTTCATCAGTT	ATTCGTGATA	GATAACGTGA	ATTTTTCCAA	AAAAATGATA	240
	AATGTGGAAG	AAAGAAGAAAT	CGTAAATCTT	CTAAATGACC	TAGATGATGA	TGCTAACTTT	300
	ACTTTTGAGA	CTGTCCATAC	TAATTTTGTG	AATAATGAAC	TATTCATGGA	ACTACATGAT	360
	CACAAGTCAG	TGATATCGCG	CGTTTGGACA	TTAGATACTG	CGGAGGATTG	CAATCGCATG	420
	AAGAAAAGGT	TACGACCATA	TACACTCAGC	TCCTCGACTA	TTTCAGGCTC	AAGTTGTCCA	480
25	ATATTGATGT	AGATCCAACC	GCCACTATGA	ATTTNAGTTC	CGAAACTCCN	TTGANCACTG	540
	TTACCTCCCT	ATTGTGTTTG	TTACNCCAAT	TGATCCCTCC	ANTTTCGGAT	TCGTGGAAT	600
	GGNGGAAAAC	CNNCGAAANT	GCNGAAAAAC	CTAAAAANAAG	GAANACCGTT	AACNGGGTTN	660
	GGAATGTCTA	TTGGGGGGGG	GCCNNANCTT	TTAAAGNNNC	TTTCNNGGGG	AANANNCCNN	720
	NCTCCCNINA	AANTTTTTTC	CCCNGGGNAA	AAANTTNTCT	GG		

1332UP

	GATCTTTTTT	AGACGCAGTG	TACTATCGAT	GAAGCATATG	ATTATTATAC	AAAACTTCTG	60
	TCCGATACTA	TTGCATTAAA	CCCGCTTAAT	AGAAACGAAT	TTTTGGAAAG	TTGCGACACA	120
	TTAGAGATGT	ATGGAGTCGC	TTCTATTGAA	AATGGCAAGC	ATGGCAAAAA	GGCCAAACAA	180
35	TTGGTAAAA	TGATCAAGAG	TACAGTTGAT	GAAAAGGAGT	TCCATGATGA	AATATGTNAG	240
	ATGGACTTGC	TTAAGAAATT	GATAATATA	AAGGCTACGA	GCTTCAATAT	TATAATACGC	300
	ATTGCATAAT	TTATTACATT	AAATTGATAT	AGGTATATTT	TTCTTCGAAG	AATTAATTCT	360
	AATCATTTTC	ATGTGAAGAT	ATCGCCCTCT	GTGTTACCTG	CGGATATTTT	GACTCTTAGT	420
	ATATCTACAT	ATTTTGCGCA	GCCATTATTT	AAACTCGCCA	GCTTGACTCT	GGACCCAAGA	480
	GCCGTAATGG	CAGCAGCTCT	TCCTGAGCGC	AATTTCTTCC	AGCAATTGAG	GCACCATGTG	540
40	CCGTCTTTTA	ATTCCAGCAC	ATATAACAGA	CCGTCCCGTC	CAATAACCCCT	AACACAATTA	600
	TTCCCTTTCT	TTCCCATCAT	GTTTCCGATA	CTGGACATTG	CCTGAAATGC	AANTTTAACA	660
	AGCCTTATAC	CAGTGAAATC	NTGCGTTTGT	AAANATGCCN	TGCCAATTTT	AACCCGTGAG	720
	GTGCGTAACC	TGAACTTTTT	TTGAAATTTT	AACCCCCCA	ATNANNTTTC	NTTTTTGNAA	780
	CCCCATGCCT	TGTTTCNCT					

## 1334RP

5	GATCATAATC	CAGTCGCTGT	CGAGATACTC	GACAGGAATG	GACGTCAGCG	ATTTTCGTCTGA	60
	AGAGCGCCGG	AAAACCTTGT	CCGTTGGCTC	CGGCGTTGCG	GTGAGCGTCC	CGGGCGGCGT	120
	GCCACCGCTC	GACTGCAGCC	GCGCACGCTT	CCGCATTATC	TGGTTCATGG	AGAAATAGCGA	180
	CGATACTGGA	CGCTTCATGA	TGCACTTTAA	GGCCACAACC	TCGGCCGTAT	CATGCTGGCC	240
	CCGCCGGCAC	CCGGCCACCC	GTGCCCCCG	CAGGACAGTC	CCGAAACGGC	CTCGTCCCTAA	300
	CCGACCCCTC	AGCATATACT	GGTTCACCTG	CACGCTTTCC	CGGCCCCCTA	TCAGCCGTGT	360
	CGTCTTTTGC	AGCAGAACCA	TCTCCACCAG	CTTGTATATC	TCCTCAAATA	ACGCTGCGTA	420
10	TGTTACTGCG	TCCCCGCGC	AACCGCTCCT	CCCCAACACC	GTGTCCGTCA	AACGAGAGCT	480
	GCTACGGCTG	GAGATGCTGC	GCAGCAAGAG	AGAGTGCTCT	CCTTCATTGA	ATTGCACGAT	540
	AGTAGGGTAC	GAAGTCATGC	NCCCTATGCC	CTACACCATG	NANCTGGTTT	CTATTGTTNN	600
	TCNNGGCCCC	NATNNTGTT	CCAACNTNTN	TTANCTGGGC	CACNTTTTTT	TNTGGTTGCC	660
	CCCCGAACCT	CCTTCCCTTA	ACCAATCCTG	GCCCNCTTTC	NCAACAGGAA	ACCTTNTGAA	720
	CACTTTCCCC	NAAANGTNGC	GAANAAAAAN	TTTTTTTNTAT	TNCCCT		

## 1334UP

20	GATCTGCGC	GGCTCCGGCG	AGCCGGACAG	CGCCGCCGTG	GCCATTCTGG	AAAGCGCGTC	60
	CGCCGGCGGG	CCGCCGGTGC	GCGGCCTAGT	CCGGGCTGTA	CAAGTCGCCC	CGAACAAAAAC	120
	GC'TTTTCGAC	ATCACTCTCA	ACGGGCTGCC	CGGGCCTGCG	CAGTACTACG	CCTCGATCCG	180
	CGCGTCTGGT	GATGTGTCCC	GCGGCGCGGC	GTCCACCGGG	CCCGCGTGGC	ACGTGTTTGA	240
	AGACGCCGTC	GCGTGCGAGC	GCGCCAGCCC	GCTCGGCGCT	GACCTCTGCG	CGGGCTCCCG	300
	CCTGTTCGTC	GCGCCGCTCG	CCGTGCAGGC	GCTGATCGGC	CGCGGCTTCC	TCGTGGGCGC	360
	CGACCGCGGC	CACGCGCTCG	CCGGCGCCGC	CGCCGTGCGC	GTGCTGGCGC	GTAGCGCCGG	420
	CGCGTGGCAG	AACGACAAGG	TGCTCTGCGC	GTGCTCCGGC	GACACGCTGT	GGCAGGAGCG	480
25	CGGCTCCGCG	CGCTCCGCGA	ACATCGCATG	AACGTGTATC	TACATACCTG	CTACGTTGTG	540
	CTCGCGCCCC	CCGCCAAGCG	CTNCCCTCCAN	CCGGGGGGGC	CCGCGGGGCC	TTCCAACTCA	600
	CCGCCGGGGG	GCCCGCGCTG	GCCCCGAAAA	CCCC'TPCCGC	AACGNCCAAN	AANNCCANN	660
	CCNTACNACN	CCCANPTANC	CAACACNTTC	NTCAACGGGT	TNNTNGCCCC	CCCCCGNCNC	720
	TTCTCCGGNG	TTTTTTTTTT	CCGGANNATT	NCTGNTCCCN	CCGTNTCCCN	CCTTATTTTG	780
	NNNGCCCCCC	CCCCC					

## 1335RP

35	GAGGCAACGG	AGGTGGCGGT	GGTATCAAAG	GTCTGGTAGT	CGCTATGTCC	TTTCCGAGCT	60
	TTTGGGGTTT	TGTGGTCTTG	CTTTTGTGTT	ACGCTAAGGT	TGGGCGCGGC	GAAATCACAT	120
	GCACTGGGCG	CGATTCCAGG	TCCGCCAAGT	TAATGGGANA	CACCGCGCCG	CTCAGCATAG	180
	TGCTGTGGGT	CCTCCTATGT	GATTGCGACC	CAAACGTATG	GTCCGCCCTT	GGGTGTGTCAT	240
	TTTCTGACGT	TGTTATTCCC	TCCGGGCCAC	TAAAACTGCG	CCTACTCTGA	TTCTCTGTCA	300
	GTAACGCAGA	GTAAGACACA	CGCTTGCTTC	GTGTGAGCGA	TAGTGTGCGA	CATAAATTAC	360
	TATGCGGGGA	NCCNTNCCAA	NTTTAACCTN	TGNNAANAAA	ANACCCAAAC	TNTTTCAAAA	420
	CCCAAANTTC	NATTTNNGGN	NCNGAAAAATN	CCGNTTGGGN	AACCCCCCGT	NNNGGGGTTT	480
40	AAATGGGGTT	TCCAAAAAAA	ACCCNCCANT	TTTCCCCCCC	CCCCCNAAAT	TNTTAAAAAN	540
	NCCTTTAAA	AANNTNNTTT	NTGTGGNGNC	CCCCCCCCC	CCCNAAAAAA	AATCCCCCN	600
	AAAAAANCNG	GTNTTTTCCC	CNTNNGGGGG	AAACCCCCC	NAAAAANNCNN	ACNTNCNANN	660
	NNGGGNCNC	CNNCCCCCN	ANCNCNNTGG	TNCCCCCCTT	TNANAAAANG	GNCCCCCAAN	720
	CNTTTTTTTN	NNNNNNNNAA	AACNCCCTTT	TTCNNCCCCC	CCCCNNAAAA	AATTTTNNNN	780
	NTNNNTTTTN	G					

## 1335UP

	GATCAGATAA	GAATTGAAGC	TCAGCGGCTG	ATGAGCGCAC	TGCTTCCGAT	ACGGTGGTCC	60
	TGTACCAGGC	TGATAAAATG	TGACACTATC	ACCATAATGG	GGTTGTAGCT	GGATACGATG	120
5	TCCGGATGCG	GATGGACTGT	TCTGAACAAG	ACGTGCAACG	TGCGAGGCC	ATAGTGGGAA	180
	ATCTAATTAA	CGTATTTACA	TATCAGTGGC	GATGTGTCTA	GGTGCCGGCC	ACCTCGATTT	240
	CCTGCTACTG	GACAGCGCCG	TCATATAAAC	ATTATTTGTT	AGGGTTTAAA	GTTGCTTTGT	300
	GCGGTGGAAA	ACAACGTCAC	ACACTAACTA	AATCTAACTC	GAGCCAGCAA	GCAACTATGT	360
	TAAATAAGCC	GAACAGTTTA	CGATTCCAAG	GGCACGGTGG	AACCCCCCAA	GGCCCCGCTC	420
	CNANTCNTTC	CCTTACAAAA	AGGGAGGGGG	GCCCTACCAC	TACCGAAACC	ATACNGGTTN	480
10	NAAACAACCC	NAANCCCGTT	TTTCCCCCCC	CCAAAATTAA	ANANTGGGCG	CCCCCTGNNC	540
	NCNATTTGTT	NNNTNANGG	GGANAGGACC	CCCCCCCCGG	GNNNGGNTCC	CCCCNNTCNA	600
	AAACCANNAC	CCCCACCCCN	ANAAAAANGG	GGGGGGGGGN	GGAACNCCCC	GATTTTCTAAA	660
	AAATTTAAAA	ATTNNNNGAA	ACCGNAAAC	GGNGTGNNCN	TNCCNNNNNG	AAAAANGTTT	720
	TTGTNGNNNA	CANCCCCCAA	CNNTTNTNAG	NNNCCCGNNC	CCCCAAACNN	AAAANTTTNC	780
	TNGNANGGGG	AACCANTCCC	CCCCCNT				

## 1336RP

	GATCATGTTT	AACCCAGATA	CGAAAACTGA	GAAGCTAGAG	TGGATAGAAA	AGCTGCGAAA	60
	AGTAATAGAG	CTGAACAGGT	TTCAACCAACC	ATGGGTTTAA	AAGTTCTTGA	ATAGCAGTGA	120
20	GAATATTCTC	TGAAGAAAAG	CATGACCACA	GGATTACATA	GAGTAACTTT	TGTGCAAAGT	180
	TTATCTGTAT	GTACAATTTT	ACGTTATAAA	TTTTTAAAGT	ACTCGGGCAA	AATCGGCACT	240
	TGGTAGCGAT	AACGCACACT	CGAGTGAAGT	CCATCCAGTA	CATAAACATT	ATGTCAACTA	300
	CTTACCATTA	TTGCCATTGC	CAGATGAAGT	ACCCATGTTT	TGGTGATTGC	CTGACCCATT	360
	GTTACCACTT	GCAGCGCCCA	GGTTTGGGGG	AATCATGCCA	GGAAAGGGAA	AGGGCGGGAA	420
	ACCCCGAACA	TGGGTGGCAT	ACCCATGGGA	AACGCCAGGC	GGCTGCGGCA	GAGAACCGTT	480
	GTTTTTGTTC	CGCCAAATTG	AAGTTCTTTG	GT'TTNCNNN	CCCCCGGCA	AAAANCTTAA	540
25	CCCCGTCCCC	CNGCCCCCN	TCCCCAANC	TTTCCCNNTG	NNGTTGGAGC	CCCCAAACCC	600
	CCCCATATNT	TNNCTGCGCC	GGGGTTTNTN	CCCCCNGGGA	GACCCCCCCC	CGCNTTGTGN	660
	NTNTTACCCC	CACCCNCCCC	CCCCCGGAA	ANCCNGTNTT	AAAAAATNCN	AANAANNTNT	720
	GGCCCCCGNG	CTCCCCGGGG	CTCCCNATA	CCCCCGGNN	GTAAATMNC	NAAGNGGNCC	780
	CN						

## 1336UP

	ATCGCCATTT	TAGGGATGAT	CCCATCACC	ACAGCTCCGA	GGCCCTTGTA	GAAAGCCAGC	60
	AAGCCCTCCC	CGCTGTAGAT	GTTGGCCCCC	GTGCGCAAAA	ACCCAGGGGG	CTTCGTGCC	120
35	TCGTTTCGCG	GCCTGTAGAT	CTGCATGCGC	ACCTTGATCG	TGTCCAATGG	GTGGCAGCAG	180
	AGCGCCTCAA	ACAGGCCCGC	GGTCCC GCCC	GCAACTAGGT	TCACGGCCGG	GTTGGTAGAT	240
	TTCTTAGACG	ACATGTGGTT	ATCAGGGTAT	GGCTGCTGGC	ACACTGCGCT	GCACGGATCC	300
	GCTACGCTTC	TGCGTCGCGC	ACCTATATAT	ACAACGGGCA	CCGACGGCGG	GCCGCCCGCA	360
	CCTTGCTCTC	GACGCAGCGC	CAATAGGAGC	TCGCGCATAC	CCCCGGGCGA	ACGCGGTGAG	420
	TCAACCCGGC	CCGAAGCGCG	GGCCAATGGA	ACCGTCACGT	GAAAAGCAAA	GACTTAAAGT	480
40	ACTATGTAGC	TACACACTTA	GGCCTCGGCC	ATCTCGCGCA	GTCTGCGGAT	CGTGGAGCGC	540
	ACGTGCGGCG	GGCAGCCGTG	GAGACGTGTT	ACGCACCACC	GGCCACAGTC	NTCCTTTGCA	600
	CNAACTTGCA	NTTCCCAAAN	NCCCGNAGCG	CCGCGCTTCN	CCGCCTTCTT	TGCCGCAAAA	660
	AGAACATCCT	TACCAACTTC	TTGTTGCCCT	NCCACTTCTT	NAACCTGTTT	CCNNCACGAA	720
	NAANCCTACC	CCCCCCNTT	TTNCCGNAA	TCCNACCTTN	TNCNTNCTTT	TACCATTNTT	780
	NTTNAAGGG	TGN					

## 1337RP

	GATCTTAATT	TAAAAATTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAAATAAAT	TAGTAAAAATA	120
50	AATAGAAAAC	CATAAGTTAA	TTGATTCTAT	AAGAAAAATG	GAATTTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420

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	TTTCATAATA	TTTATTTTAA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TCCCTTTAAT	480
	TGGATATTAC	TACCTACTAA	ATATTTACCT	AATAATATAT	TATTAAGAAT	ACTTAAATCT	540
	AATAATTTAT	TATCTAAAGG	TATATAAATT	AATTAAATCC	TTTTTTATTA	TTATTTAAAT	600
	TATTATTAAT	AGTAAATTAT	ATTATTTATT	TTATTCACCA	TAATTTTTTTT	GATNATAATA	660
5	TATCCTTTNN	TAAATGGGGA	ATTTATNAAT	AATTANCTTC	NANGAATTTT	AATGAANAAC	720
	CCCCNTTANN	ATAAAATTAG	TTAANNNTGN	NCTCAAAANN	CCNATCA		

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## 1337UP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
5	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACCTAAT	AAAAATAATT	420
10	AATTAAATAA	ATAAATAATT	AATTAAATTT	AAAATGTTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACATCACCA	540
	TGACCAATGT	TACATCATTT	AGTTTAATAG	GGTTTACTAA	TAACCTTTAN	CCTTTTACCA	600
	AANNANNGGT	ANTANTNGGA	AAAATTATNC	CCTTAATAAT	AACCTTNATN	AANNNTATNT	660
	ATATACCAA	ANNNTNTGAN	ATTTNAAAAA	ATATNGGCCG	AANCNNCNTA	TTTTGNGTAN	720
	CCCCNCNTA	CNCCNGAAAA	AANGNTTACC	CGTGTTCCCC	CNTATNNTGN	NTNCCCNAAA	780
15	ATAAAAAATG	NGCCCCCAC					

## 1338RP

	GATCAACCGC	AACCCGTCAC	TCANGTCCAG	ACCGTTATAG	AGACGGTCGT	CGATGGCACT	60
20	ACAAGGCCGG	CAAAATGCTTT	GCTTATGAAT	AGCACGGTTG	AGGTGATAAC	CGTTAAGGAA	120
	ATAGTGAAGG	AGACAGTTTT	CGTGACTGAG	AAGGTGACTA	ACTAACTCCA	ATGCAAGCAG	180
	AACGCTTTCT	GTCTTTTTGT	CCAAACCTAC	CTGAACACCT	AAACTTAGTT	ATTACAACAT	240
	GAGTTTTATT	TACACAGTAG	GGTGCCACAG	CCACAGGAAA	TATCCAAAGA	AATTAGCTTT	300
	GCCTTGATA	AAGATATTCA	TCCCTATTCA	GCGACCCCTC	TAATACGCAT	TCTCTAGAAA	360
	GTTCCTTGGC	TTTCATTTTA	AATCCTCGTG	CACCTCGTCC	GTAACAGTGT	CTATAGTATC	420
25	ATTCCGTATC	ATTTCTGAAT	GAAGTAGATT	CCATATCAAC	ACTTGCTTTG	GTGGAAAGCT	480
	CATTATTCTG	AGCAGTAATG	GCTTCACCTC	TATCCTGTTC	CAACATACTT	TTTTTAGCTG	540
	CCCGGATTAA	CCTCCCTGAA	TTCCCTTACG	ATGCAGTCGA	GACCCATGCC	GATTTATCAA	600
	ATTTATCTGT	CCTTTAAANA	ATTTTAAACC	TTTGACNCCC	CTATTATTAT	TTTTTAGCNT	660
	ATCGTAATGC	TGCCNGANCC	CCCNAAANGAN	ATGGGGTTTT	CCNTATTANC	CCTTGGTTCC	720
30	CCAANTTAAA	ACCCNCCCCG	GNCCCCCCCC	CCCCCACCN	GGTGGGANAA	T	

## 1338UP

	GATCAGGTTT	TCCGGTACGT	GAGAACGTAT	CTAAGGCACA	AAGGGCTTTG	GGCGACTGTG	60
35	CGGACGCTTG	AGTTGCNAGA	TACAGGACAA	AGCTGTTACG	GCGGCAACTG	GTGCANCACG	120
	AGCAGCCGAG	GAGCGATTCT	GCGCGAAGCG	ACGGTGAATT	CGAGCCAGCT	GGTAGCAGGA	180
	GTGCCGGATC	GTCTATTTAG	TTGCGACGGG	CGTCGGAACA	GGATGCACGT	AAACGTTGCG	240
	GTAACACGCG	ACGCTGACGC	GACGGCTGCT	ACGCCGATAG	CACGGGAGCG	CAAACGACGG	300
	CAGCCGCTGT	CGCCAGAGAT	GTCTTACACA	CTGCGCGGTA	GCAAGCTGCA	GCGGCGGAAG	360
	CAGACACTGT	AGGCCGGTCC	GGGTGCGGCC	AGTGGGACAC	ACACGGTGGA	CGAGCTGGCC	420
	GCGCAGCTGG	AGCGCGGCTG	CGAGCAGGCG	TCGGAGCGGA	AGCCGCCGTA	CTCGTATGCG	480
40	GTGCTGATCG	GCGTTGCGAT	CCTACAGTCG	CAGGAGGGCA	GCTGACGCTG	TTCGCNAAAA	540
	TACCGNTGNA	TTTCNCNCNT	CTCCCCTTAN	TAACCGGTGT	TTTAAACCCG	GGGTTGGAAA	600
	ANANCTTCCG	GACNACNTNT	TNCTTAAACA	ANGGTNTTGT	TTTAAAGGGN	GGNNNCCCCC	660
	TCAAAGGANG	GGCCTTTTGG	AAAATTAAGG	GGGCCNTTNA	NGGGGGCCTC	NCTTNNCCAA	720
	AAAGGGGGAA	TNATTTTNNG	GGCCCANATT	TNNCAAAAAT	TNTNCANTAG	GGGGNCTNNG	780
45	NNAANTTTNT	TCNCTT					

## 1339RP

	GATCATCGCC	TTTAGGCCCA	TGTCAACCTT	GCCCGCACCG	ATCAACTCCG	TCACGTCCGA	60
50	CGGGTTCGTG	GGCTCGAGCA	GCGCAATGTC	CACACCCTCC	TGCTGAAAGT	AGCCCTTGGA	120
	CTGGGCTAGA	AAAATCGCAA	TGTGGTATGG	CGCAGGCTGC	CAATTCAATA	GGAATGAAAC	180
	TTTGCTAGAC	ATCTTCGGTG	CAGTCTCCGC	AGCTACACCC	CATTGCATCC	AGGCTCATCA	240
	GCCGCTTTAT	ATACCGCTGG	GCCAAAGATG	ATTGAATACG	GTTCCGAGAC	GGCTACTGGA	300
	ATACCCGTCG	CGCCACAAGC	CCGCCACTGG	ATGCCATGCG	CCAATGCGGA	AGCCTCCTAT	360
	GTGACATGTA	CTAACAGAGC	AGCTTCCTTA	TGCACTTATC	GAGCCAAAAC	CAACATCTGC	420
55	GGAATCACAC	TTGACGGAAT	CCGGCCCCAT	GCGCAGCTGC	TGGAAACACA	AATCCAGCAA	480

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	CTAATAGGGC	TCAGTGGTAT	AACGGCCCAT	CGCTCTCTCA	ACGCCAAGTC	CCTCTCTGGG	540
	GAAAACATGT	GATCACGTGC	TACATATTCA	ACCCCCGTCT	TACCTCATAG	CTGCGCATGT	600
	CCAGCCCTGA	ACTGTTCCGA	CCTTCCGTCT	TCCNGAAANC	CTGATTGCCT	TGCTTTAATT	660
5	CCCCCTCTCC	NCCAACCATG	TNTCGCCCAT	TTACTTCCGT	TGCTTTTTTA	TTTCGTGCAT	720
	TGTTTTTNTA	AAAGNNCCTG	TTAANTAAAT	NCCNTCATTN	TGGA		

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## 1339UP

	GATCAGCGCA	TTTGTGCGATA	GTGGCTTTGA	TTCGAAAAAT	CCGATCATTA	CCATGCTGAC	60
	TATACGTCTA	CTGACCAACG	CCTTTGCAAA	CAAAGACTGG	GGCGTTAACC	TAATGTGCTC	120
5	TGCGCCAATG	TATAACTCGA	TATTTGGGTT	GATTGATGCA	GACCACCCAA	CTTGTCCTCC	180
	TAAGCAACAG	TCATCACTGG	CCGTAGCAAT	AGCTACCCTA	ATATACAAC	ACTCAGTGTT	240
	GGTAGTAAAA	GAGAACAACC	ATGACATCCT	AGCAATTGTT	GCAGAGGTT	TAAACAACAA	300
	ATACGGCTCC	TCTTCCTTTA	TCCTGCGGAA	CGAGGAGGCC	GCATACAGAC	TCCTTGTTGC	360
	TTACGGAAAC	TTAAGTACTG	TGGAAGGCAC	CCTCGCACAG	TTTGCTCCTT	CTATCTCATG	420
	GATAAGGAAG	CTGAAGAGCC	AGTATGGCCA	CATATCGAAA	TTCCAGGATA	TTTTAAATGA	480
10	TATTTAAAGA	AAGGTGTACG	TATATATCCT	ATTCTTTTCA	TCGCTGTCCC	GAGGCCTTCC	540
	CGGAAAAATG	GTGAAAACCT	CGCTCTTTGA	CACACAGCCT	TTGCCCTTCA	ACAGGATAGT	600
	TTGAAGGGAC	ATGTTCTGTT	GACAANNCTT	GAACCAGGGT	ACTGGTGNAA	AATTTNAANA	660
	TCTTTTCTCC	NCCGAAANCN	ANTTCTNCGG	AANTTAACGG	GAAAAAANC	CCCCTCNNNC	720
	CTTTNTTTAN	TAACCCCCC	CAGGNTTNTG	ACCTTGATTT	TTACAAAACC	TTTTTNTT	

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## 1340RP

	GATCGCCTGA	TATCGACAGG	CACTTTTGTA	TATTAGCAGT	ATTCTTGACG	AGATAATGCA	60
	GTCAACTCCT	ATATAGAAAC	CGGATACAGT	GGTAAAAACG	CAAATGTAGG	CAATTATATA	120
20	TTACTCTTCT	CGACACCACT	AACCTCTCGA	TAGCGGCATA	TCCTGTAAAT	TTGCATACAC	180
	CTTTTCCCAA	CTTTCAGTGG	TCTCGTTGGC	GTACTTTTACA	TGCATCTTGG	CCCATTCCCTG	240
	GAAGACATGT	GTGATACAAA	ATTGAGTCTC	CTGGAAAAAT	ACAAATTCCT	CTAAAAATGCA	300
	CTTTCATATT	AGCCAGGACC	TGTTTAGTTG	CTCAGCAATT	GTCCGTTTGT	CCCCTTGAAT	360
	TGCTGTCTGT	AGTTTATCAT	ATTCTGCACC	TTTAAACGTC	GGATTACTCT	CCATAGATTG	420
	AAGTTTGTCC	ATATTTATTT	CCACTCTCCT	CTGCAAATGT	GCTATGTTAT	TCCCCGCCAT	480
25	AATTTTATAC	CTATCAAAGA	CCCCTTCAGT	GCTATAATAA	TATCTATGAA	GGTCTTAAAC	540
	TTACCCGATA	GGTGTTCCTC	CACTTCCTGA	CGCTCCTTTC	TTAGAGGTAT	CGGCCACGCT	600
	ATTGAGATGT	TTTTGATATN	NTGGAATAT	GANATTTAAA	TATCNTGAAT	AGTGCCTCTT	660
	CCTATTGGGT	ANAANTGTN	CNGAATTATC	AANCAATTCC	TCCATCACNC	NGCCAAGCAC	720
	CCNCCGTCTC	TCNAANACCT	GCNCNTNGCC	CCGTNCGGTT	NNNNNA		

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## 1340UP

	GATCTGCTGT	ACCTGAATGG	ACTTTGTCTC	CTGAAGTAGA	AATGTAATGG	CCCCTTCGGG	60
	AATACATAAC	AAACATAGCG	GAGACAAAAA	CAAAAGCGTT	ATACACGCAT	CTGCCGTTAC	120
	ATCACCGTCA	GCTCCTTGCA	GACCAATAAG	CCTTCAAGTT	AAATATAGGC	TAGCTATAAC	180
35	ATATTATGTC	GCTAAGAAGG	GCCAAATCGT	TGCCATCGCT	TAAGAATATC	GCTGAGGTGG	240
	CCAAGCCCCAT	CACCAAGGCC	CCCCCGCTCC	CCCTGCTTGC	GTTTGAGGGC	CCTGGGCTGT	300
	CCACATGTCG	CTGGTATCCC	ACCACCGTGC	GCACAGTGCA	CAATACCCCC	AGTAAGGCGC	360
	AGACGACGCT	GCTCTCGACA	GCGAAGAAGG	AGAGTGCCTT	TTCCGCAATG	AACCTGAAGG	420
	CCTTGCGGAA	CGAGTGCCGC	TCCCGAGGCT	CAGGGTCTCC	GGGCGGAAGT	CGGATTTGAT	480
	CGAGCGCATT	GTCGACTTCG	AGCTGAAGGG	ACCGCTGGGC	AGGCGCGGGA	CACGGCGGGC	540
40	GTTCCACAGC	CCGGGCACGA	GCAGCGCCAG	CGTATGCCGC	CCGTGGACAA	GGTCACCATG	600
	CCCGACATCG	CGCTTGACAG	AACGAACCCC	GTGCCACACC	CTGAGAAAAA	CTACATACTC	660
	CGGANTCCNT	CNTTGTNCCN	CCAAGGGGGT	TTCCCTCCCC	GTTACCNATT	CCNAAAAGAT	720
	TTTTGCCNCG	GAACCCANGA	AGAAACCACC	CGAACTCCCA	GAAGGGGGNT	TTNNNANCCG	780
	AACCGAANCT						

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## 1341RP

	GATCACATCC	GATGCGAAAC	TCGTATATTG	TTTTCCCA	ATGATGAAGG	TGAGTGTGGG	60
	GCAGCAATTG	TCCGGTTGAC	GACTCCTATA	GGCCCGGGCA	TGCCACAGTG	ACCAGAAATT	120
	TGCAATGTGA	TTCATGATGC	AAATGGAAAC	CCCATCCAAG	TTCACAGTC	GCAAAAGAAC	180
50	AGTTGGATCC	TGACAAGGTT	CTTCTGTTAG	GCAGCTCTAT	AGACACTCCG	GTTGCTGTTG	240
	CTGCGGATGC	AACGAAAGTG	TCCGCCCCATG	CTTTACTCCA	GGCCCTTTTT	ACCTCTAACG	300
	AAAGTGAAGT	AACCTCTGGA	TGTATTACCT	TTTCAAGT	CAGAAACCTG	ACCAGTTTCG	360
	ACTAGTTTTT	TATTGAAGTC	CGTGCTGTCT	CAGTATTTGA	AGCAGTTAGT	CCCACGAATG	420
	AGAACTTAA	AGAATAATAG	AATGGGGAAG	ACTCAAAAT	TACGGCTACC	ATAAGACTCA	480
	CAGACTTACT	CGACTCGAAC	GTTTTCGTCC	GCACCTTGTG	CTGCGAGTCA	TATACAGAGC	540

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CCTGTATCGC	GTAAACACC	GGATGCGCTA	CAGCAAGGTA	CTCGCCTACA	AGACAACACC	600
CTACGTACGC	CGTTTCACAG	TATGCAAATA	ATNGAAGGCA	TTTCCTCCNG	ACTTTTTCAGC	660
NAAAGGNITT	ATNCGAACTG	ANCCCTGTCC	ATACTTTATT	CCCCCNANCC	CNGTTTTCNA	720
AAAANCAGNG	AACCATACNA	TGCGTTTAAT	AATGAACNTT	CACNT		

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## 1341UP

	GATCAGAGTA	GATTTAGTAA	AGAGGTAACC	ACCACTGTTC	CAAGAAGTCC	AGGGCCTTGG	60
	CTTGACCAGC	ATTGGTAAGT	GCTGTGGCTG	GAAATTTGCA	CTTAAACGGT	CTGAGCTCAT	120
5	CTGGTTTCGCC	AAAGACCTAT	GAAGTTTCAA	AACACCAACT	TTGCTGCCCA	TTCTATATTG	180
	AAATGTATGA	CAGATGGCAG	GTGCCTTACC	GTACACTGTT	TTATTGGTAA	CTGGGTCTAC	240
	ACCTTTTCACG	TTCACCTTTG	CCACATGGAT	CAACATAGAA	ATTAAAAGAG	AGCCAACCTT	300
	AGCCTTGATA	TTGTGCGGCC	AAAGAACTTT	AGACTCCTCA	ATTTGTGTAT	TTCTAAACGT	360
	GGTTTTTGCC	CTTTGGACCA	GCTTCTTGAA	TTGCTTACTA	TTGGCCCTAA	CTTCTTTAAA	420
	AATCGATTTT	TCACTCTTCA	ATAGTGCTTC	CGATCTGTAT	TCCATCTCGA	CAGCCTTACC	480
10	TATAGCCAGA	ACCGCTCCTG	GTTGTTCTCA	TACCTTCACT	GACGCCCTCA	GTTAGAAATC	540
	CAAGCCTTTA	CCNATTCCCC	AAATTGTTTA	TGAANACACA	TTTCNCCTNG	ANTNACCCCA	600
	AAATTGAAAT	ANGGGGNCTT	TTCCANNCCN	TGAAANAAAA	TGTNGAACGG	NGTTTCAGTT	660
	AAGCCCATNT	ATCACTNNGN	ANCATTNNNN	AAAAANGCTT	CCCCCTCCC	TTTTTAAAC	720
	GGGATCTTNC	CAAAAAACCN	CCCCCTNAAT	GAACCATTTT	NCGAAANCCG	GAAGCCCNNG	780
	CCCTCNCCGN	CTANATTCCN	GCAANNCATN				

## 1342RP

	GATCCTGATT	TTGATTTCGC	CATTGCTGAT	GTTAATGCAC	TCAGTGCTGA	TGTCCTATAT	60
	ATCCAGCATG	AATTATCCTG	GTGGATATGC	GCTATCTGCA	TTCAACAAAT	ATGTGCTGGA	120
20	CAATAATATC	TCGAATGCGA	CCGTCCACCT	AGATGTCTTC	ACTTGTATGA	CGGGTGCAAC	180
	GCTGTTTGGA	CAGCTGCCGG	ACTCCTACGG	GATCATATAT	GACAAGACTG	AAGGTGATGA	240
	ATTATTGGAC	GCATGGTCAT	CGTTTCGATTA	TGTCATTACA	ACTGATCCCA	ACAGCTCACT	300
	GCCTCCTGTT	ACAGGCTACA	AATGGGAGCG	CATCCAAACT	ACTGAGGCCT	TTGACCGCTT	360
	CGACCTTAAA	ACTATACCGG	AAATAATCAA	CTCAGAAGTT	GCTAAGGGAT	TCCCTATCTT	420
25	AAAAGATGCA	ATACTCTCTG	CAGACCTGCA	ACCTGTGAAG	GCTGCGTTCA	CAGATGTGAT	480
	CAGGTGCAGG	GATTTCAGTG	ATACATATAA	AAGAGTTGAG	AATTAATAGA	ACCAGCGCTC	540
	CGCTTACGGA	CAGTTTCCAT	ATAAATATTT	ATTTATTAAA	CTTAAAAGTT	CTGCGAGTTG	600
	AGGAGGAATT	TGACTGCTGG	AGATTCCGAC	ATACTGAAAA	CATAAAGTGC	ACATTTACAG	660
	GATTTCGGCAG	TTACTTGATT	CCCCNTCCTN	NNCCTTAAAT	GCCTGATCNA	ACTTNAACA	720
	TCCTATTGAA	CCCCCTTTGG	TGNTCCAANC	AAANTNTAA			

## 1342UP

	GATCGGGCAG	GCCGCGGAGC	AGCAGTCGCG	CGCCTTCAAG	GAGGCCGCGC	ACTTCGGCGC	60
	CATCATCCTG	ACCAAGATGG	ACGGGCACGC	CAAGGGCGGG	GGTGCCATCT	CCGCGGTGGC	120
35	CGCCACGAAA	ACACCCGTGA	TCTTCATCGG	CACAGGCGAG	CACGTACACG	ACTTCGAGAA	180
	GTTCTCGCCG	AAGTCGTTCG	TGTCGAAGCT	GCTCGGCATC	GGCGACATCG	AGTCGCTGCT	240
	GGAGCAGTTC	CAGACCGTCT	CCAACAAGGA	GGACACCAAG	GCCACCATGG	AGAACATCCA	300
	GCCAGGGCCG	TTACACGCTG	TGGACTTTCA	GAAGCAGATG	CAGACCATCA	TGAAGATGGG	360
	CCCGCTGTCC	AACCTCGCCA	GCATGATCCC	CGGCATGAGC	GGCATGATGA	GCGGCATCTC	420
	CGAGGACGAG	ACCAGCCGCA	AGATGAAGAA	GATGGTCTAC	GTGCTCGACT	CCATGTCCCG	480
40	CGAGGAGCTC	GAGTCGGACG	GCGCTCTTCA	TGCACGAGCC	CGCCCGCATG	CTGCGCGTCG	540
	CCCCGCGGNC	CGGGCACCTT	CCGTCTTTCC	GAAGTNTGAA	AATATCCTCC	NTTGCCTCAG	600
	CCANATGATT	GCCCCGCNTT	GGCCCCANGG	GCCNANAACA	TTGGCGGCTC	CCCTGGCNTG	660
	CCCGCCNGCC	CCNGGNATGT	CCCCGCCTCT	CNCCTCCAAA	NGATNTNACC	NGCCCNANCN	720
	TCNNTTNNCT	CAACCCNCCC	NTGANNNCCN	CATAATGGCT	NNNCCGNNGG	GGNCCNNGGC	780
	CCCCATGCCC	CCATTAGGCN	AT				

## 1343RP

	GATCAACCAA	TGTGTTAAGG	AAATTTTAA	CGTTTTCCGG	GGATTTGGCC	ATCTTTCCCT	60
	CTAATTGGTA	GGAAACATAG	TCTGTAGCAC	CCATGATATT	AGCAAGTTTC	CGCCGAAGCT	120
50	GAAGCAAAC	CTTAAGCCTC	TTCACTTGTT	TTTCGGAACA	ACTAAACATT	GCGGTCCATA	180
	CCTGCCTCCG	AATAGCCTCT	GAAGGACAAG	CATTCATAG	TGTATACGGA	GCATACCCAC	240
	TAGTTGGTAT	CTTATAGTTA	TTACCCATGG	TGTCCTTGGT	GAGCTGACGA	AGAACAAGAT	300
	GGCTAGTGCC	AAATCTTTGC	AAATCTTTGC	ACCGAATCTT	TATGTAGCTG	GAAGATAATG	360
	ATTCTGTGTT	GTTGATGAAG	TCTTGGCCAA	TAATGCTGAT	GTTTTGGGAT	AACTGTATAA	420
55	ACTGCTTTCT	GACTTCGGGC	GACGCATATG	CGCCTGCTTT	TTCAAAATCC	TCTAGCAATA	480

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5 TATGGCCTAC CCGTATCTCC TCGCTGCTCA GTTTACTGCT TATATTCTCG TCCGATAGCA 540  
 CTTGTTTTAA TCTTTTGCAA AGCACAACAT CTGTATTCAA GATATCATAA TCTCAAACAT 600  
 CTGTTTATGA CATTCCTTGA GCTGCGGCAA CAAATTGTTT ATCCGGATGT TGCAACCCGT 660  
 TAAACTCCNC ACAATNCAAT CCCCCGGCAT AAAATCCTGA TTTGATCTAT CNAATGATNT 720  
 NCNCCCAACC TCTTGTGACA ACCCTCNCAG TCCTTACAAC CCTACCCGTT ATGATTTTNG 780  
 NAATTCCTAC CCTCCNGCAT TTAGTTGTTT NNNATACCTT TNGNCCCCGG GGNGGACTTA 840  
 TCAN

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## 1343UP

	GATCGATTAA	AGGAAGCATC	TGCTTCCCGT	CATATCATAT	AACATTGTAC	CCGGGGCTGA	60
5	GCGGGACCAG	TAGCGAATTT	GATAGCAGTG	TTCTCCACGT	CCCCGCTCCA	CTGTGAGCTC	120
	CTTAAAGTAT	ACCGGCTTCA	TACACCAAGT	CCCACAATGA	TGCGTACTTG	ACTTGTAATC	180
	GAGAGCATTG	GGCTTATACT	GTGATTACGA	TGAATGTAGC	CAAGAGAGAA	AAGGTTTCATT	240
	CACGATATAC	AGTACTCACA	TTCATGGCAT	GCCATCCCCA	AATTCCAATA	CAGCCATTAG	300
	CACCAATGTA	GCGCTACTAA	TCCGGCGAGC	TTAATTGGCG	TCAGTTCAGA	GTGAATCTCG	360
	AGCTTAAAAG	TCAGATTGAT	TAAGTAAGAA	AATGACGATC	AACAGGGTGC	TCAAAATAGT	420
10	TGATTACCAG	ATTCCGGGCGT	GTGGtCTAgT	GGtATGAtTC	TCGCTTTGGG	TAAGCGAAgT	480
	TGCGGtTCAC	TGcGGcTTAA	CTACTAAACA	TGTGAgAGGc	CCTGGGTTCA	ATTcCCAgCT	540
	cGCCCCAAAT	TTTTtGCTCT	CGCCTCCCGC	GGGAAAGGTG	AATATCATT	TACAAGTAGT	600
	TAACCTCTCC	CACGTTACGT	CCTTCTGCAG	ACAAGTTGCA	GCGGTTTACA	ATGCTCAGGC	660
	TATTTTGCGG	CTTCAA					

## 1344RP

	GATCCTTGCG	TACTAAGAGT	TAGACTTTAA	TTAATAATAT	TATTTGTAGA	AGATAGAAAC	60
	CATACTGACT	CACGTCGTAT	TFAACCCAAC	TCACGTAACC	TTTTAATTGA	CGAACAGTCA	120
20	AACCTTACTT	AGCTGTTACA	ACCAAGAGGA	TAGGTTGAGT	CGACATCGAG	GTGGCAAACA	180
	TAACCTACAA	TAGCTACTCT	ATCGTTATAT	TACCCTGTTC	AATTTGTFTA	TCATAATAAC	240
	ATTTAATTAT	TATTTCAATA	ATTCTCATTA	TTGTTGAGAC	TATTTCATTA	TGTATTATTT	300
	ATTAATTTAT	ACATATTGGG	CTTTCGTGGA	TATAATTAT	GTTAATCCTA	CTCATATATC	360
	TAGTCGTTGA	ACGTTCTTAT	AACTTTTATA	AAAGGATTGT	TATAAGCTTC	GCTGCAGATT	420
	GTCCCTTATT	ATTATAAAAT	AATATTAGGA	GTTCCTTGCA	ATTAACCCAA	TTTACTCAAT	480
	ATATTTAAAT	ATTGATAAAT	AAATTTTACA	ATTTAATGGG	ACTATTAATT	AATCCCTAGC	540
25	GTAACCTTTA	TTCGTTTATC	AAATACCAT	ACAATATGTT	ATATTTGTTC	ATTATGCCAA	600
	ACTTACGTTA	TTGTNCTACT	TGTAGTATTA	CNATTATAGC	ACAGTTACCC	CATCATATTT	660
	ATTTAATANA	TACCCCAANT	AGNTTTTTTT	ANCATAAAAA	GGANCTAATT	TCCCTTTTTT	720
	CNCCAANTCC	NNCTCTCTCA	ATATTTNTAA	AAATTTTAAA	CNNAANTAAG	AAACCCCNMN	780
	TNAACNCAN	CTTTTTCAN	GGCTTTCNAN	CCTNTTNAAT	ANCCCN		

## 1344UP

	GATCCTTATA	AAATGGGCAA	TAGACGTGTT	ATAATATAAT	ATACAAAATT	ATAAATAAAT	60
35	ATTTAATAAA	ATATAAAAT	AATAAATTAAA	GTATTATAAT	AATTAATAAA	ATTATTATTT	120
	AATAAGTATG	GATTTTTAAC	TGAAATTTGT	TAAAATGAAA	TAAGAAATGC	TAGTAATCTA	180
	TTAATAAGAA	AGTAATGGTG	AATACCTCTAA	CTGTTTCGCA	CTAATCACTC	ATCACGCGTT	240
	GAAACATATA	ATTAAATAAA	GAATATTAAAT	TAATTTATTA	ATTATTAAAT	ATTATTAAAT	300
	TTATTTAATA	AATATAATAA	ATATTTTAAAT	TTAAATTTATG	AATTAATGCG	AAGTTGAAAT	360
	ACAGTTACTG	TAGGGGAACC	TGCAGTGGGC	TTATAAATAT	CTTTAATATT	CCATTTTTTAT	420
	ACAAATAAAT	ATATTTTFTA	ATATATTTTA	TAATAACTAT	AATTAATAAG	TTAAATTTTA	480
40	AATTATAAAT	TAATAATTTA	ATAACTTATT	AATTAGAGAG	TTAGGGTACA	TCCCCCTAA	540
	TGCTATGCAT	TATGGTTGGT	ACCACTCTAA	TTAATAAACT	ATAATAAATA	AATACTAATA	600
	TTTTATATCA	ATTAAATTAT	AATTATTTTT	TATTAATATT	TTAATATTAT	TTAATGAAAT	660
	ATATAAATAA	AGTATTATAA	TTTAATAAAT	AAATAAGAAA	TGAAGANAAC	GACTCTCANA	720
	ATTAAAATTGC	ATTNATAGTT	TACCATTAAA	CAACATTCCC	TTATTTCATAT	TATTTNATCN	780
45	ANTAATTAAT	ATCTTATTAT	TNATTAGAAG	GANAGGNTNC	CNCCCCAAT	GCTNNGCATC	840
	TTGTGGTACC	NCNNATTAAA	AAGTTTACAT	NA			

## 1345RP

	GATCCCAACG	TCTGATTATG	TGTGTGAATG	CTGTTCTCCT	GCTCCTCCTG	AGTCTCCTTA	60
50	GCCTTGCCCT	TGTACACTTT	GCCGTATGTT	CCTGCTGCAA	TATAGCCGAT	GATTTTCGTAC	120
	TTCTCCAGCA	CTGACACCCCT	ACCGGCGTCT	TTCCGCTGCC	GATATGGCCC	TATCGAGAAC	180
	ACATGTGTTAT	TCGCCATTAG	CATCGGCAGT	TTGGACGTGC	TGGCGCTGCC	TTTGGTATCG	240
	AGAAGCTGCT	GTTGCTGTTG	CTGCGACCAC	AGGCTCCGGG	TGGATGCCTG	GTTGGATACG	300
	TTGAAATACT	TATTCGTGTTG	TGTTTGATGC	TGATTATTCA	TACTATCGGA	GGACTGTAAA	360
	CGTATCCCCA	TAAAATAGAG	AGCTCGAGCT	ACCACCTGAC	GACTTGTGTT	ATTTGTAGTG	420
55	TTAAATGGAT	ATCGGCATG	TTCTAAGCTC	GTTTTTAAGT	GTAACACATT	GCAAATCCAT	480

ATGCACACAG CTCATCCGGT TCTACCGACA ACCCTCTTGC GACCGGAGCG GTGGAGCTGG 540  
 GGTGGATAGT TCCCGAGCCC CTATGTAGTA TATACAGCGT GCCACGGCTG CGCCTGCGCG 600  
 GCTGCAGGGC CTCAGCACGA NTGCCCTTC CNCCACTGCT TTATCCTCCT GAAAGCCGTA 660  
 CAACCNCCGG NNAAATACGG GGCACCCAAA GCNGCCCGAN GCCCCCCGAT AANAACNTGA 720  
 CCAGCCNTAG NGAGGCCCCG AAANAACANT GCCCTTTTTC AGCGGGCCGT CGCACAAACC 780  
 CCAAGNGNGN TCCCNNTTGG GNNTTTTAAT NGCCNNGGGG ANGCCCCNTT NCTCT

## 1345UP

GATCCGGCGT CAGCGCAAGC CAGTCTACTG GGGGACGGAG ACGCGCACAG CATTGGCGGA 60  
 GGGAGAGCTG GAATATCGCG ATGACCACAT TTCGAAGGCA GCTTACGTTT ACTTTCCGCT 120  
 AACGGAGGGC GCGAGCGCCA CGCTACGCGA GCGCCTGGGC ACGTCCCTCC CAGAACAGCC 180  
 CATCGTGTGT CTCATCTGGA CGAGTACACC GTGGACTCTG CTGTCAAACA GAGCCATCTG 240  
 TTTCCACGAT GACCACGCGT ACCTGCTTCT GCAATGGAAG GGTATGCTGG TGGTAGCCGA 300  
 GAGAACTGAA CTAGCTGACT TTAAATGGAG TGGTGACACG CCGGTGGTGG TCACCTCATT 360  
 CCGCGTTCCT GACCTCCGCG GGCTCTATTA TACCAATCCA CTCTTTGGGG ACGCCGTTAG 420  
 TAGGCCGCTG CTGCATGGAG ACCATGTCAC CGCCGACACA GGTACTGGTC TGGTACATAC 480  
 TGCGCCAGGG CACGGCCAGG AAGACTACCT AGTAGGTCAG GCGCACGGCA TTGAAGTCTA 540  
 CTCGCCAGTC GACCATGAGG GGAGGTATAT TCTGGATGAT ATTCTCCAC ACCTCCGTGA 600  
 TATGCTAAGA GAAGAGAGCG GTAAGCCGCT GAAGGTTACA GACCACAAAG ANTGCNNGNT 660  
 CTTTCATCAGT TTGCTANAAA AACCCTAAGT GCTCCTGCAT TCCCTGAATA CCACNCTCNT 720  
 NTCCCTNCAA TGGAGTCNAA NAACNTGTTT TCNAGANCTA CCCNNCCGTN GTTGCNAACT 780  
 GATGGACTGA ACTTCCCCCN GGAAACCTGA ACACTTTATT TTCCCTNCC AGGGGAAAAA 840  
 NCGNTCAAGG TTCTCNAAAN CGA

## 1347RP

GATCATCATG CCAGCGCCCA TGCCGCCGGC GGCACACCTT CACACCCACC CGTAACTGAC 60  
 AATACTCGAG CACCTTCGCTG CGCTGGCCCCG CTGGCGGCTG CCTGGCCCAT TATGCAACCA 120  
 CCCACACGTT TTATTCCACT TAAAAATTAC TTAAGCTGAC GTTACGCCTG TTGAAAAATT 180  
 TTCGCTTCAC GGAATTTTTT TGGGTGAGAT ATAAAAGGGG CTAAGTTGCA CAGTGAAAAG 240  
 GTGAAGTTTT TTGTGTTTAG ACTTCMTTA TGACCTCATA GAAGGAATTT GGGAAATCTG 300  
 ACTTTCTAGC AGCCTCTCTC CAGTTGGAAG TGTTTACATA CTACTGCTAA ACGTGCGCTA 360  
 AGTTAAGATT TTCTTTTCTT TAGTTTAAA CTCAGTACCT TATTCCATAA AGCGACACTA 420  
 CGATGTCTTT TAGATTCTCC CTCGTCTCGA ACCTAAGCCT ATCCTTGAGC TCTGTGGGGC 480  
 GGATGCCAACA GATGCGGTTT GCATCGTCTG AGTCGATGAC TGTGCGGGAT GCGTTGAACA 540  
 GTGCGATGGC CGAAGAGATG GACCCGTGAT GACGATGTGT TCATCATCGG AGAGAAGTTG 600  
 GCGCCAGTAC AACGGTGCCG TTACAAGTCA CCCAAGGCTT GTTTGACCGT TCCGGNAACG 660  
 CGGTTNGTNG ANACCCATCA CCGAAANGTT TTTGCCGTCT TGCGTGGGTN CNCCTGAAGG 720  
 CNTGACCTA TGTCATTGAN TNGTTCACTC TCCAGCAGCA NGACANTTCT GAATCCGCGC 780  
 CAAATACANN TTCGTGTGTG CNACNNTCAN TGTTTCCAGC NAAGNGCGNC NCGNNC

## 1347UP

GATCCTACAG AACTCAACTC TTATATCCAG GACTCAGTCA CGGCGTCTGC AATCCGCAGC 60  
 AGCCACGCGT GCTCCAGGCT GGGTGGCCAT TGGATGGGTG GGCACGACCC GAGTGGGCAT 120  
 GTATTCCCTGA TAACGTTAAT GTGTATGTTT ATGCTGGGCG AGCTGCAGGT ATTTGGCCGC 180  
 CGCGCAATCG GGAAGCTTTC TGCTGATTGT CAACAGCTGC AGGGCGCTCC TGGTAAATTT 240  
 GTGGCACGCA TTTTGCAAGC AAGTCCGATT AGAGAGCTAA TTAACCTCTGA AGCCCCCAA 300  
 CATATTTTAA GACGCCTTTTC CGTTCAACTG CCACTAGAGA GTCTTGCGAT TCTGGTGAGC 360  
 GCGGTTGTTT TTGGCTTTCG GTTCATTGTG CTGGAAAACC CGATTCTATT GCTTGTCTGGT 420  
 CTTATTCTGA CATGGACCTG GTCACCTCTG GTAACATATC TCTCTTTCCA TTCGTTTGGC 480  
 GAGCATTTGA CCGGTTTGCT CTTCGCATAC CTTCTAGTTT TGGCGTTATA CTGGTACATA 540  
 TAATGATCTA AGTAAAACTT GCAATATTAC ACACGAACGT TAAACTCGCC AGCTGGATAT 600  
 AGGCAAGAT TGCAGATGCT GTGCTTTCCG CCTAATATGC GGAAAGATGA GCAGGCCAAA 660  
 CCCAATGCAG AGTAGGTTTC TCATATAGTA ACCATCGCGC AGAATGACAA CTTCGCCCCG 720  
 CTTTCGAAGC ACTCCCCCTC GGAAGGAACA TCCNATGGGC GAATTTTGGC CACCTTANAA 780  
 TTNAANAAAC ATATCATCGC CGANACAATT ACCCCCANAA TATCAAGTAT 840  
 CNGAAATTTT CNTTANTTCN CCAATACGN

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1349RP

	GATCGTTATA	TATCAGTCTC	TTGCTATAGA	TTACTATAGA	GCCCACCACT	AATGTACAAG	60
5	TTATAACTAC	TGGTAACACG	TTATATAACA	GGTAGGAAAC	GGGGCCGCCG	GGGATTTTGT	120
	CCTATGGCTT	GGCCAGGTAG	CAACTGCTAT	AAAGGCGGAC	GTTTCTCCCG	GAGCTTTTTC	180
	ATCTTGCGCA	GTTTCACATT	CTAGTTAGTT	TAGGGCTAGG	TCGACAAACA	TATTCCACAT	240
	CGTTTTAATG	GCTGGTGTAC	CTGATAACGT	CAAGGGCGTG	GTTGAGCTGG	ACCCCTGGTT	300
	AGCTCCTTAC	GGGGACATCC	TCCTCTGCGAG	ACGGTTCCCTT	GCCGACAAGT	GGAGGCACGA	360
	TATCGAACAT	GCGGTGCCCG	GCGGGCGGCG	CAGTCTAGTT	GAGTTTGCGC	GCGACGCATA	420
10	CAAGAGCTAC	GGGCTGCACG	CGGACGCGCA	GAGCAAAAGC	ATAACGTACA	GGGAGTGGGC	480
	GCCCAATGCA	ACCCGGGCGT	TTCTAGTCCG	CGACTTCAAC	GGGTGGATGA	GACCTCGCAC	540
	GAGCTCCAGA	ACAAGGACGA	GTTCGGGTGT	TCACGGTGTG	TTCGGACCTG	GGCGGACGGC	600
	GAATTCATAA	TCCGCNTACT	CACCCTTTAA	GTTGTGTTCN	AACTTGCCAC	CGGANCCCCGA	660
	TACCCGGTTG	CCACNTTGAT	TCAAAGGNAC	CCACCCACC	AGAANCCCAA	GATTTGGGCC	720
	NCCTTACAAG	CCGTCTGAC	CCNCCCCCT	ACATTCCACA	CAAAGCCCCC	NGACCAACTG	780
15	ATNCCTNAAA	NNACAGNCNC	TTGCTCTCAC	CCGACCCGTT	TGT		

1349UP

	GATCGCGAAA	ACTAACGCAC	CAAACCCGAC	GGAAGCCAGA	GCTCTCTTGT	AAAGTGGCAA	60
20	GATAGTGAT	GTCTGGCCGG	ATGGCTCAGA	GGATTTCTTG	CGAGCATAGT	GGCAGCGATT	120
	GACATATGGA	GTTATCATTG	CAAAAGCAGT	GGCAATAGCA	AGACCGGTTT	TGTTCCAACC	180
	GCCGTTCTCT	TCTTTCATTA	TTGGCCACAA	GGGATTGTTT	GAGTAGAAGG	CCATCTTCAA	240
	CACAACGCTC	GCAACAAGGC	CTAGAGACCA	AGTAATGGCA	AACTGCGCGA	CACGCGGTT	300
	GTCTTTCACA	ATGCTCTTCA	AGGTCACTGC	AAAGTTCATC	GTGCTGAGAC	CCGTGGCAAC	360
	CGCAACCGTC	ATCAACCTCC	ACTCCGGTTT	CTCAACTATG	TACGCTCCGA	TACCGATTAC	420
25	ATTAGCAAGT	AAAGGGCCGT	ACTGTTGAAT	CAACGTTGGG	AAAAATGGAA	CATAAAGCAG	480
	AACTGGGCTC	AATAACGCGC	CTATACCCCG	CCTCATAGCC	GGAGATACCC	ATGTACCAGA	540
	GCGGGAAAAA	CCATATCATA	CACAATAGGG	CAGTCAAGTT	CGTCCAGAAC	ATAAACGAGT	600
	CAAAGGTACT	GACAACAATG	TAAAACAGAC	TTGCCTGATT	GGTGATGGGC	TCGTCCGGCA	660
	GGTAAACGAG	TTCTCGTGCT	CCTGCGTGAT	AATCACCTCC	TCCCAGCATT	TCCTCCATTG	720
	CGCCGCGGCC	GAGTCCCTTG	CCGGCTGAGA	NAGCNNGGTG	CTTGCTTTTG	ANTGCACAAC	780
30	CCCCNCGAAG	GCCTGTGCCC	TGGGTTGCCN	AACTTTNCCT	NAGTCTCTCC	AGTTTGCTNT	840
	ACTTACCCTC	CNAAAAATTC	CAAATATCCN	GGACNCCCN			

1350RP

35	GATCTCTTGC	AATTCCCTGCT	CGGTCTCTCT	GTGATCTCTA	TTGATCACCT	TTTCGAGTTT	60
	GGTCGCTTGA	GAAAGCGTCG	CAAAGTTGTT	CATAAGTTTC	TTATACCGTG	CCAGTTTCGC	120
	AGCCAGCACA	TCGTGCTTGA	TCGTGTGGAG	CGCAATTGGA	TCCCATCGG	CGGCCATGTT	180
	ATCCTTGACC	GCGATATTGC	GTGTTGATGA	AGTCTGAACG	GCCTCGTGCG	CTGGACGTAA	240
	GGCGAAAAAG	TAAAATTATA	TAGAACAGGC	ATGAGATTGG	CTGGAAGTTC	AGGGAGCCAG	300
	GCCTCGTGCG	AAGCAGCTTA	GAGAGCCATA	GGAAGCCACA	TGCGCAGGAA	CTAGAGATGA	360
40	GACCCACCCA	AGGTGAACTC	GCCCACGGCA	CAGGGGCAGT	CCTAGCAACG	TGGTAAACAT	420
	TAAAAATAAT	ACATACGTTA	CAAGCAGCCG	GCATAGCAAC	TGCCTGGAGT	CATGTTTTAG	480
	AGAAAAATAG	AAAAATTATT	ATAATATTCC	TTGTGTATGA	AATAAAGCTG	CTTTGCAACA	540
	CGCGGCAGAG	ATTGAGACCT	GCCTGAAGCC	GTAAAAGGAC	GAAAAACCGA	ACGAATAGAA	600
	TTAAGATAGA	AAAGCAGCAC	TCGGCCAAGG	CGAAGCGGGG	CGCGCAAGCC	GCCCGCGCTT	660
	TCCCTCNCNC	TCAGCTGCAA	ATGCTCCTCA	GTGGATCCTG	CTCCCCCTGT	CCCCGTCTCA	720
45	CCTCCTCCAC	TCCTCGTCNT	ATCCTTTTGA	TGAAACNAGG	CTGACGCGCG	TGTTCACTCC	780
	ATCTTCNCNC	GCNCCGCTCG	ATAAATTGCT	CAGCNCTACC	TCTTGNNNG		

1350UP

50	GATCCGCATT	AAGCGCGACG	ACGAAATCAA	TACCAAGAAG	CTCGACGAGG	AGAAGGAGCG	60
	GCGCCTCAAC	GCCATCATCA	ACGGGGGAGC	TAGTCATATA	AGCGTGCATA	TAGCGCAATT	120
	AAAGGTTTAG	CGTCATCGAT	AGTTACATAA	AGTTAGAAATG	CATGCTCCGC	CACGCGCGCG	180
	TTCGACTCGG	CGAGCCAGCG	CGAAAGCGCG	TCTTGCGCCG	CGGGTACGAA	GAACCGCCGC	240
	AAGAAGTGGA	GTTCCCTCCG	CCACCGGTCG	TAGAGGTCCT	GGCTGAGTAC	GTTGTACTTG	300
55	ATCGGGTCGC	CCTTGAGAGAT	GGCATTTCATG	AGCCACTGTG	TCTCGTGCAA	CGAATGCGTC	360

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	GGCGCGCTGC	TGTGCGACTT	CATCATCGAC	AATTCGCGGA	ACGGCTCGAA	CCGCGTGATA	420
	AGCGCAAGCA	AGCAGAGCCC	CGCAGCGTAC	ACGTCCGTGC	TGTGCGTCGG	CTGGCCGCCG	480
	CCGATCAAGC	CCGGCGCGCA	GTACTCAAGC	GTCGTCTGTA	GCGGCTCCGG	CGCCGCGTCG	540
	CACACTGCCG	CCGACGTGAA	GTCCGCCAAG	AATGCTCCTG	CCCGCGCACG	AGCACGTTTCG	600
5	CGGTCTTGAT	GTCCCGGTGC	ACCACGCAGC	TCTCGCGAAG	GAAC TGGAGC	GCCCCAACAA	660
	GGTCACGTGC	GTACCGCCAC	CACTGGCCCT	TGTCNCGGGC	GCGCGCCGGT	GCNCCGCTTC	720
	CANGTGGGGT	TCAACCGCTC	TACACAACGC	CGGGACCNC	TCGCCACCGC	GAANCGGCGG	780
	GTATCCCNAC	GTTTNCGCC	GCNCCCCGN	GGAANGGACC	ACTTNCGGTC	NCGANCCNCC	840
	CCCGCCNGGT	GGCAAGNGGG	AATTNTTTAC	CNTCT			

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## 1351RP

	GATCATAATG	ATTTGTCTTA	ATTCCTTTCT	TAATTATTCA	TTAAATAATT	AATTAATATT	60
	TTATTAATAA	AAAATATTTA	GAGTTATGTT	CGTTTATGAT	AAATTCTAAA	ACTTTGCAGC	120
5	ACGAACTGAA	GACAACATATG	TAACGCCTGT	AATTAATTAT	AAATTATTAT	AATTAATAT	180
	TCAAAAAATG	GTAAGATTTA	TCGAGGATTA	TCGAATTAAA	TAACATGTTT	CACGTGCTTA	240
	GTCTGTAACC	GTCTATTGTT	TTGATTTTAA	TTATTGCTAA	CGTAGTCATC	AGGCGGAATA	300
	CTTTAATTTT	CATTTAATTT	ATTCCTTTAA	TAATAAAAAA	TAAATAGGTA	TTCATTGTTT	360
	ACTGCTAAAA	CTACTCGGGT	ATCGAATCCG	ATTTGCTACT	TTAGCCTTCG	TTCCCTCAATG	420
	TCAATTAATA	TATAATTTAA	ATTTTCACTT	TATAAGTCTT	ATTTCATATA	TTATTATTTT	480
10	ATCTTTACTT	GAATAATTC	TAAATTATTT	TTATTAATTC	TAATTATTAT	TTTAAATAAT	540
	CATCTACGAA	CCCTTTAAGC	CATTACGAAT	AACGCTAACC	CCTTTGTCTT	ACCGCAGCTG	600
	CTGGCACAAT	TTTGGTTGGA	NGNANTTAAT	TATATATCTC	TTTTAAAAAT	ANAATCTCCC	660
	TCATATTAAAT	AATTTTATAT	TGANANTAAT	TATCNNTATT	TAATAATTAT	TGAATTTATT	720
	GTTACCCANA	NTAANAANAN	ATTATTTATTT	ACATCCCCNA	GTACNGANCA	CTTCACATTG	780
	CCAAATCCCN	CGCGTTCCNA	NAAATGATAT	ATTCNANCAC	GGATNTCTTC	TT	

## 1351UP

	GATCATTATA	TTATAAAATA	TAATAAGAA	TATATTTAAA	TAATAATAAT	AATATGAAAT	60
	ATTATATTAA	TTCTCCATTG	GAGCAATTTG	AGATTAGAGA	TTTATTAGGT	TTAACATCAC	120
20	CAATAATAGA	TTTTAGTTTT	ATTAATATTA	CTAATTTTGG	TTTATATCTT	ATAATTCCTT	180
	TATTAGTAAT	TTTACTAATG	AATTTAATAA	CTAATAATTA	TAATAAATTA	GTAGGTTCTA	240
	ATTGATATTT	AAGTCAAGAA	ATAATTTATG	ATACTATTAT	AAATATAGTT	AAGACACAGA	300
	TTGGTGGTAA	AGTATGAGGT	TATTATTTTC	CATTAGTTTA	TACATTTTTT	ATTCTTATTT	360
	TTACTATAAA	TTTAATTAGT	ATAATTCCTT	ATTCATTGTC	TATAACTTCA	CATGTAGTAT	420
	TTGTAGTATC	AATAAGTATA	ATTATTTGAT	TAGGTCTAAC	TATTATTGGT	TTTTTACTCT	480
25	ATGGTTTAAA	ATTCTTTGGT	TTATTTTTTAC	CACTAGGTAC	ACCATTAATT	TTAGTACCAT	540
	TATTAGTATC	AATTGAATTA	TTATCATATT	TTGCTAGACT	TATTTTCATTA	GGTTTAAGAT	600
	TATCAGCTAA	TATTATAGCT	GGTCATTTAT	TAATGTTATT	TAGGTGGTTT	AATATTTAAT	660
	TTAATAGCTA	TAAATATTTT	AACATTTTAT	TAGTTTCTTA	CCCATGAATG	CNAATTTAGT	720
	ATGGTTGTTT	ANAATTGGCC	ACCCTANTAT	CCACCTAANT	TGAGGTTTTT	TAAATCCNC	780
30	ATTTTAAAAA	TCCATTTTAT	TACATNNATT	AANAATAANA	TATTTAATAA	TATCCANNAT	840
	TNAANATTTT	ATAANTTTAA	AAN				

## 1352RP

	GATCCTGCAT	CGTTTCGTCG	GCCTGCAGGT	TGATTTTGTG	GCTCTCAATT	TTATCCTTTA	60
35	TCAAATTCAC	AACCTGGCAA	TCCACCTCAT	GCCTTATCTT	CAACGAATGC	CTCATCGTAT	120
	TGTCTAACCT	GAGGACCATC	TCCACCTTCC	GTTTAACAAG	CTCGACGGTA	TCCTGTGTCA	180
	ACAGGTTTAT	GGCTGGGTCG	TCCAGCCCCA	ATTGGGCATC	CCAGGCAGTT	ACGTGATCTA	240
	TGTTGTCTCT	GGTGTTCGGA	GAGAAGCGAT	ATGTAACCGA	CTGCATGTTA	AGAAGGCCGT	300
	AGGGCGAGTC	CTGCTCCCGC	ACGTCCGCGT	CGAGCAACTC	GCTGGTGTG	ATGTTGATGG	360
	CGTCTTCACA	CAAATCGCTC	AACAGCGAAA	GCTGCTTGAA	GGGGAAGCGC	ACGTGGTGGA	420
40	ACAGCGACCG	TGCGTCTTGG	CCCGAGCGGC	TCGCGCGGCG	GAACGGGTTG	TGCTCGTCTG	480
	CGGACAAGTT	CGGGCAGCTC	AGGGACGGAT	GGAGCATCAC	GGGCGCCTGC	TTCCGAGGGC	540
	CCAGGTCTGT	AGGGTCCGGC	TGCGGCAACG	CGAGACCTTG	TACTCCGCGG	CCGCGCCGGG	600
	CTGGCCGAGC	GCCCCNGTCA	GTCTTCTACA	CCNCTTGACT	CCCCCACTC	CTCCGTNGAT	660
	GACTGNCCGC	GCTCTNCATC	CGGTGCTCGC	ACACNCACAT	CTCCGAATGN	TTTCCACCAC	720
45	CACCCNGNAC	AACCTTCCAC	ACCCGGAAC	TCNNTNGNNT	TTNGGACCCCT	GTCTTTACNC	780
	TCCAATCCCN	TCTGCTGCAT	TTTTGNAAAA	CTCCCCCAA	CCCACCCCTC	N	

## 1353RP

	GATCTAACTA	TTAATGTGTT	CCTTGAAATT	GTGCTGAAAT	ATAACGAGCT	CTTAAATGAT	60
50	GTCTATCTTG	ATGACGATGT	CGTCAAGTTG	AGCCAATGGG	TACTTCAAAC	GTGTAATGAA	120
	TAAAAATATA	CAAGCGCAAA	GCCCAATAAC	CTTTACCCTA	TATATCTTGT	AATATATTAA	180
	GTTAATTGAA	CCATTTACGT	GCCATATTCT	GCGCTGGCAT	GGTATCCGTG	ATTTTATAAT	240
	ATATATTTCT	CGCAGGGGAA	GCAGAAACAC	TCAAGATCGG	CGATTGCCGA	TAAAAGAATT	300
	GCTCCCTGAT	TGATTGTTGT	TCGAAGGAGA	TGCAGATGGA	TTGTCCAGAA	AAACCGGTTT	360

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	TAAGACTCGT	TCATCAAAC	TGTTAAACCA	TTGCCCATCG	GCTTGCACTA	TATTGCCCAA	420
	GGTTTCGCGG	ATATTTCTTC	TGTCTAATGA	TAATCGTCCC	ACAGGCTGGT	CAGCGCCTGA	480
	TGCAGAGCGC	GAAGAGGGTC	GGTCTATCAT	AGGAGGAAAG	CTTTCTTGAT	CCGGGGAGCC	540
	GGTCGGGCTG	TCGGCTAAAA	ATGGAGGTGC	GTCTAATGAA	GACATTAGCT	GGACAGGTCT	600
5	AGGGGCTTCC	ATATCAAATT	CATCATCCGT	ATCCTCCTGT	TCTTCTACGC	ACCCGTGCCT	660
	TATGTTTAGA	TCTCCAGCAT	ACCGCAGTAT	ACCTCCCAAT	ATGATACGGT	GAGAACCCCA	720
	CTACCACCCA	GTGGCCNAAA	AGAACTTGAC	CCCCTGTNAC	CCTNCATGCA	TCCACNACCC	780
	CACCCCCCA	ATCNCNCTGT	ATGGTATGAC	CCTCAGANAN	CCNCCTCNGA	TC	
10							
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## 1353UP

	GATCGGCGCA	CTCTGTGGTT	CATGTCCTGC	ACAAGTTGAC	CACTGTATAC	CAGTTTGACA	60
	TCAGAGGGCG	AAATCATCAG	TGTGTGGCCG	TACACAGAGC	AAATAAACTC	CTTTACTTCC	120
5	TGCACGGTGG	TGTCGACTGT	CACTTTCATA	GTCTTCATCG	CCAACACGGA	GTCCGAAACG	180
	AACTCGATAG	TTACACCATC	CCCGTCCTGG	CCGTGGTTGG	TACGGAACAT	AATTAAGCAA	240
	TGCGAGAAATG	GGGTGGGGCG	AAAGTCAAAG	CCCAATACCT	CCTGTAGGCT	CAACCCCGCG	300
	TGTTCTGCCG	CGTCTTCGGC	GCCCAGGTAC	ACAGGGGTAC	GATCGCCCTG	CAACTTGGA	360
	TGCAAGCATG	TCGTGGGGCA	CATGGTTCTT	GTTCGAACAC	AGGTTCTTGC	AGCTGCTGCG	420
10	CTCGTACTCG	TTCACTATAT	CACATGCCAT	CGTCCGCAGC	GCCAGCACAG	ACGTCTTCAG	480
	AGGCACACGT	TGCCTTATCA	CCGCCACCAC	TTTATCCATG	GAAAGCGTGT	TGACCTGGAA	540
	CTTGACGTTT	ACATACGCAA	ACTCACTGTC	GCCATCGTAA	GCCAGGTCTA	CAGTGCCGCC	600
	TCCGACCTGC	TCCGCACATC	CAGCTCCAGA	TGGACCAACC	CCGCGCCGCA	GCCTGCAATC	660
	TCCTCGCACA	ACATGGTCAG	ATTTCGAGCGG	ACGCTGTTGG	TATTCAGACA	GTATTGCTCA	720
	GGCGGCCAAG	CGCCATGTTT	TCCCCTGATG	CATGATAACC	AATGCCNTAC	TGCNATACCT	780
	NGCNACTGAT	AANTTGGGGG	ANGCCCGCCC	NTTCACGAAG	AAGATCCANG	CTCCNTTCA	840
15	AATAGNAANN	CNGANTGAAC	TGGCGNATNC	CNAATCT			

## 1354UP

	GATCGAACAC	GCCTGTGCCA	GGGAGCTTAG	GGTCGTGTGC	ATCCAATTGA	GATCGAAGCA	60
	AAAACCGACC	ATGCTTGTTG	AACCGAAAGG	CGGATGTAGC	ATGGCCCTTT	CCCAACGGTT	120
20	GAGATCCTGG	TTGCGCCCTC	TTACCCTTGT	CGTAAATTCT	CGCAAAGTCA	GCCTGGTCCG	180
	TCGTCAAGAG	CGCCTCAAGG	GCATGGCCCA	AATGATCTCG	CGGTCTGCG	CGGTCTGCG	240
	AAGAGTCTGA	GCTCAAGCTG	AAAATTGGGG	GGGCTGCGA	CCGGCGCTGC	AGCAGCATTG	300
	ACGACGTCAT	CTTGCGAGCAC	TTCTGTCACCT	GGGCGTCTTT	CCGCAGCAGC	GTGCGCAGACA	360
	GGTGCCGACC	ATTTCAGAGG	CGGAAGTTGG	ATAGCAGATA	ATGCAAGTGC	GACAGCACAC	420
25	CAGACATCGC	ACTGGTTGAC	GATACATACC	GTGCTTGCCC	TTCTTGCGCG	CGTCCAGCA	480
	GTGCGAGGTC	CCGCGAGGGC	GGCACGAAGT	CTGCGATGGC	CTCAAATCGA	AGTCCTGCAC	540
	CTTGATCACC	CGCTCGATGA	AGGGCTCGAA	GTGTACACAC	CCCGACCGCC	GGTCCCGGAG	600
	CGGCACCACC	GACAGCGGGC	TGGAACAGGC	AGCGTTCCAG	CCCGTGCGCC	AGCCGCGGCG	660
	CGAGCTCTGT	TGCACTGCTC	NTNCCACCCC	ATTGCTGAAC	GCCCCNTGAT	TACAAATTGT	720
	TCNCTCCCG	GCCCCGCTTG	CCCCGGTTGC	CCCTCCCNCG	CGCGGCACCC	CCGCNCCNNT	780
30	GGATGANNGT	TCNCTGATTN	NCCAAACCCG	TTCANNTTGT	CCGGTTTTNT	CANGGNCANT	840
	NCCCNNTCNT	TGTNCCNNTT	NAATGCCCN	N			

## 1355RP

35	GATCATGGCC	AAAAAATTGG	GAATAGGAAA	CTGTTTCCAG	TACTCATCAA	GGTCAGTAAA	60
	AATGTTTGCC	AGCAGTGAAG	ATTGCATCCT	TATCTTGCCA	TTTGCGGATA	GGACATTTGT	120
	TTGCATATAC	CTGTGGTGAG	AGGAAAAGAG	TGTTGCCAGT	TGGGTAAGTT	CTCGTAAAAA	180
	CAAAATAACT	TCTCTTCTGG	AAGTCTTACC	GTACGCGATT	CTATTCAAAA	TCCTCTCCAA	240
	GTCTTGCCCA	TCACGCAACA	TATTATTAA	CGACTCAATG	AAGATATTAC	CAACTTCGGT	300
	TGAAATGCAC	TGAAGTGGT	CCAATCTCTG	TTGTATCTGA	TCAATATTTA	TTAAAGGCTT	360
40	TGCAATCCAG	TTCTTCAAGT	TCCTTAACCC	GTAAGTTGTT	CTAGTATGAT	CTAATACCCA	420
	TAACAGGGAG	CCTTTACTGC	TCCTATCTGT	ACTGTTCTCA	AAAATATCTA	AGCTTTCAAT	480
	AGCGCTAAGA	AGGAAGAATC	ATGTGCGTCT	tCGAgCAGAA	TGGTTTAAAG	TTTTCCCTGA	540
	AGAAGAGTAA	ACnnncATTT	TTGAAGTTTG	TTAGGTAGCC	ATGCACCAGC	ATGAGCGCTG	600
	TTTGACAGAG	AACGTTGCCC	TTAAAGGCTG	GGTGCGGCTC	ACTGAAGATT	TCTTCATACA	660
	ACCCGACGAG	CTCGATCCTA	TTTAGAGTGA	TATCGGAATC	TGAAGTATGA	AACACCTTTT	720
45	CGATTTCTGA	GCCAAGGCCA	TCTCCGACCA	CAACTTCACT	CGGGTTTGTG	TATTTTATTTC	780
	GCGTCTCCAA	AGCCTCCGTC	AGAAAACGCT	CCTCTTTGAA	GTCATCGAAG	ATAACTTCAC	840
	CGCTGTTGAG	ATTAACACTA	ACCAGGAAGT	ATCGCGTGTA	TGAAGGTTGT	CGCTTGACAC	900
	CAAGACCCCA	CACAGAAGCG	CTATCACCCA	GGACCCGACG	ATCTTTGGTT	CGAACGCTCT	960
	ATTGATGCCA	TAGGTAGCCC	TCGTGAATAT	ATTGGGTACT	TCCCTCGAGA	AAACAGAGCT	1020
	TGAgGTCCCA	CTGtTCTTTT	TCACTGCGGA	TGTCTCTGtC	TGcTcCACGa	CCCCACTTTT	1080
50	CAGATTGtGG	tGCATcAAGC	GCTGCAAGtG	GACTTcGAGA	CgGGTGTCTg	GGaATGGTGC	1140
	AgTACGCAAA	CTTcTTGtGC	tTGtGA				

	GATCATGCTA	TCAAGTGCAG	AGAACACGGA	TAGAGCCTAC	TCTGCAGGTT	CGGCCTCGCT	60
	GAGCGCGGCG	CAGAAGTCGA	AGAAGCCGCC	AAATACCGCC	TTCCGGCAGC	AGAGGCTGAA	120
	GGCCTGGCAG	CCCATCCTGT	CGCCGCAGAG	CATCCTCCCA	CTGCTAATAT	TGCTGAGCGG	180
5	GGCGTTTGCG	CCAATCGGGA	TTGCGCTGAT	CATCAGTGCA	AACAACGTGC	AGAACCCTGGT	240
	GATCGACTAC	AGCCAGTGGC	GCAAGCACGC	CACGTCCGAA	TACACGCCCA	TCCCCGAGAA	300
	CCTGGTGAGC	TACCACTTCC	GGACGTCCAT	GTCCGAACAG	CCTAAGTGGC	GGCTGCATTG	360
	CAAGAATGAG	TGCGAGCTAG	AATTTGAGAT	CCCCAACGAC	ATATCGAGCT	CGGTGTACAT	420
	ATACTACAAG	CTGACGAACT	TCTACCAGAA	CCACCGCAAG	TACGTGCAGT	CCTTCGACCT	480
	CGACCACTT	AAGGGCAAGG	CTGTTGCACC	AGACAAGCTG	TCCGACACGT	GCCACCCGCT	540
10	CTCGACTAAG	GACGGCAAGG	CTGTCTATCC	CTGCGGCCTG	ATCGCCAACT	CAATGTTCAA	600
	CGACACCTTC	ACGCCGGTCC	TCCGGGGTGT	CCAACGGCGT	CCCCCGACTA	CAACTCAGCC	660
	AACAAGGAAC	ATCGCCTGGC	ACACNGACCG	CAACAGGTNN	CAAGAAGAAC	AAGCTACAAC	720
	CCGCCAGANA	TNGTGCCGCC	CCCCGCCTTG	GCACGAACGT	TTCCCCCNAA	TGGNTANNAC	780
	AANCCAACCT	GCCTGACTNN	CTACTTGGGA	GAATTTCCCG	TNTTGGANTG	NNCCCTGCAG	840
	NCTGCCNCCT	NNTAAANCTN	CNTNCAAAAA	AAAAGCAACN	CCCTCCC		

## pAG1355up

1	GATCATGCTA	TCAAGTGCAG	AGAACACGGA	TAGAGCCTAC	TCTGCAGGTT
51	CGGCCTCGCT	GAGCGCGGCG	CAGAAGTCGA	AGAAGCCGCC	AAATACCGCC
101	TTCCGGCAGC	AGAGGCTGAA	GGCCTGGCAG	CCCATCCTGT	CGCCGCAGAG
151	CATCCTCCCA	CTGCTAATAT	TGCTGAGCGG	GGCGTTTGCG	CCAATCGGGA
201	TTGCGCTGAT	CATCAGTGCA	AACAACGTGC	AGAACCCTGGT	GATCGACTAC
251	AGCCAGTGGC	GCAAGCACGC	CACGTCCGAA	TACACGCCCA	TCCCCGAGAA
301	CCTGGTGAGC	TACCACTTCC	GGACGTCCAT	GTCCGAACAG	CCTAAGTGGC
351	GGCTGCATTG	CAAGAATGAG	TGCGAGCTAG	AATTTGAGAT	CCCCAACGAC
401	ATATCGAGCT	CGGTGTACAT	ATACTACAAG	CTGACGAACT	TCTACCAGAA
451	CCACCGCAAG	TACGTGCAGT	CCTTCGACCT	CGACCACTT	AAGGGCAAGG
501	CTGTTGCACC	AGACAAGCTG	TCCGACACGT	GCCACCCGCT	CTCGACTAAG
551	GACGGCAAGG	CTGTCTATCC	CTGCGGCCTG	ATCGCCAACT	CAATGTTCAA
601	CGACACCTTC	ACGCCGGTCC	TCCGGGGTGT	CCAACGGCGT	CCCCCGACTA
651	CAACTCAGCC	AACAAGGAAC	ATCGCCTGGC	ACACNGACCG	CAACAGGTNN
701	CAAGAAGAAC	AAGCTACAAC	CCGCCAGANA	TNGTGCCGCC	CCCCGCCTTG
751	GCACGAACGT	TTCCCCCNAA	TGGNTANNAC	AANCCAACCT	GCCTGACTNN
801	CTACTTGGGA	GAATTTCCCG	TNTTGGANTG	NNCCCTGCAG	NCTGCCNCCT
851	NNTAAANCTN	CNTNCAAAAA	AAAAGCAACN	CCCTCCCN	

## 1356RP

	GATCTACATA	TGCATCAAAA	CATGTGCCTT	CATGCCGATC	AGTAGTTATG	TTTGCGCTGA	60
	GAGGCGAGCC	ATTTCCAGCT	TGTCTGCACA	ACTCCATATC	ATTTGCATCA	TCAACCTCAT	120
5	TATCGCTATC	ACCATCCTTA	GTCGAGTATG	GAAAGGAGGG	TGACACAGCA	AGGCCAGAGG	180
	TATCAGTTGA	AGACATATCT	GTGCTCATGC	GGTGGGCCGC	ATCATAGTCC	GATGACTTCG	240
	TGGAGGATTT	AAAGTCATT	TGCGGAGGAT	TCTGTGGCTC	TACTGACCTT	GCAGATTTCG	300
	TTTCACTTTC	GTACAGAATG	GACTCATCTT	CGAACCTGAG	ATCTATCCGT	TTGTGATCAT	360
	ACGCGACTCT	TTTTTCAACC	TTCTTTGTCT	TCATTGGCAC	GGAGTTTATC	AAGCTAGAGC	420
	CCAAGGAATG	CTGCTTATCA	AAGTTCTTCT	TAGCCATGGG	CATTTTCGTAT	CTATCATCTA	480
10	TCCCTTCGTT	CGAACCATAC	TTCACTGGT	AGCCATACTT	TGTATTATAA	TAAGAGTTGC	540
	GATAATGCTT	CGTACCAGAA	CTACCGGCAC	TGCTAGACTC	CAATATGGCT	TGGATGAGGA	600
	CTGCGCACGC	GAAGTTTACT	GCCATCCATA	TCAATTGGG	CNTGGCTGCC	ACATTGCAAA	660
	ANANTAAGAA	GAAGTACGAC	TAATCCTCCA	CTNGCTACCC	CGTCCNTAGC	AGCGAACC GG	720
	CTGCTGTCTN	NCNCATCCAC	CCCCGTGCTT	GCTTAGCTCC	TACNCCNTG	TGGTTCCATA	780
	ACCCACCCCG	TGTCACCCCA	TCCCCTGANC	ATTNTGAGAG	ANN		
15							

## 1356UP

	GATCTGAACC	ATATTACCAA	AACCAAAACA	AGAATTTCGGG	CCCAAGCGAC	CCGTCCGCGC	60
	GTAAAGCCCT	ATAACCAGCT	TACGCGTCTG	TGGGCGCCAT	AGAAATTTGC	ATTTTCAACG	120
20	GAACCAACAC	GTCAATCCCA	AAC TACACTT	ATCATGCCTT	AAAAGGGATT	ATCTTTTCTA	180
	ACGAGGAGGC	CCGCCTGCGC	AGTAGGAAGC	GGATCTTAGC	GGCGTCCGGC	CGGCACATTC	240
	GGCCGTTGGA	CTGCAATATC	CTACTTCTGC	AGCGGAAGAT	AGCGCACGAA	AATCTGCGGC	300
	GGAGCAAGCT	CAGAATTATA	TGTAGGACCA	AACATTGTCA	GCAACGCCCTG	CGCCGAGTTC	360
	TGTTATCGAG	TAGGGGGATT	TCCTGCGAAT	GCCGTTCCCTT	TTTATCGTTT	CTTTTGTGAG	420
	GGGCATCTGC	AGAAGCGATG	AGGTCCAAG	CATCTTGTG	CATCGATCAC	CGAGCCCACA	480
25	GGGCAGGTAG	AGTAAAGCCT	AGTCACCATG	TGTGTAGTTG	ATAATAGCCG	CGGAGGCGCA	540
	TTCGCATACT	ACGCGGGTAA	GCTGCGAAAC	AAGGTAGCGA	CGCGGCGCGG	GC'TTTTAGGC	600
	GACTACGACT	ACAAGTACCT	GTTACGCGCG	CAGATATTCA	AGCGCCAGAG	AAGCTTCAGC	660
	CATTTTCTCG	ATCNATGCAA	AATCCCCGGT	GGTGC'TTGGG	TGGCNTTTGG	GGNTNCACNC	720
	CCCNNGCAAN	NCTGGCGGNT	TNNTTNCNCC	NCCAA'TNNTG	AATACCGGNG	GNGGGAANTT	780
30	TGAAAGNNAA	NCCNACATNC	TTATTGGGCT	TNCCNGNTGT	NGAACGGGGC	TTCNTNNAAG	840
	GNGNAATANN	CCCTTGNGAA	TCCTTAANAA	AAT			

## 1357RP

	GATCCCAGCG	AGGACATCGA	AGAGGGACTA	CTGTACC GCA	TGGACAAGCT	TCGCTGCCGA	60
	TTGATGAGCG	AAGACCGAGA	TGAAATGACA	GATGGCGGGA	CCGTCCGGGAG	CGTGATCTGG	120
	AAGGAAATGT	TTTCTGCCGT	CGGTATGGTG	TCCAGGCTCA	TGGTAGTACC	TGCATGATTC	180
	TGTCTTTCCG	TGATCGGCTT	CATGGTGGGC	GTTAGCGACT	TATAATAGTC	GGTGC CGGTT	240
	GCTGGCGCAA	GCAGCTGGCA	TGCAGTGTG	TCCGACAAAT	AGGAGTACCG	GTTGGTGTTC	300
	TTATTTCGTGG	TGTTGTCAGA	AATGTTTGCA	AAGGAATAGA	AACCA'TTTTC	CATGGTGGTC	360
40	GAGGGGACTT	GCGAGTTCTG	TGCGGGTGTC	TGCGCGACAT	GACATTTTCAT	TTCTTGTTC	420
	GCGCCCGCTT	CCGCAGGAAA	ATGCGGCGGC	TGTGCCGCCA	TGTCTCTTTC	CTGCTTGTGT	480
	CCGTCTGTGC	CCATCTCCCC	TAGGGGCTTG	CCCTGAAGAG	TTTCAAAGCT	TTTGAAC TTC	540
	AAGGAGGGCG	ACGCCGGGCC	CACGAAACGA	TATCGCTTTA	CTCCTCCTCA	GC'TTCCCGAT	600
	AGGCATCTCN	ATGCCATTTT	ATTAATATAT	TTCCCCCGTC	CGAACC CCA	ATGTATGTCT	660
	CCCGGTTGGC	AAGGGATTCC	GACTTATATA	TTATTTGATG	TCCACCACAG	GTTTCCNAAA	720
45	TATTATACAT	CNATTGCCNA	ACCTCCCCNT	TATNCATCAT	CCGACCNCNC	CNCATTTGTA	780
	CNCACTAACN	TGCACATNNC	CCNATNTNNT	AACCCATCAA	CNCACCTTNC	CTGCCCATCT	840

## 1357UP

	GATCCTCGCG	TTCCCATGCA	ATTGTGTTGC	TTCCGGTTGAC	CCGATATGAC	CTCAAAACCG	60
	GGTCCGAAGC	CACCAGCACC	TTGTGCTAT	GTGACTTAGC	CGGCTCAGAG	AGAGCAGTGA	120
	CACAGATAGT	ACGCCGGAAG	GAGGGTGCGT	TCATCAACAA	GTCATTGCTA	GCGCTTGGAA	180
	CGGT CATAGC	CAAAC'TTAGC	ATGTTGGGAA	GCCAGGCCAA	TGGCCTGCAG	CCGTCTCCCG	240
55	CAGCCGGCCA	CATACCGTAC	CGTGACTCAA	AGTTGACCCG	CATCCTTCAG	CCAGCATTGA	300

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	CAGGAGACAG	TATCATTACG	ACCATCTGCA	CCATCGATTC	GAAAGCCGAG	TCCTCAACCG	360
	AAACGACCAA	TACCGTCCGC	TTCGCGTCTC	GCGCCAAGAA	TATCGCCCTC	AACGTGCGCA	420
	AGAATGAAAT	GGACTCGCAC	GCCGAGAAAG	ACACCATCAT	CCAGAACTTG	CGCAAGCAGC	480
	TTGACGAGCA	GCACGAGACC	ATTGTGATGC	TCCGGCGCAG	TGCTGCAGCG	CCTAGCGGCA	540
5	ACGGCTCGAC	CAGCCCCTG	GACAGCCCTG	GCGTCGGCGG	CACCCAGCTT	TGAGCGAGCG	600
	CACGCCACAA	CATTGGAAAA	AAGGNTTGCT	AAAGGTNGAA	AACAGCATCC	TCCAAGAAGA	660
	ANCTCCGAGC	CATTGCGAAA	AAGCNTCTCG	AANNAGGAAA	TGATGTCCTC	CGAAGAACCG	720
	CANTTTCNCA	NATTCCTNAA	ATCTCCCCCT	TGGAAATCCC	CCCGTCCCCC	CAAAACCAGG	780
	NTNCAGGGGT	TGATTTCCNC	NGCCCCATTA	CCGNNTTACT	TTCAAAANTA	AATNCACNCC	840
	CCCAGGNCCN	NGAAAAATNCN	TTCCCCCCCCN	TNTGGNGTTC	ACCGCCNA		
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## 1359RP

	GATCCATGTT	TATTCACCCC	GCTCACTCGC	GTAAACGATG	CTTTACGTTG	CTCACATCGC	60
	CGCCACCAAT	AACAGCGTAT	CACATTTTAC	GTTTCCGTCG	AGCAAAAAGT	CGGTCCGGAAC	120
5	ATAATGCTCC	AATACCACGA	TAGGTCCGCG	CAAGCGCCTA	ACACGTGCCA	TCCTGCTCGC	180
	CTCCCCACGG	GCCGCTCGCG	CTGTGCTGGA	TGAAACTCCC	CTCCAGCGTA	TGAGCGGACG	240
	GGCAATTCGCC	CTGCCATTAC	TGCACGCCCC	ACCGACAGGT	TTCCCATGTC	AGCATCGACG	300
	GCAAACCCGC	AGAAATCGAT	AAGTAGCAGG	ACACGCGTCA	GAAAGACCAG	TGTGGTATCA	360
	TGGCGCACGA	GGAGCTAGGC	AACCTCGCTT	TTCCGCAACC	ATGCCCGGCC	GCAGGTTCTGA	420
	ACGCGGGAGC	GCCTCACCAA	GCCGGGATTG	CTAATGTCCC	TTCCGGCCAA	AGGCCGTCAC	480
10	AGCTAAAAGA	GAGGCGCCCC	CGAAGGCATA	TAGCTGGCAG	GAAACGATAC	GATTCAGCGC	540
	ACTCGCAGCG	TAAGGAACAG	GAGCATCACA	TGGAACAGTC	GCCTGTGGTN	TCCATCCCCTG	600
	AAGGTNGACA	CTAACCTGAA	AAGCGGCGGT	TGGCACTAAN	TACAAACNTT	ACCACAGTAG	660
	ATGCCNAATA	CTGCTGACAA	ACGAACTGGG	ATTNCTNACC	GGTGTGNGG	ANANAAATCT	720
	NCCAAGAACN	TTNAACNCAA	TTGGCCACTA	CCCCCTCTGA	TCCCTCTTNN	ATCNCACGGT	780
	TTGGGANCCG	GNGNGCAAAG	CCCTGATGGN	ATCCCTGACN	AANTTGACT	NNT	

## 1359UP

	GATCGGTGTA	GTACACGGTT	TCCGGCGCCG	CTTC TGCGAG	AGCAGCTCCG	ATCACCGCGG	60
	TACCCAGAA	CTGCCCGGGC	GCGTCGCAAC	ACTAGTGCC	GCTGTGATG	CCCGCCTTCT	120
20	AGTCGTTGCC	TATTTTATTC	CTGCCGCGCA	TGTTGCCGCT	GTCACGGCGT	ATCTCGATGT	180
	GCGCGAGCAG	GACGGCTATC	TTCCGCAGAC	CGTTCCCTGT	CATCTGGTGG	CACCACCGCA	240
	ACCGCCGCAC	GAGCTGCGTG	ATGCGCTGGA	CGCCCTGCCC	TGTGATTCCG	TTTCTGGACT	300
	ACCCGTCGTA	CAATCCGTCA	TATACATCGG	CATCCCGCAT	GCCGCCACCT	TTGTTGGTCC	360
	AGAAGAATCG	CAGCGCACTG	CTGCCGTGAT	CGCGCACAAT	CACGGGCCCA	GTGGGCCCAA	420
25	CTACGAGTAT	CTGAAGCTGC	TCCACAGCGC	GCTGCACTCA	ATAGCCGAAA	CGTTTGGCGC	480
	CCGCTTGTTG	GAGCTGGAGG	ACCATTATCT	GGACGAGCTG	CTCGAAGCGG	TCCGACCGTCT	540
	ACGGGCCCCG	CGCTGTGCCG	CGGTAGGTGC	CTGATCTTCT	GCTAAACCCA	CGCCGAAACA	600
	AAGATAGCAC	CCGCGCTCC	GGGTAGCGGC	CGGCCGTCGT	GACCAGTTGC	TAGCGTTTAC	660
	TTGCATACCC	GTATCTGCTT	TAACCGTTTG	GAAGGTTTAN	CATCATTAGT	TNNTTTGTGC	720
	GCTTTGCTGC	CCCTGCNTTG	GCAAGGGGCN	CCTATTTTAA	NTTACCNCCC	GNTTAAACGNC	780
30	NCCTGAACAA	AAATGAATTC	NTTTNGANAN	TCCCNATTT	TNAGGATATC	CCNGTTTGA	840
	ATTGANAANA	CTGATTTGCC	NTTTTTNTNT	A			

## 1360RP

35	GATCCTTCTC	CTCCGCATTC	ACAGAATATA	TCCTCGCGGT	CATATCCTTC	GCGGTGCAAA	60
	TAATGAACCG	TGAGTCCCGC	GACCATGTGA	GCGATGTGAT	GTCGGCGAAA	TGCCCCGCGT	120
	GGACCCGGTA	GCGCACAAAA	GGCGCAAAT	GCCGCTCAGC	ACTGACCCCT	GGAGTCCGCC	180
	AAATCTGAAG	AAACCTCCCA	CATGCCAGAG	CAAAGAGCTT	ACCGTCTGTC	GAAAACTTCA	240
	CGTCGTTTAC	TTTGTCCTTA	AAGTTGAAAT	GATGTATCAC	ATTCTCTGTC	TTTATATTCA	300
	CAAGGATTGC	CCGACCGTCC	ACGTCAACCG	AAAGAAGCAG	TGTACCCTGG	GCATTGACGT	360
40	CGATCCTCCG	CTATATTCTT	TCTATGCTCA	TATTCAAAGG	TAAACGACTT	GTTACCAATC	420
	AGGTCAAACA	CCGATACCTT	GTTGCCAACG	GGCGAGAATA	GCAGCGTTCC	ATCCTCCGAA	480
	AACACCACAT	TTCCCTGTCT	GTATACAGTG	CCTAGCAGAT	TGGAAAACTT	GAAATCAGAC	540
	TTCATCGTAG	TCCAATGCCT	TGCCCTTGCTT	GATCTTTTCA	TGGTGTAGCT	CATCTCATCT	600
	CGAATTAAAT	TTTCCGTACC	ACCCAAAAAA	ACANATCCTC	CANCTGCATC	TCAAGATTAT	660
	ATATATATGT	TCGAAAAATTG	AANATCCACT	CNTCTAAATG	GTACACNGTC	ATATGAATGT	720
45	GTTTNTTTGC	TCCANTATCC	CNACCATTAC	CCACTCCAGA	ATGGGAATAT	ATGCCAGGAT	780
	NTCCGCCACT	TCACCCTGTT	TTGACANATT	TCTTGAGNTG	CTGACAGCCG	AGAAAAAAGG	840
	TCAAGGTTAT						

## 1360UP

50	GATCGATGCA	AACCAGGACA	ACTACTTAGA	AGAGTGCTTG	AAAAATTAAAA	GTGTATTGAG	60
	TGAATTTGAA	AATGACGTAC	CGGATAAGAC	AGATATCAGA	GGAGTTCTCA	ATCCGGTTCG	120
	AATTGTGGT	TCCCGTGAAC	ATGTGTTCTC	TGAAAAAACC	GGGTATTGG	GAGATCTCGC	180
	GGCTGAAAG	GAGCAAGTAT	TCGGAACATT	CTTTGCACGT	ACCTTTTCGT	ATATGGGTGC	240
55	AAAGTTACAC	TATGGCCATC	CTGATTTTGT	TAA TGCTATA	TTTGTCACTA	CCAGAGGTGG	300

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	TGTATCGAAA	GCTCAAAAGG	GCTTACACTT	AAGCGAAGAC	CTTTTGTGTG	GGATGAGTTC	360
	CATATTACGT	GGGGGTAGGA	TTAAGCATTG	CGAGTACACT	CAATGCGGGA	AAGGCCGTGA	420
	TTTAGGATTT	GGGTCCATTT	TGAACTTCGC	TACTAAGATT	AGTGCGGGTA	TGGGGGAGCA	480
5	AATACTCTCA	AGGGAATACT	TTTACTTGTG	TTCAAATCTC	CCACTCGACC	GTTTCTAGTT	540
	TCTACTATGC	ACATCCGGGA	TACTACTTGA	ATATGTTTCC	AATATCCCTT	CTAACCCCTT	600
	AATTANGNAA	TTTANTCCCG	NATTAATGGC	GGTCCTGGTC	AANCCNACCA	AAAATNTNNA	660
	NATTCTNTTA	ACCCCCAAAN	CTGCAAAATT	TATTGTTGCC	ATTNAACCCN	TAACCAAGGT	720
	NCCCCNTCNC	GNTTNANCNA	TCCNTNTCCC	NCCGGTNCCC	TTCCCAGTTT	TGNAAGAAAA	780
	ATTTAAAAAC	CNACNCCGGG	TTNCCCCGAA	AATGAAACTN	NTANAAGNGC	CCCCTTTCAA	840
10	ATTTTTTTTTT	C					
15							
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## 1362RP

	GATCATAAGC	TATTGGGTAC	CCGTTGTAGC	CTAGCCTTAA	AATAATCGAC	ATTTTGAAT	60
	TTAGTTATTG	CGTGGAATA	AGGTATATAT	ATTGCTTCCA	AGTTTAAATGT	CGCTTTTAAC	120
5	TCACTAAAT	ATGGATGTAA	ATTGTCTCAA	TTGGACTTTC	ATGTTCTATC	TATACACTAA	180
	CTGCGATGCG	ACTCATTGTG	CTTCAGTATT	CAAAACATGT	TTTATATATG	TAATATGCGG	240
	ACGTAGAAGG	CAACTAAATA	TGAGAGGCCAA	CTTAGTCGCT	GTCGCTGTG	CTGTTTGAAT	300
	CGCTGGAATC	TTTTTCATAC	ATGATCTCGT	CGCCATTATC	TTCTTTTAGA	ACGCTAAGTT	360
	CCAAGTCCTT	ATGAGATTCC	TTGTTCTCTT	GAGAGACCTC	GTCATCAAAG	ATGATCTTGG	420
	TGTTGGAAC	GACAGGCAGG	TTTTCTGCTT	GCGACCTGTG	ATAGCCTTCA	CTTAGCAGTG	480
10	ACCCCTCGAG	GGACACCATT	CTGCCCGCAG	CTGTAGACATT	TTTAACAGTA	AATTTGAGTT	540
	TTCCGTCCAG	CTGCTTACCG	TTGCCGTCAC	CCAGTGCCCT	AGAGACCGGG	CCTTGCGCAT	600
	CCCTGTGGAG	AATCGTTTCG	CTGCTCCCGT	TGGTACTCTC	TTCGTTATGA	ATAAAGTCCA	660
	ACCATCCGGA	ATGTTATTTT	CTAATGAAGC	GTTTGAACTT	CGTGATCCAN	CAACCATNTT	720
	GTTGAGGTGA	CNNTTGAAAT	CNCCCNCGA	CNATCCCNAT	TTTNGNGACA	NCCNCAATTT	780
	CCCNCGCCCN	NTTAANCCAG	GNTATCTGNT	CCANTGANTA	CATCTCNCTT	T	
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## 1362UP

	GATCATAGCT	GCAGGCTGCC	AAGCAGACAT	GCTGACATCA	TACAGCCAAG	AGAGCAGCTA	60
20	CGCTGTCACC	GAGCTGGAAC	AGAGGCTAAA	CGAGTTTCGC	ACTAAATGTA	GAAAAAATGC	120
	AAGCCACTTT	CAGGCACTAC	TTTCACTGGT	AACTGAGATA	GACCATCCCG	ACAGCAGCCG	180
	GCTAAGTCAC	CGTACAGTAG	TCTTGACATA	CATGGAATAT	CGCTAAGGAA	GGAGGTGTAA	240
	TAGGACACAA	AATCATGAGA	AGAGTATTGG	CTTGTGCACG	ATGCCGTGGG	CACAAGATCA	300
	AATGCGTGCA	CAACAACGAG	CCACCCTGCT	CTTACTGCCA	GCACAAAGGC	ATAGCGGAGA	360
	AATGCGTGTT	ATCATTTCCG	CCCAAGAAGA	GGCGCAAGAA	GCCGGAACCTA	TACTTAGAAG	420
25	GGGTTGGCAT	GGCGCTGGGC	GGGTATCCGG	TGCAGCAGTT	GGAAACTGCA	GATCTGCACG	480
	AGCATAAAGC	CAGAGCGGAC	GGCTCTGATG	AAAGCCAAGC	TCCTGTGCAT	GCGCAGGACT	540
	ATACGATCGG	GAGCAAGCTG	CGCAGATGTA	CGAGCTGGCC	AGCAGATGTA	CTACGGCTGC	600
	CCAGGCGTAC	TCGACGGTTA	TGTCGAGTAG	TGCGAAGGTT	CCCAGGCGGG	TTGATTCTCC	660
	CGCCAATTGC	CACCCGATT	CTAAACCGAA	ANAATGCAAC	NCATGGAACC	NGCCNTACTT	720
	TNTTGACTG	CCCCCAGTGC	CNATGTCATN	GTGCACTTGC	ATNGAGANNT	TGTCATCCTT	780
30	CCCCACTGCG	NTGTTTANAT	GANACCNCCC	AAGAATACCC	CCTGACCGTC	TTTGGTTCTT	840
	TTTGCCCCCC	NCCT					

## 1363RP

35	GATCATTATC	AGCATTAATC	TTCAACTCCG	CATTGCCTCT	TAAACCAATA	ACAAAACCGG	60
	CAGATTTGCC	TCCAATTGCG	TAAGGATCCT	TTAACCCTTT	GAGGGATACT	TCAAAAAGCC	120
	CTTCACTAGG	CCAGCGAATA	TTAATCTTGG	CATGGAACAT	ATTCTTAATT	TTATCCCGAG	180
	AGCCTATTTT	CTTGGATGGA	TCAACTGGAG	GTTTCGAAAA	ATTGTCFAAA	CAATTCATGG	240
	CCTGTTGTAT	AGCAGCTTCA	TAAGAGCCAC	CCCATGTCAC	CATCGTGATG	TCTTTGAGT	300
	GTATATCCAT	TGTTACCTGA	CTGTAAATTT	TAATAGGCGT	TAAAGACCGG	CGGAAGCGCA	360
40	ACGAATAATA	TAGGCTCTATC	TCAGAAGAAG	TAACGGAAGG	AACAAGCGGC	ACAAATATCG	420
	TTCGTAGCTC	CTTGGTTGAT	TGAATCATAT	CCTCCAGTAA	TAAAGAGGTC	ACCATACAAA	480
	TGTATAGCCG	GAAAAGAACC	TTGTTGGGAA	GGCATAGCTT	CGGCATATGG	ACTAACGGTA	540
	GTNNGGTTAA	CCTTNAAANA	GCCCCCTTAA	TTCACCCANC	TTGGCTTCCA	ATNTAAAAGG	600
	GAAGCCNCCA	NTTATTTCTGG	GTTANTTTTG	GAACCCCNNT	TNCCCNCAAN	TTTAATNAAT	660
45	TCNCNNTTTT	ACCCCTTCCCA	CATNANGGCT	TAAANTNNCA	TGTTTTTACCC	CCCCNGCCAA	720
	GANNNTCCNCC	ATTTTGGAAA	TGTTANANTC	CANACCCCTT	TTNCATNTTN	NAGGANCTTC	780
	AACGTGCNT	TTNCCCCAAA	AANTTAATCC	CCCNAAAAAT	TCTTTCTCTC	TGGGNTTTT	840
	CCCCCTTAC	CNT					

## 1363UP

50	GATCGAGGAT	ATTTCCGTAC	GCTGGATGTC	GCTCGATGTC	AAGTACATGG	GTGATCGGTT	60
	GGCCTTTTCA	GTGTCGCTTC	AAAAATCAA	GCACAATAAG	GTCTGTCTGC	TGAAGTCTGG	120
	TGCGCTCGAG	GTTCTCGGCT	GTTTCACAAA	AGACAGTCCC	TTTGGACTAA	CATGTGTTGA	180
	ACTGAGTGTC	AAGTTTCTTC	AACTCACAGT	GCTGTGAGT	AACCTACTAG	CACTATTTAC	240
55	CTTGGGCAAA	GAAGAAGATG	AGGACGTCGA	AGGCTTTGCT	CGTAATATTT	TCGATGGCAT	300

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	GACCGAAGAT	CCACAACCTGA	ATGCACAGAA	TTGTGTGGAG	ATGATGAGAT	CAAGAGTTAC	360
	CACGTTGCAT	AGCTACTTTT	CCCATCTAAC	TAAGGTTGAT	TTTTTTGTTG	ATAAGGTTAA	420
	CCTGGCAGAT	ATACCACCCA	GCTTATTGCC	TGAGTTGTCA	TCTGCCTGTG	AGCCTTTGAA	480
5	ATACGAAGTT	GCGCTTTCTA	GTTTTACTTT	TCAAGTCACC	CGTTTTAGCA	CCCGAACAGC	540
	CAGGTATAGT	ATCCTTTTCA	AAAGTCTGAT	AGACCGTAGG	GTCCGTATCA	CATTGTCATC	600
	GTTGCAGTGC	GCTCTCAGTT	AATGCCCTA	AAATCCCCCT	GAAAAGGCTC	CTGAATACAT	660
	CCGGTTTTTG	AAGTTCCCAN	TTATATCCAT	ATGGTGANAC	TATACTTTTC	CTGAAAATTT	720
	GACTGGTCCA	CGCTGTTTCT	GANACAAAGT	CAATGGTGGG	CAGTTTCTCC	CCTACCNTAA	780
	NATTGAAATG	AAACCCCCAN	CTTGAACCCC	GTTNGCAATA	CTGTANGACT	ATTTNTTCCN	840
10	CANAACCCCN	CCACGNAN					
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## 1364RP

	GATCAGATCG	ACGTCACGTT	CCGTGCGCTG	GGCACACCTA	CGGACAAGGA	CTGGCCTGAG	60
	GTCTCGTCC	TCAGCGCGTA	CAACAAGATC	CAGGTATACC	CGCCTCCGTC	GCGCAGCGAG	120
5	CTGCGCAGCC	GCTTCATCGC	TGCAACTGAG	AATGCCCTCG	ACCTGATGTG	CGGTATGCTG	180
	ACGATGGACC	CGCACAAACG	GTGGGACACG	ACTCGTTGCC	TGCTCAGTCA	GTATTTTGTA	240
	GAGCTTCCGG	AGGCGACACC	TCCTACGGAA	CTTCCAAAAC	TAAATAAGTA	ATGACTATGA	300
	TAACCTAGAT	GGTATACTCG	GACGTTTTGT	GTTTGTGCTT	TGAGGCGATG	ACATTGGCTT	360
	TTATGGTATC	GCAGACGTTG	CCTGAAAAAG	ATTCAACGTC	TCGGTAACAG	ATTTGCGCAG	420
	ACTACTTGTT	GAAAGAACAA	AGACCAGAGC	GCTGGGATGC	TCACCCCAAT	GACGAACCCA	480
10	CTCCGCTTTA	TTGGCGCTGG	CTGCAGGTTT	CTTAGCACCA	ACAAAGGCC	GCCACTGCAC	540
	AAGACTTTTC	CCTCCAAGAA	GCTGGTGAAC	AGGATGCTGT	TCCGACCTTG	ATAGCCGACT	600
	GACCTTCCGG	AAATTACTTG	CCTTGTATAC	GAGCAGTTGT	ACACCCAAAT	AGACAGTTAT	660
	TACGGGCAAT	TTGTTATACC	CCNCGNCTTG	ANGGCNCCGA	CNTTNTATCC	TGAAAAGNTG	720
	CTNGAAAAAA	TCCCCGCNAA	NGAAAAANNCC	ATCGCCATCT	ANTTGNCTNG	AAACAACTGC	780
	TTTACTGCTG	CCCAATNGAN	ACCAAAATCN	CGGCCGTACC	TTGACCCNT	CACCCGCTNC	840
15	CT						

## 1364UP

	GATCTAGTGC	TTCAACAAGCT	AGAAGCTCCA	ACCATGAAAG	AGCGATCGAT	CCTGAGAACA	60
20	CTTTTTCTGT	GGAGGCTTAT	CAATGCTCTT	TCTATCCGCA	GCTTCTTCCA	GGCAGATGAA	120
	TACTGGCAGT	CGCTGGAGCC	TGCGCATGTT	AAGGCGTTTG	GATATGGTGG	GCTGACTTGG	180
	GAGTGGCAGC	ATGGGCTGCG	CAGCTATGCA	TTCCCCGATGC	TCTTTGAAAT	GTCGTACTAT	240
	GTGGCGTGGA	TACTGGGTGT	GGCCACCCGG	ATGGCGCTGC	AGGGGTGGC	ACATGCGACG	300
	GCGCTGTGTG	GGGCGGTGGT	GCCGAGCGGC	GCGGCGGGCG	TGGCCGCGAT	GAAGGCCGTC	360
	TGGGAGCTGC	CGGAGGCAGC	GCAGGAAGTG	GTGGAGTACT	ACGGGGTATT	GTACGGGCCG	420
25	CGAGTGGTGA	TGGCGGCTGT	AGCAGCGTGC	GGGGAGTTCT	ACAGCGTGCT	GCTGGTGGCG	480
	AAGCTGTATC	TGCGAGTCGC	GGATAAGGGG	GACGACCCAG	AAGGGCGACG	CGGCGCCGGT	540
	CAGCCGGTTG	GCGCTGAATG	CTGACCATGA	CAAACCTCTT	CAACTGTTTC	TTGCGGAACG	600
	CAACGTTTAT	AAATAACCCC	CACNGCGNTC	CCCTCTAACC	NATTTGGATT		660
	GGANCCGGGG	CCCANCTTTG	GTTCTCNTGG	GCTTCCACCN	CAACTTTNGC	GGTGGCTGCN	720
	TTTGCTTGCC	CTGCACGGCC	NATACTTTTT	ATCTTGGCCT	CCCTGCCTGT	TCTTGTGCCA	780
30	ACCTGTTGCC	CACCAAAGGT	GCACTCNNTT	ANCCTGTCCC	TAGGTTGCCC	CGNGCCCCGC	840
	GGGTTTTTCN	ATACCANTNA	NACNCTCCT				

## 1365RP

35	GATCTGCGGC	CGGCGGAAGA	CGCAGAGGAA	AGCGAATCGA	GCGCGGGAGA	GCGCTACTCG	60
	ACGGACAAAA	GCACTTACGC	GTCTTCCGTG	CAGGCGGTGC	TCAGAGCGAG	GACAGCGTCG	120
	GCAGCCAGCG	CAGATACAGC	AATGAGCAGT	TCAACGGCAG	CCAGCGATAG	CGCGGGCGGC	180
	GCTAAGATGG	ATGCAGCCGA	CGCAGATGAC	GCGACGCGCA	GCTTGGAGCT	GCGGCTTGCA	240
	GCCCTCGCCA	CGCAGGACCC	GGCTGTGGAC	AGCGCAGACA	CGGCGAGCGG	CGCGTCGCCG	300
	GCGTCCGCCG	CCGCGCCGCC	CAGCCCGCCG	CCCANCPCGG	CGACGGAGGG	GTCGGACGAG	360
40	GCGGCCGCGC	CGCTGGAGGT	GCCCAAGCAG	CGCGGCGACG	CGGGCACGGC	GGCCGGCGGC	420
	GAGCCGCTGC	GGCGGCGGCC	CACCAACCCC	TTCCGCGTGA	TTTCGGTCCG	CGGCTCCAGC	480
	ACGTTCAAGC	GCGCGGCGGG	CGCGGACGGG	CAGGCGTCGC	GCACGTCTGC	CGCGGGCGAC	540
	AAGGCCGCAC	CCGTGTCCGC	GAACGAGCAG	AGCATGCTCA	AGTTGCCGCG	CNAGCNCANC	600
	TACCTTGACC	ATGAATTCNT	CNACTGTTC	AAGANATTAA	TTTCCTGANA	ACNTGAANAA	660
	ANCGGTCCCT	GTNCTTGAAG	AAANCCCCCN	ANTAACNACC	CCCTNGACAG	CTCNGATTTT	720
45	CTCCNCCTTA	TTNTAAAAAA	TTTCAAATNC	GGGTGGTNCT	TCCCCCNCTN	CCCAACNTTT	780
	TAAAANGTTC	CCACGGCNTN	NTGNNCCCN	NATTTGGCCC	CCCGTTCCNT	TNCCCNNGT	

## 1365UP

50	GATCACGTGA	CGTTCATGGA	GCGTGACGCA	CTGCACGACA	GCGAAGCGGT	GGTGCGCGCG	60
	ACGCGGCGGG	CGGCCGTGCA	GCTGTATGTG	GGGCGCGGGG	GCGGGCTGCG	GGGGCGCCTG	120
	GCGGAGGCGC	TGGACGAGTT	GCTGGGCGGA	CCCTTAGCGG	CGAGCCCACT	GCGGCGGGCG	180
	TGGGATGTGT	ACTTTATGCA	GCTGGCGCGG	CTCGCGGCCT	CCCGTTCCAA	CTGCATGAAG	240
	CGGCGTGTCT	GGTGCGTGAT	TGTGCGCGCC	TGCGCGCTCA	TTGCCACCGG	GTATAATGGG	300

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	ACGCCGCGCC	ACTTGCGCAA	TTGCCACGAC	GGCGGGTGCG	CGCGCTGCAA	CGGCGGCGGC	360
	AGTGCGCTGC	ACACCTGTCT	CTGCTTACAC	GCGGAGGAGA	ATGCGTTACT	GGAGGCCGGG	420
	CGGGAGCGCG	TGGGCGAGGG	CGCGGTGCTG	TACTGCGACA	CCTGTCCGTG	TTTGACATGT	480
5	TCGGTGAAGA	TCGTTCAGAC	GGGGATCACG	GAGGTGGTTT	ACTCGCAGAC	CTACCGGATG	540
	GACAGCGACA	GCTTCAAGGT	ACTGCGGGCG	GGCGGCGTCA	GGTCCCCGGCA	GCTACAGGAC	600
	GCGTTCCCCC	GCACTTTTTA	TTATATNNGC	NGGCNGCTTT	CCCNGCAACN	GCTAAACTTG	660
	CTGTTTTTNC	ATATAAGGNC	CCGGCGGTNC	CGACTNCAAA	GNAATNCCNC	AACCNITCTT	720
	TNTTCCGAG	GCNGGGGAAT	TTTCCCCGGA	TNTNNGGCC	CCCCCGTNN	TGCCGTTACC	780
	CANTTCCCCT	GCCCAATCCT	CCCCGCGAAN	CCNCCNCCAA	CCGTCTCGNN	TTNCTCCACC	840
10	CGNCCTGNCC	T					
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## 1366RP

	GATCCAACGG	TCAACCAATG	CCTCCGAGAT	TGCCGGCATA	GCGGATGAGA	TTGCCAAAGC	60
	GGAGAAGCAG	GACAGCTCCG	CGGCGGTGTC	TGCCATGGGT	GCCGTCTTAG	GGCATGCAGC	120
5	GAGTCCTTTC	GGTGCTTTGA	ACGTGCTTAA	CAGTTCTGCC	GAGCTCTTGA	ACCAGCCGGG	180
	AGCAAAGCCT	GCTGCCGGTG	CTCTCAAGGG	CATGATGGAG	GCTGCGTCTA	ACACGACTAA	240
	GGCAATTGAC	TTCATCATGG	AGCGTGCAAG	TCATCCAAAG	GCTGGCGCGG	CAGAGCAGGT	300
	GATGGGTCTA	GATATGGTAC	TCCAGAATGC	CGTGAACCTA	AGCGAAACCT	TTGCAAAATAT	360
	CATAAAAATG	CAGATGGCAT	CGACCGAGGA	GTCGCAGAAAG	GCCCTCCCAA	GTTTGTGTGGG	420
	CTTGTTGTCTG	TACTCGACTG	ACAAGATCGA	GAGCATGAAA	TCCGTGATTA	AGCTGATAGA	480
10	GTTCCGGTGAA	AAGAGCCCTG	ATGTATTGAA	TCCTGTCTTA	GAAGTGCTGC	AAGCTTCCGT	540
	GAAGGTCAAC	AGATTGATAC	CCTCCGAAAG	AATTTTNGAC	TTACACCCAC	ATCCTGGAAA	600
	CTTCATNTTT	GCTGCGAGTT	ACAAACTGGC	ATTTCCCAAT	CTGCCATTTG	TTCCCTTAAC	660
	GGNCCCCAAA	GGTTTGACA	CCNCNNTCCT	NCAGGNTTCA	ATNCCTACTC	CTNTNNCCNA	720
	CCNANGAATC	CNNTTGGCCC	TTNTTTAANN	CAAATCNGNC	CANATNTACC	CCCAGGTTTTT	780
	TTTGTGGAAN	CCCTTTTANA	CCTTTCCCCC	CCTCCCTTTN	NAT		

## 1366UP

	GATCTTATCA	GGATAAATGA	TTTGCTCCCC	GAAAGTCGAT	AAATTGCTCA	TATATGCCCT	60
	CTGGGGGAGA	TAATATATCG	GACTTTTCGCC	ATTTTCAGCA	TTTCTACGCG	GCATGATTAG	120
20	CTTCGTAGGC	TTCTTAGGGT	TAGTAAACGA	TTGCAAAACA	GGCCACAACC	CCCCAAGGAC	180
	CCTGAAAAGA	GAAGACTTGC	CGCAGCCATT	AGGACCTATA	ATCAATAGAT	GGTTACCATG	240
	CTTCAACTCG	AAGTTAAGTT	CGGGGATAAG	GACCTGATTA	GCAGGTGTCA	CTAGTGGAAC	300
	ATGAACGAAT	TGAATCTTAG	AATCGTCGTA	TTCTATAATG	ACCTTTTPTCC	CATCAGTCTT	360
	CGAACTACTT	CCAGCGTCTA	GCCTGTCAAT	GAAATTTGTT	AACCGTAGGG	CCTCTCCCTT	420
	TAGCTGCTGG	ATACTACGGC	GCAGTTTCGAC	ATAGCGGCCA	ATAGATGCGG	ACGCAGTTAG	480
25	CAGTAAACGT	CTGTTGGTGA	TAAAATCAGC	GGTGACATCC	TCAGCCATAT	TAGAACGAAA	540
	GAAGACGGGG	ATAGAGCATA	ATATCAAGCC	CAGCAGCGCC	CCAGACGTAC	TTCAACCAAA	600
	AGCTAGTACA	ATTCGTACAG	TGCTCTTAAA	TTTATCTCCC	CCGGCTNAGA	ATAAGTTACT	660
	GGTTANAAAN	AAAAACCCAA	TCCCATATTC	GGTNTTTGAC	CNTGAATAAA	CNNTNCCNCN	720
	TTGCTTGACC	NCACTTGAAT	TTATGACCGA	ATTACCNCCA	TTTTCCCCCTG	ACATACCGTT	780
30	CAATTGNNNG	TTTGACCTCC	CACTNATTAT	GATTNAAATC	AACCCATCCN	GTCCTTCNGC	840
	TTTCCCTTGGN	GATC					

## 1367RP

	GGATCCGCCC	CCGTTGCCCC	CGTGTGGCCC	CGTGCCCGCC	GCCAGGGCCT	GCGCCGCGCG	60
35	CAGGCCACCC	GCGCCTCCGC	CGTGTGCCCC	TAGCGGATTG	TTCAATCCCT	GTGTTGCCCT	120
	CTGACTGTCC	ACTCGACCTC	TTGTATCCGC	ACCTTTCTGC	CAAGTGCGCC	CCAAACTCTG	180
	TTTTCTGTGC	TGTCCAGAGT	TTCCGTCTCT	GGCTGCGCTA	CTGCCTACCT	GCCGTTTGGT	240
	ATGGAGGAGA	AGTGTGTGTG	TATCTGATTT	GTTTATCTGC	TTTCCTTCTC	CTATAAGCTT	300
	TTTGTAATGA	AAAAAATTAT	GAAAACGGGA	AATCTGTGGA	ATTTGGAAAT	GCTGCTGGCG	360
	CTGCGTTGTT	CAACTTCCAG	CGCCGCCGTC	TCGTTCTACT	GCTCTGTTCT	TGGTCTAGCT	420
40	TTCCGTTATTT	TTTCTGCTCG	GTTTTCGCTTC	TTTTTTCTGC	AACGCAAGGG	CGCGCTGCGT	480
	GCCTGAGGTG	CCAGGTGGCT	GCACAAGTGC	GGGCGCCCGG	GAACCGAGCC	GGGTAGTTAC	540
	CGGGCAACTC	TGCCGCCGAT	CCCTTGCGGA	GGCTTACGGC	AGCGCTTATT	TAATTGTTAC	600
	GTAAGTCACG	TGGAGCTAGC	ACGTGCTTGG	CAGCTCAGCC	GCACGTCACG	TAGCGTGTGA	660
	CTAATCGCGG	CGACCTGGTG	GGTTAAANGA	CGGGTTACNC	CGTTAAGTTG	GAAACGCNCC	720
	AATAAATTAC	NTACCCNTTA	AACACACGGG	ANAAAAANAN	NCCCGGCNCA	NAAGNANCTT	780
45	TTGCCCTTGA	AGCCCGGTGC	CCCAAGCCCG	GNCNCCCCCA	GAAN		

## 1367UP

	GATCTTATGG	GTGGTTCTCT	AGGGCTGAAA	GGCGGATATG	GACAGTCGAA	ATGGGCAGCA	60
50	GAATTTATTA	TAAAACGTGC	AGGTGAGCGT	GGGTTACGCG	GTTGTATATT	GAGGCCAGGC	120
	TATGTGACTG	GTTCCCTTTC	TACAGGAGCT	TCTAACGCGG	ATGACTTTCT	GCTCCGGTTC	180
	CTACGGGGAT	GTGTTCAATT	AGGCAAAATT	CCTGATATTG	AAGGAACTGT	TAATATGGTA	240
	CCAGTTGATT	GTTAGCAACG	GTTAGCAACA	GCGGCTTCCT	TCTCGTCATC	AGGCAATACA	300
	CATATGATGG	TTGTAAATGT	CAATGCGAAA	CCAAGAATAT	CATTCAGGGA	CTATCTACTA	360

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	GCACTGAAGG	AATACGGGTA	CCAGGTAACA	TCAGTTCCTT	ATGACGAGTG	GAGTAAGGCG	420
	CTTGAATCGT	CGAGTGATGA	AGAAAATCCT	TTGTATCCGC	TATTGTACCT	TGTCCTAGAT	480
	GACTTGCCCTA	AAAAC TGCGC	AGTCCTGAAC	TCGATACTAC	TAATGCGAAA	TTTGTTTTAG	540
	AAGAAGATTT	TGCGCGGACG	AATATTGAGC	CAATTATCAT	TACTTCGGTG	TCATTAGAGT	600
5	TGTGGGTCCC	CATATCTCAT	TTTTGCATAA	TTTAGCTCCC	NANAANAACC	ACCTAAAGTT	660
	CCCAGCCCCT	GCCNATATTC	NCTCTCCCGA	CGAACAAATT	CCTTAATANC	NCATACCNCT	720
	GCNCCGAACA	TACANCAACC	CNTAAATACC	NCAAATTGTN	GACAACATGA	NTGTTTATTT	780
	TTTTTATATT	ACAACCTATT	ATTAACCAAA	TTNTNATCAC	GATCNTCTNT	GACGCCCTCT	840
	CTGACAAATT						
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## 1368RP

	GATCATCTGA	AGTAATATAG	AATCTGCATG	GGCGCAAACC	GTTGCGGTCC	AATGTAGCGC	60
	CGGTGTAGCG	GCCATCGGTA	AAGGTGAGCA	ACGCAGGGCC	ATCCCATGGT	TCCATCAAAC	120
5	AGGCGGCCCA	GTCAAACCAA	GCCTTCAGGT	TAGAATCCAT	GTCCCTTGTG	TAGGCTTCTG	180
	GAACCATCAA	GCACATCGCT	TCGGGTAATG	ACAGAACACC	ATTTATCACT	AGTAATTCTA	240
	GCACATTGTC	CAGCGCGGCA	GAGTCGGATC	CGCCTTCTTC	GATAATCGGA	TAAAGCTTCT	300
	CCAGTTGGTC	TTGGAAAACG	GCGGATGCCA	TGACACCTTC	CTTCGCACGC	ATCCAGTTTT	360
	TGTTGCCCTCT	TAGGGTATTA	ATTTACCGT	TGTGTGCAAG	CCAGCGCAGA	GGCTGGGCAC	420
	GGTCCCAAGA	TGGGAATGTA	TTGGTTGGAG	AAACGAGAGT	GTACCAGCGC	CAGGTGAGAC	480
10	TTGAAATGAG	CATTTGGTCAA	GTCGTGGTAA	TAATTATACA	CCTGGCAGGG	TCAATTGACC	540
	TTTGTACACA	ATTGTCCGGT	TATTTAGGAG	CACACAGTTA	ACAGTCTCTG	TACCGATGGC	600
	CGTTAAACCC	NNCTTTCTTT	AAATNTTAAA	CTGGCATCCN	GAAGTCTCTC	GTNATTANCC	660
	TGAATCTNCN	CCCGATACTC	CTGCCCATAT	TTCTTTTCNCN	CAACAACGTT	TTTGAATG	720
	TTTCCCAAAA	CCAAGGAACC	NAAAGAAATN	CTNTGGACNC	CTCCAACCCN	AACCCNNATT	780
	TAACAATCGG	TACTNGCCAA	TTTNTTCAAG	CNNAACCTGT	NNNCT		

## 1368UP

	GATCGTGACG	ACTTTGTGTT	TTACTTCAAC	CGTATTGCAA	CGATCTTGGT	TTGCGGGGCT	60
	TTGGATGACA	TTGCTATCGT	GCGGGATGAA	CTGCCATTGG	TGACTGCATC	CGGATATCAA	120
20	CTGGAGAAGC	CTGTTTCATGT	GAATTTTGAC	AAGATTACGG	CTGTGAATAT	TGTGCGCTCT	180
	GGCGACTGTT	TCATGGCTTC	CCTACGCCAA	ACAGTGCCAA	ATATATCCAT	CGGTAAATTG	240
	CTCATTTCAGT	CTGACTCTCA	AACAGGTGAG	CCGCAGTTAC	ATTGCGAGTT	CTTACCAGTG	300
	AACATTGGCG	GCTCTTTTCGA	CCAGGTCCTA	TTGATGGATG	CACAAATAAT	CTCAGGCGCA	360
	GCAATTATCA	TGGCTAITTCA	AGTGCTAGTT	GACCATGGTG	TTGAACTATC	AAAAATAAAG	420
	GTTATTGTCT	ACTTAGCCAC	TGAAATTTGGA	ATAAGAAGGA	TAATAAATGC	CTTTAACAAC	480
25	AAAGTATCAT	ATATGCGGGC	GAAATTATAT	CAGACGAAAG	TATGACAGAT	GGCCAATGTA	540
	CTGGGCGAGG	GTGAGATTCA	TCGACTCAAG	ATACTTTGGC	TGTGACTGAT	TCAGAGCTTT	600
	TGCTGCCCCAN	GCAGGAATTA	ANAACTTTTG	GTGCTATTGC	ATGTTACAAT	ATTAGCATTT	660
	ATCATCCATA	CCATAGCTGC	TTTACNATAG	CATNTAATTT	TACTATCTTT	NAACCCACCC	720
	AGACTATTTT	TCCCCCNCNTA	CTTTACNAAN	ANTTTAANCA	ACTGACCCCC	CGNTATAATT	780
	GCCCATCCAA	CACCCCCCNC	CTCNTAANAA	ANACCNACTT	GGAACGAGTG	GGAACCNCC	

## 1369RP

	GATCGCCTAC	TTGTCTCAGG	AACTTGTATT	CATGAGAGAT	GATATGTGCA	ACAGGTTTTAA	60
	GCGCAATAGC	ATTATTTTCC	CAACAGTGGA	AGAGGAACAG	AAACAGGAAT	ACATGCTGTT	120
35	ACAGCAGGAG	CTCCAGGATG	ATGAACGTAG	TTCCGATCTC	TCCATTAGTC	AACTGATTAA	180
	GTCCAGGGAC	CAATTGCCGTG	CCAGTGTTCA	GGAGTCCAGG	AAGATAGTCA	AAACCATCCT	240
	CGATCAGCAA	CACCTTTTCGC	CCTTTACCTC	GCAGGTGCGC	CCTATAACGT	GGGACTATGA	300
	CTACACGTTG	CACCTGTCCC	CAATACCCTC	CACATATGATC	ATTTGCGACC	CAACTGCACC	360
	GAAATATGAT	GTTACTTTACA	ACGGCTGCAA	GAGTATCAAT	CCAGGCTCAT	TTCTCCACAA	420
	GCGGAGCGTC	AACTATACTG	AGTACACTCC	TTCTGTTACGG	AAAGCAACAG	AGGAAGAAAT	480
40	TGTCGTGTAG	GACTTTAAAC	TTACATATAA	TGTCAAATAT	AAAGGTTTCA	GACGTCGTCA	540
	TGTTTCGTAT	GGATATTTCT	TGAACTTTTC	CCGTAATATC	GTATGGCATA	CAGTAGAGGG	600
	GGTCAATNGG	AACAACCCGN	CGTGCTTCTT	CAAACCTGGNC	CCCANNCAAT	CCCAAAAAAT	660
	TNTGGAAAAC	TTCCACCTAG	ATTTTCTGGC	CATCGCNGAT	GCCCNCCNCT	CTTTGATTCC	720
	TNCANCCCCA	GANNAATCNC	CCNCTTTCTT	GNTCATCCAT	NCCCNNTNGC	CCAATTCCNA	780
45	NCGTAAANG	CCCCCCCCNC	TTTTCAACTT	TNGGATTTTN	NTNGTTTCCG	TCGGCINNCC	840
	CCGTNCAGAC	C					

## 1369UP

	GATCAAGACG	AAGCAGAAGA	AGACGCGGTA	CGCATGTACG	TGCCACCTGG	TGCCGTCGGA	60
	GGCGGCCAAG	GCGATCGCTC	TGGAGCGCGA	CACGCGCCTG	GGGCTGGTAA	TATGCGTGGA	120
50	CCCGACGGTG	GACACACGGG	CGCCGCACAT	ACAGAGCATT	CTGGCGCAGC	AGCAGAGGAA	180
	GTACGGGCGC	ACGGTGCCAA	CCATCCGTGT	GGCGGTGATT	AATTCGATCG	AACATTGCGA	240
	GTGTTTTTTC	GGCAAAACGC	TCGACCGGAA	CACACGGGAC	TACCTGGTAA	ACGTGAGCGC	300
	TGCAATGGTG	GTGTTGCGCG	ATGTGGTGGG	GACCCTGCCG	CCCGACCTGA	GGCCAATATA	360

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	TTCGCAAAAC	CTGAGGTACC	TGATAGACTG	GTGGGATACC	CCTGAGAGGC	CATGGCCGTT	420
	GCCGGACTTC	TATCCGGTGA	AGGTATACAC	TGCAATGGAC	GTGGAGCGCT	CGCTGCTGAC	480
	CGAGGTGAAA	TACTCCCCAG	AATAATGACT	CCCTTGGAGG	ATGCGTTTTA	CCAACGGCAA	540
	GAAACTTACC	ATAGTTCCNT	GGACAAAGGA	ACCGTGGAAA	TGCGCCGATC	TCCCTACTAC	600
5	CCAAATAAGC	GTTTGTGAAA	ATGACTACAT	TNGAATCCCN	CCNACCAAAA	TTGAACACTC	660
	CCCGGAANNA	NCATACNAAN	CCAAAAGTTT	GCTAAATATC	TCCTTCCNTN	GTACACTGAC	720
	CCCNACTNNT	GCAGGGAAAG	GNCTGTTTTT	AAACTTCCAC	TCNGACTTNA	TTTACCCCT	780
	CCCNGCATCC	ACCNAANCAA	CACCTNTTCN	AACCATAGAA	CNNTTTTCCT	TTTAAACAC	840
	TNAGAAGCAT	TTNAAAAT					

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## EP 0 866 129 A2

## 1370RP

	GATCTTGTAC	AACTGAGCCT	AGGTCTTGTT	GTTGAACGGT	AACCTCCACA	TTCATTATTG	60
	GCTCCAATAT	GGAGAACGCC	GAAGTTGGTA	AACTCGTCAG	TGCTGATATG	ATTAAAGGAC	120
5	GCACAGTCAG	CAGAATGGAT	GCAGCTGCTG	CGCAGTCTAG	CGGTAGCCGC	CAGCGTTTAA	180
	CATGAATCAC	ACACGAGTGT	AGAGGAAAGC	CTGCGGTTTT	ACCACCTCTT	TGCAAGCCA	240
	CTATGCAACA	CGAGATGATA	GAGTTCACGA	ATGCCTCATA	TTTCAATGGA	AATGGCCAAT	300
	TGTCTTCGTT	AAAGCGTGGG	TTTGGATCTA	TGACAAGATA	GTTATTATCG	CTTCCCAAGG	360
	GGTACCATCC	GTTACTGAAT	AGTACTTTAT	CTTCTTCATT	GTATTGCCGA	ACTTCGAGTT	420
	CGAACGAATA	TCCATCATCT	GTTTCAGAGT	GCTTCCTCTC	TGTAGCAGTA	TTAATGGTTT	480
10	CCTTGTATGA	AACTGCTACC	TTGCCTACTC	TTACAGGCGC	CTTAAATTCA	TTGAGCAGCC	540
	GTCCGCTGCT	ATTTCCAGTG	CATTCCCCCC	ATCCCATTCA	TCACTGTCTG	ACCAGTCTCC	600
	TCATCCCTCA	CNAATACCAC	NACGGTTCCC	CNCTCGTTAG	CTGCNNCANG	ATCACCCNAT	660
	ANCCTTTTNT	TCCCCAANTT	CCCCGGTCCN	NCANCGNCCT	AAAANGGTGG	NGGTANTCAT	720
	GGGTNTTTCC	CANTTGNANT	TCNGCTTTTG	AAAAACAATC	CCCTTTAAGN	TNNAAGNCNA	780
15	AANGGGTTCC	CTTCTAANTG	TGTCCCTTGT	GGCCNCNNC	CCCAATNCCG	AGAT	

## 1370UP

	GATCGCAGAG	GAGGAGCCCA	TTCCGACGCT	TGCATGGAAG	GAGGACACCT	TTGAGAATTT	60
	TCTGGCGGAG	GTGACATCCG	ATGAGGCGCG	CGAGACGCTG	GTTTCCGAGG	AGGATGCCGC	120
20	CACCTACCTG	GCCAAGCTTT	TATGACGGCT	GTCCGTGCTT	TTAAATTGTT	ACATACTGTA	180
	CATATTGCTG	TTAGTCGTAC	CACATTTTGA	TCAGCTCTTC	GGAAACCGCG	CTGGGCGTCA	240
	GCACGCCCAG	GTCTGTGATC	AGCGCGGTAA	TGTGCTCGTG	CGAGGTGTAG	TCGATGGACG	300
	GGCTTAGCAG	CTGCTCTGAC	TCGTGCTGTC	GCGAGAAGTC	CAGCGGGTCA	CGCTCCATGG	360
	GCAAGTCGTC	GGGGGAAAGC	GGGAACATCC	TTACAAACTT	GTGCGATTTC	CTTACCACGT	420
25	AGAATGGCTT	GCGTGCGTTC	TTGGCGAGGA	CCCCTACCGT	GTACGTCCCC	ACGAGATTTA	480
	TGATGCCGCC	GGACTCGGCC	ACGCCCCCTC	CGCCAACCAG	CACTTGTCTGA	TTTGTGTAT	540
	GATGGACCCA	CCGCGCTGTC	CACGATCATC	GTCACCGGAT	GCCCTTTGCT	TGCAGCAGGT	600
	CATACAGCTG	CTTGCCCTGC	CCCGAAGGCC	CGTGCTCCGT	CACGANACAC	CGGAAGCAAT	660
	CACTCTCACC	TGTTACTCAC	ACGAAANNCG	CCCGCAAACC	AGTTCCCAAA	AAGTCTCCTC	720
	TGTTAGATCC	NCCCCATCTT	GTNCTTTTTN	TNGACGCTTG	CCCGAANCAA	AACGTCCNTT	780
30	CCNCNGTTGC	TGCTGNACCC	CCCTCCCANA	TNTTTTTTCC	CCCCCNCCC	NATTTCNTCT	840

## 1371RP

	GATCGAGAAC	AACTACGACA	ACAGCCACGC	AGACGGCGCG	GAAGCGCTCA	AGCCGAGCTA	60
	TATTTTGTAG	TACCTTGCCCT	CGCTCATGTA	CCAGCGCCGC	TCAAAGCTGA	ACCCGCTCTG	120
	GAACGCCATC	ATCGTCGCCG	GCGTCGAGGA	CGGCCAGGCC	TTCTGCGGTT	ATGTGGACCT	180
	CAAGGGCGTC	AAGTACTCCG	CCCCAAGCTT	GGCTACTGGC	TTTGGCGCCC	ATATGGCCAT	240
	TCCTCTCATG	CGTAAAGTCG	CAGATGCCGA	AAAAGACGTC	GCCGGCGTCG	ACCTCTCAAT	300
	TGCGCGAGCG	ACTATCCTGG	AGTCCATGAA	GGTGTATTTC	TACCGCGATG	CGCGTAGTTC	360
40	CCGTGCGTTC	TCGCTTGCCA	TCATCGACAA	TGATGCCGGT	GTCAGCATGG	AGCAACTGGA	420
	AGTGGAAC	ATGACCTGGG	GGTTCGCCAA	GGATATTCCG	GGCTATGGCA	CCCAGAATGT	480
	CTGAGTACCG	GCGCGCAAGC	GCCGCACCTG	TATACTATCT	TGTCGCGGCT	GCTCGCCAAC	540
	CGCTGGCTAC	TCACATACAT	ATCAAGATGC	ATAATCAATC	TGCTCATGAA	CGCACCTCTG	600
	TTTTGTGGAT	ACTCTTCTCG	CGCGTATCCT	GAGTACGCTG	GAGTGCAAAA	AGAGCCACTT	660
	TGAAACAACA	CGAGTCGCAG	CTAAGGNGAN	ATCCGANTAA	NCAACNCACA	CTTCAATTGA	720
45	CTTATGAAAT	GCCCAAGGTT	GATTGAACTG	ACGTCTTTGG	AACNNTGGGN	CGTGGAACG	780
	CCCTCTTCAN	TTGAACCAAA	GTCCACAANN	AGGTATTNT	TTNAACCGTT	CCGCC	

## 1371UP

	GATCCATTGT	GCGTTTGGAG	GTCACGCCAC	GGACGTGGAC	ATGTACGTGA	TGAGCTTCGA	60
	CGGGCAGCTC	TTCAATTCGTG	CGGCACGCCA	GAAGCTTGAG	TTCCCGACGT	CTCCGCGGGA	120
	GAGTTGGGCG	TACCTTGCGT	ATTACAGCGG	ATACAAATTC	GAGCGCATGG	CGCTCCTGGA	180
	CCGTCCGGTG	GCCGAAACTC	CGCGCGAGGT	TCTGGAGAGC	CGCGGCAAA	AGGTGCTCCG	240
	CAACGGTCCG	CAATACAGGA	CTGTGATGAG	AACCGGCGTC	GGGGAGCACA	AGCTGGTGCT	300
55	CGGAGCTGAG	ATCGACGGCA	TCATTGACTT	CCGCGAGCCT	ACGGGCGACA	ACCTGAAGCA	360

CTACGTGGAG CTGAAGGTGT GTCAGAAGAA CCGGAAC TTCAGAGAAAC TTTTCTCTTC 420  
 TTGGCTGCAA TGCTTTCTGG TGGGCATAAA CAGGGTTATT ATTGGATTCC GGGATGAGAA 480  
 ATTTCGTCTG AAGAGCGTCG AGGAGTTTCGN TACGTCAGAG ATCCCACACC TGTAAAGGG 540  
 CACGGAATAT TCCAATGTAT GTGTGGACGC AATAGAGTGG TATGGTGCTC TTACGAAGTG 600  
 5 GCTATGTGAG CTCCGCGGGG CCTGAANACA CTTCAACTGT ACAGCTCTCC NGCTCCCNTG 660  
 GTGCTTACGT NTGCNCCCCT GCCCNACAAT ACTCCCNAN NGGGACNATT NTCCTGTTTG 720  
 TTCCCCAATT GGCGCGGGCC CNATATAANN CANATTCCNN CNTTNTTTCC CTTNTGNTTT 780  
 TAAAAACCCN TTNTTCCAC CNATTTNCCC AGANNACANA GGNNTTCCCC ACCANNCTTN 840  
 CCCANCCNCA

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## 1372RP

GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGT 60  
 ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT 120  
 15 ACAAAATAATG AAAAGAAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA 180  
 TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240  
 TGTACATGTA ATAGCATTAAT ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA 300  
 TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT 360  
 CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420  
 GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480  
 20 GTTAAAAATA AGATAATAAC ACCAACTGTT CATACAATA CTCTAGGTGA TTTATAAGAA 540  
 CCATAATATA AACCTTTACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA 600  
 TTAAGATGCA TATATCTAAT TAATCAACCT AGTTGTACTC TCTCATAATA TGTTCTACTG 660  
 ATGANAAAGC TAATCCATAT TANATGAATA AGCATNNCTA AAAAATACCN GTNAGAATTG 720  
 AATACTAACN TAACCTATAA AACCNAATTC NTCCATATAA TGAGAAGGTG AGGGAATCAT 780  
 ACNACTATAA CNATTTAATA TATTGATTCT ATTNCCATT TMTNTNAAT TTTTC

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## 1372UP

GATCTAGAAT TATTAAGTCA ACTATTAAC TATATCTATA ATAATAATGG TTTATCATT 60  
 AAATCATTTA AGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA 120  
 30 AATTATGTTA ATAAAATAAA TAAATATAAT TTACTAATTA ATAATAATTT AAATAATAAT 180  
 AAAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATTCCT 240  
 AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTAAA GGGTAGACTA 300  
 TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT 360  
 TATATATATC AATGAAGTAA ATTAATAAAT TTATATAAAT TAAATTATAT ATCACTTAAT 420  
 ATTAATAAAC TTAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAAATTTAA 480  
 35 TTAATACTA TTTAATAAAT ATTCTAAAGT AATTTCTTAT TTATTTTATA ACATTTTAAA 540  
 ATGTTTATG TTAAATAGAT AATAATCAAT TAAATAATAA AAATTAAGAT GCCACAAATA 600  
 ATTCCATTTT CTTTATGAAT CAATTAACCT ATGGTTTCTA TTTATTTTAC NATTTATCNC 660  
 ACTACTNATG TTTTPTTACC NNTGAATTTN ANAATATATA CTCNCNANTA NATATTNCNA 720  
 AATTATAATA TTAATTAAT TTAATTAATC TATTATGATC CTNNTTNTAA ANATATCAGA 780  
 ANAATTTAAT ATATATATNG AAATATNTTT ATCCCCNGG NCACCTGAAN AAAANTATAG 840  
 40 TTTTNTCCCC ACAT

## 1373RP

GATCTTAATT TAAAATTTTA ATTAAC TATT TATAATTTAG AAATATATAA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180  
 ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTAATATT 300  
 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
 50 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
 TTTTATAATA TTTATTTTAA TTAGTCTAGT AATATTCTAT TTAATAGTCT ACCCTTTAAT 480  
 TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAAT ACTTAAATCT 540  
 AATAATTTAT TATCTAAAGT ATATAAATTA ATTAATCTTT TTAATTTATA TTTAAATCAT 600  
 TATAATAAGT AAATATATTA TTATTTTATT AACATAATTT TTGATAATAA TATACCATTA 660  
 TTAATGGNNN TTATAANAAT TATCTTNAAG GATTTNNTGG AAANCCTTNN TTTTAGAAAT 720  
 55 TNGGTAAANG TGNNCTAAAN NCCAATCCCN AATTATTAAA TTAATTTAAN AANAANNANC 780  
 CTTTNTTNA ATTTAGTTTN AATTTAACCC NCTCCCTNT TTAANAT



## 1374RP

	GATCAATGAT	AAATCGAAAT	AAACTGATAC	TATTGTAGCC	ATTTTCTGA	ATTAGCACCT	60
	GGAAACACTT	TTTAACCTGT	TCCGGAGTGG	TCTCTGACTG	ATTGGAGTTG	AGCGTCTCGC	120
5	GCGTAACTGC	CTCTGCTGTC	GTCTTAGCTC	CGACGTTTTC	CACTGCCCCG	CGCTGGGTGC	180
	CCACACGCGT	CTTCTTCTGA	ACTGCGAGTG	GCCCCAACAT	GTGGTCCACT	AGCGTTGGTG	240
	CGCCGCCAAG	TTGCTGGAAT	AACGCACCCA	TCTTAAACCA	GTTGAACTGT	GCAAAATCTC	300
	CATACGCTTC	GAATTGCCTG	AGATAGGAGT	TGCGCTGCAT	GCTCTGGCGA	AGAGCAGCAT	360
	CCGCATGCTG	ATTGGTGCTC	TCATCTAGAG	CGTCGCTGGT	AGCATCTCCA	TCATTTTCGA	420
	TGCTGTCTGT	CTGGGTATTG	CTAGCATCGT	CTGTTTCCGG	ATACATAGAG	CCAGGTACAC	480
10	TCACTGATT	CAACTCAAGG	TAGTCTTCCA	GCAGAAACCG	CTTCGCCCCG	TTGACAAACT	540
	CCTCAGGGCT	CAAAAGCTTC	CCGCATTTG	TCAGTTTTAG	ATTGCGTATA	CTCAAGCTTG	600
	CAAGTCGCTG	ACGCTCATCA	CGGCATGCGA	ATCCTGGGCA	AAAGAGAATT	GACCTCAGTT	660
	CAATCGCCCC	CCCTGCTTTA	AAAACATATT	AACTCTCCCN	CCGCNCNCAG	GANAGAATNC	720
	TCCCGTACTT	CNANGNAGNC	ANCTNTGCC	NTCATCTCAA	ATTGCGNACC	TNGTNANTTG	780
	GANCCNTTCC	CGAGCCCCCT	TGCCCCCCTA	TTGANGNTCG	NCCCCGTTCC	A	
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## 1374UP

	GATCTTAAAG	GCGGATATAA	AAGCTGTACA	AAAGAAGATG	AACAAGCTTC	CAACGCTTCT	60
	AAACTTTGAT	ACTTCCGCCA	TTGCCTTGGA	AGATGAAGGC	GAAACAAAAG	AAAGTACCGA	120
20	ATTTAGGGCT	ATTATTAAAG	AGTTTGAAAC	ACAAAATAGT	TTCCAGAAGA	TTTTATATGG	180
	GAATTAATAG	ATAAGACTAG	CATCTTTTCGA	AAACTTTATA	TAAACCAGGC	AGATTAGCTA	240
	CCTCTACAA	GTCTTCAGA	AGTCTCGTCG	ACGCTAGGAG	TCGCCTCTTT	ATCGTTGGGA	300
	AAACCACTTG	TTCCAGAACT	GTCCCAATAT	GCTCTGCCTT	GGAAATATAA	TAAGCGCGAA	360
	CATCGCCATC	GATTGTGTCT	TCGTTTATAT	CTACGTGCTC	AATAATCTCA	GGAATATAGA	420
	ACAAGGCAAG	TTGTGGAAGG	ATTCTTTCTA	GGCACTCCTT	TTCCGACGAC	CAATCTACCT	480
25	TAGTTCCCAT	TCTGTAGAGG	AAAAATGGAA	GTTTAGAAAG	AGGCGGGACA	TAACTCTTTA	540
	AAAGTAAGGG	TACACTCTTA	ATGCCAACGT	TCGTCAAATC	GGTCTCGTCT	CCACATATTT	600
	CAATCGAGTA	ATAGTTCTCT	AGCATTCTCT	CATGTCCACA	CTGTTGAGTT	ATTCCAAATA	660
	TCGAATGCGA	CGCATATATC	ATCTTAGATA	NCGTTGGTAT	ATCGCTAACT	TCCGCAATCT	720
	CAACNCANC	CTNGATATNA	TTTCCCGAAN	TTTGNNAAATN	NNNATCCCAT	TGANAAAATT	780
30	CCTTCTTTAG	GACCTATCAC	CCAAATANTT	AACGCGGNTT	NANGATCCCT	GNTTGGTCAC	840
	AACNCNNGGT	CTTNNN					

## 1375RP

35	GATCTTAATT	TAAAATTTTA	ATTAACATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
40	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCTTTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCT	TTTTTATTAT	TATTTAAATT	600
	ATTATTAATT	AGTAAATTAT	ATTTATTTAT	TTTATAACAT	AATTTTTTGA	TAATAATATA	660
	TCATTATTAA	ATGGTAATTT	ATTAATAATT	ATCTTTATGA	TTTATGACAA	CCATATATTA	720
45	TAGANATTGT	TAATAGTTGA	CTAATATCCN	ATCCAACCTN	TATTNATTTA	NAGATCATAN	780
	ACCTTTTATA	CAATTATTTT	NATATAACAT	NTACCTNATT	ANAATATN		
50							
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## 1378RP

	GATCCTTATA	AAATGGGCAA	TAGACGTGTT	ATAATATAAT	ATACAAAATT	ATAAATAAAT	60
	ATTTAATAAA	ATATAAAAT	AATAATTAAA	GTATTATAAT	AATTAATAAA	ATTATTTATT	120
5	AATAAGTATG	GATTTTAAAC	TGAAATTTGT	TAAAATGAAA	TAAGAATTGC	TAGTAATCTA	180
	TTAATAAGAA	AGTAATGGTG	AATACTCTAA	CTGTTTCGCA	CTAATCACTC	ATCACGCGTT	240
	GAAACATATA	ATTAAATAAA	GAATATTAAAT	TAATTTATTA	ATTATTAAAT	ATTATTAAATA	300
	TTATTTAATA	AATATAATAA	ATATTTTAAAT	TTAAATTATG	AATTAATGCG	AAGTTGAAAT	360
	ACAGTTACTG	TAGGGGAACC	TGCAGTGGGC	TTATAAATAT	CTTTAATATT	CCATTTTTAT	420
	AAAATAAATA	TATTTTTTAA	TATATTTTAT	AATAACTATA	ATTAAATAGT	TAAAATTTAA	480
10	ATTATAATTT	AATAATTTAA	TAACTTATTA	ATTAGAGAGT	TAGGGTACAT	CCCCCCTAAT	540
	GCTATGCATT	ATGGTTGGTA	CACTCTAATT	AATAAACTAT	AATAAATAAA	TACTAATATT	600
	TATATCCATN	AATTATAATT	ATTTTAAANA	NATTTAATAT	TATTAATGAA	ATATATAATA	660
	AGTATTNTNA	TTTINATAATA	ATAAAAAATGA	NAAAAACGACC	CCTAATAATA	ATTTGCATTT	720
	ANANTTACCC	TTACACCTCC	CNTTAAATTT	TTACCCTNAT	ANCCNTNTTA	ATTAAGGANG	780
	GNGNNCCCCN	TGCTCCCCNN	TGTCCCCCCC	ATTNNANTTT	A		

## 1378UP

	GATCCTTGCG	TACTAAGAGT	TAGACTTTAA	TTAATAATAT	TATTTGTAGA	AGATAGAAAC	60
	CATACTGACT	CACGTCGTAT	TTAACCCAAC	TCACGTAACC	TTTTAATTGA	CGAACAGTCA	120
20	AACCCTACTT	AGCTGTTACA	ACCAAGAGGA	TAGGTTGAGT	CGACATCGAG	GTGGCAAACA	180
	TAACCTACAA	TAGCTACTCT	ATCGTTATAT	TACCCTGTTC	AATTTTGTTA	TCATAATAAC	240
	ATTTAATTAT	TATTTCAATA	ATTCTCATT	TTGTTTCAGAC	TATTTTCATTA	TGTATTATTT	300
	ATTAATTAAT	ACATATTGGG	CTTTCGTGGA	TATAATPAT	GTTAATCCTA	CTCATATATC	360
	TAGTCGTTGA	ACGTTCTTAT	AACTTTATAA	AAAGGATTGT	TATAAGCTTC	GCTGCAGATT	420
25	GTCCTTTATT	ATTATAAAAT	AATATTAGGA	GTTCTTTGCA	ATTAACCCAA	TTTACTCAAT	480
	ATATTTAAAT	ATTGATAAAT	AAATTTACAC	ATTTAATGGG	ACTATTAATT	AACCCTAGCG	540
	TAACCTTTAT	TCGTTATCAA	ATACCATTAC	AATATGTATA	TTTGTTCAT	TATGCCAAAC	600
	TTACGTTATT	GTTCTACTTG	TAGGTATTAC	AATTATAGCA	CAGTTATACC	ATTATATTTA	660
	TTTATATATA	TCCCATATAA	GTTTTTATTA	ACATATAAAC	TGTNCATTAT	TTATCTNTTT	720
	TATATAAAAT	ATNATTATAT	TAATNATTTA	TTAANATTTA	NACCCNTATA	TTAAATATAA	780
30	TCNTTTTAA	TAATAAATTA	TTAAGGACTN	TCCAACCTTT	TTGAAAGACC	CCCCACTNCC	840
	ATTAATGTGC	NT					

## 1379RP

35	GATCCAATTC	TCTCGGTAGT	TTCTTCCAT	ATAGAGACTG	ATCAACTAGC	CACATTCCCA	60
	CAACAAAAGA	GTTTCTATCT	AACGTGCCAT	CGCGTCTTGT	ATCTACCATG	TCGTAGATTT	120
	GAGCCAAAGT	ATCTTGAGGT	AGATTGCTTC	GAGACCAGAT	ATCTGTAACA	ACTAAGTTCA	180
	ACATTAGACC	ATCCTCTGGC	ACCTCTCTTG	TCTCATCGTA	GTTACCGTTA	TTCCACCATG	240
	GGAGCAAGTC	AAGATAAGTG	TCTCTATTGC	TGACCCACAT	TCCCTCGTAA	CGCTTTCTTT	300
	CCCTTTCAGT	TACGTACCCA	ACATCAAGGT	GCGACTTCCA	AGGTTTGTCT	TCGTTGAAGG	360
40	AATTACGGTA	TCGAAGATTT	TGACGTATCT	TCTCGCGCTT	TTTGCCGGAT	CTTCTTCTCG	420
	GACTTCGACT	ACGGGAGTTG	CGGTGCGTTC	CGTAATCCTC	TTCAGAGTCT	TCGCTGTCAT	480
	CGCTTAGTTG	ATGGGGCTCT	GAGCTGGAAC	TGTCATTAAAG	TATACCCCGC	ATAGTGTTTT	540
45	TTAGCCGCAC	ATGCAATTTA	CTCTGCACGA	GAGCGTTATC	GTTCTGCGTA	TATATATGTG	600
	ACGTTGGCGG	GTGATTCTTG	CTGGGGCCTA	GCCCAGTTTG	CCCATGGCGC	TTGAAAGCTT	660
	CATCCACTTG	GANTGCTGCG	TTGANANTTT	GGTATTAAATN	CAGGAANATT	CCTCCGTAGT	720
	CCAGTTCATA	GGAATTTGTT	CATGTCAATT	ACAANCTTTC	NACGGGAATC	TTTTGCGACT	780
	CNTGTACAGT	CGANGNATNT	GTCNTCCGTA	CANCTCCCGA	TNCNCCAAAN	TNNCCNCATT	840
	CNCNN						

## 1379UP

	GATCCGGAAG	TTAACACTGC	CTGGGATTCA	TAAC TTGGCA	ACAGCGTATG	TGCGTGTGAA	60
	CATAGTCGAT	GGAGCACATG	AATTGGGGTA	TCAATAC TGA	TTTCATAATG	CTTTCTGGAG	120
5	CCATTGACCT	TGCGTGACAA	CCTCAAACAT	ATTTGGAGCC	AATGGTTGGA	CTTTATGTGG	180
	GGAGATGCAG	TATTCCGATG	TATGCACTGT	TGGTAGTTCA	ATCTTTCCGG	GACAAAAACC	240
	TGGTAAGTGA	ATTGTCTCTT	TGAAGCGCCA	CCCGCTCCAT	CATCCAGCAG	GTTTCCTAAG	300
	TTTTTAGCAC	GCGAAAGGCT	CGCGCCTTCG	TGTATACCCT	TAAGTGGTGG	TGCTTTGTGC	360
	TCGACCAGCA	AGAACTTCTT	TGTAGGCTCC	ACTCGGTGTA	CTTTCCGACC	TTTACAATAA	420
	TACTCTAAAG	TTTCCGTCAG	GAATATTCTA	ACCTGTGGA	GCACGAGATT	AGCCCGTGGG	480
10	TTTAGCGAGA	GCGATATTGG	TAGAAATGCG	TCCAAAAC TA	TATCTTTCGA	TGCAATTACG	540
	ATTTACATAAC	TCAATTCTTT	TTCCCAGTCA	CGTGATATGA	CTATCGGTTC	GGTATCTTCT	600
	ACAGAGTTCC	GAGATAGTGT	GCGGATAAGT	TAATCGGAAC	ACGACGTGGA	CATTGGACTT	660
	AAGGTCCTAT	GCCCTCAATG	TCACTCAAGC	AGGTATTTAC	GTTCCCNATG	TTACTAGAAT	720
	CTTCTTGCTC	GACNCCGGAN	TNGANCCCCA	AGAAAAATA	TCCCCGCCNG	AAAANAATTT	780
	CCCTGGNGTG	ACGTGTGNAT	NACCCNACGA	AAACNTCCTC	CTTCGAANGT	NCCTTATATT	840
15	CNNTNAAANA	ATANA					

## 1380RP

	GATCGCATCG	ACCTCGCCAA	AGTAAGGCAG	GCTCTCGACG	GAGATCCAGT	CGACAAGGTG	60
20	AGGAAGCGTG	GTGTTCTTAC	CCTCGAACAC	AATTGGCTCC	TTCTCGCCCG	GCAAGTGGAC	120
	CGCCAAGGTC	GGCTTCTTAG	TTGGGTACTG	CACAAATACA	AAGTCGTTCC	GGAGCAGGTT	180
	GGCCAGTTCC	TAAAAGGACT	CGTTCAGGCC	CTTCACGCCA	CCGTCAACCA	CCACTGCGGT	240
	CTTGGACTCC	GCAAGCAGGT	CCTCCAGGTC	CTGGGCGGCC	TCCTTGCCCT	CCAGCACCGT	300
	CACGGCCGGC	TCGGCCTGGC	GCAGCATGTA	CGCCACAATT	TCCTCGGCCT	TGCGTGCGCC	360
	CGTGTATGGC	ATGCCCTCCT	CTGACGCCCC	ACTGTGGAAC	ACCTTCAGCG	TCGGGTACCC	420
25	GCGCACGTTT	TGGCCCGCGC	ATAGATCCAG	CTCCTGCTCG	CAGTCCACCT	GCGCCAGCTT	480
	GATGCCCTTC	TCGGCCAGCT	CCCCAGCCGC	CTTCACGTAC	TCCGGTGCCA	GGTGCTTACA	540
	GTGGCCACAC	CATGGCGCAT	AAAAC TCCGC	CATCACAAGC	GGGTTCTCCT	CTAAGAACTT	600
	CCCGAACGTC	TCTCCGGTCA	ACTTGACACT	GCAGAGTCCT	CTGGTGCACT	GGCATCTTGG	660
	GCCTGTGCAA	CTGTGCCAGC	AACCGGCGAT	GGACAACACA	AACCGCTTGT	CCAAAANCNT	720
	TCTCGTGCGG	TCTATCCTAC	CCGTGGTTTN	GTGNACTCTG	TGGCGATCAA	ANCCGGNTNG	780
30	CNATTTTGT	TTTATACTGA	TCCAGAATTC	ACCCTNTCNC	AAAACNNTTN	CCNGAAAAGA	840
	NCNGNTN						

## 1380UP

	GATCTCGCCT	GTTGTGAGTG	ACGCCGAGTT	GCGCGAATTG	TAGCAGTGCG	AGAGGAACGT	60
35	GCCGACGGTA	TCGTTTGCCA	GCGCGACAAC	GCGCACGCTG	CCCAACCCGA	CCGCGTCCAA	120
	CTGCTCTGG	TACATCTTGA	CCACGTCCTT	GCCGATCGCA	TCCTTGATGT	TGAAGCCCTT	180
	CGTCCAGCGG	ATCAAAGTGC	CGCTCGATAG	CGATGTCTGC	GCCACGGGAT	ACGAGAACGT	240
	AAACCCGAGC	TTCACTTGGC	CGCCCTCGCT	CTGGAGCACT	TCAGAGTGGT	AGCGCTTGAC	300
	AAACGCCATT	GTGCGCTTCG	CGATGAAGCC	GAACAAC TCG	TCTGATGTTA	CGTCGTCTGC	360
40	AAGGAGCTCC	TCGGGGATCT	TCGACTTCAA	CTGCTCCAGC	TTGAACGTGT	GATCACC GTT	420
	GAGACGCACC	GAGCACACCC	GGAAATTCGT	GCCGCCAAGG	TCCGCCGCCA	AGAACGTGCC	480
	CTCCTCAGTG	CCATTGGGCC	TGCCCATCAC	GTACGACGGG	ATCATCGGAA	GCCCACGGTA	540
	CTCCCGTCCG	TCTCTCCGTT	CTTGAGACCT	GTTCCATACA	TTCGATGAAG	TACGCGGTCA	600
	ACTCGCGGAG	TTTGTCTCTC	GTCACCTCGA	AATCCTTACA	TATTTCTGTC	ACTGCTCCTC	660
	GACTTTCCCG	CGTTGCGCTT	GTGCAAATCT	TCNAAAANAT	CCTGGTACTG	TAAANATTAG	720
45	ACTTCGANAC	GTTGGTTCGAG	TCTTTCNNGC	TTNCCTACTC	NCCNGCCNTG	TCNTANTATT	780
	TTGANGGCGN	TCCAATAAAA	AACCCTTTNG	GGGGTCNCAA	GNGACCTCCC	ACCCTCTTTT	840
	GTTTCCCCNT	CCCNNAATGA					

## 1381RP

	GATCATTATA	TTATAAAATA	TAATAAAGAA	TATATTTAAA	TAATAATAAT	AATATGAAAT	60
	ATTATATTAA	TTCTCCATTG	GAGCAATTTG	AGATTAGAGA	TTTATTAGGT	TTAACATCAC	120
	CAATAATAGA	TTTATATTTT	ATTAATATTA	CTAATTTTGG	TTTATATCTT	ATAATTCTTT	180
55	TATTAGTAAT	TTTACTAATG	AATTTAATAA	CTAATAATTA	TAATAAATTA	GTAGGTTCTA	240

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	ATTGATATTT	AAGTCAAGAA	ATAATTTATG	ATACTATTAT	AAATATAGTT	AAGACACAGA	300
	TTGGTGGTAA	AGTATGAGGT	TATTATTTTC	CATTAGTTTA	TACATTTTIT	ATTCTTATTT	360
	TTACTATAAA	TTTAATTAGT	ATAATTCCTT	ATTCAATTTGC	TATAACTTCA	CATGTAGTAT	420
5	TTGTAGTATC	AATAAGTATA	ATTATTTGAT	TAGGTCTAAC	TATTATTGGT	TTTTATACTC	480
	ATGGTTTAAA	ATTCTTTGGT	TTATTTTAC	CACTAGGTAC	ACCATTAAAT	TTAGTCACCA	540
	TTATTAGTAT	CAATTGAATT	ATTATCATAT	TTTGCTAGAC	TTATTTCAAT	AGGTTTAAGA	600
	TTATCAGCTA	ATATTATAGC	TGGTCATTTA	TTAATTGTTA	TTTTAGGTGG	TTTATTACTT	660
	AATCTAAANC	CACAAATATT	TAACNTTTTN	TTAAGTTCNN	CCNATGAATG	CTATTINAGT	720
	ATGTNTGTTA	GAATTTNTAT	CTTATACCNG	CTTANINTGA	AGTNTNAATA	CNCCNTATNA	780
10	AAC TATTTAT	TCCTTATTAA	ATTAACANTT	NAACNCCCNA	TTANTTTNTA	TNCTT	
15							
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## 1381UP

	GATCATTGTC	CAATATTCCC	CACTGCTGTA	TCATATAGAT	ATTGATTATA	ATTTCTAAAT	60
5	CAACGTGATT	GTTCTAACTT	TAATTAACAA	TTATGAATTT	TTGGCTAGTT	ATTATTTTTT	120
	AATTAACATA	TACCTAAATC	ATTATAAGCT	TGACTTAAAA	CAAATAATTA	TTACATTATT	180
	CTTTATTTAT	TATTTAATAT	TTAGTTAAAT	TTTAAGTTCA	TTATCTTAA	TTTTTACTCA	240
	CGAGTACACC	ACTTATTAAT	ACTATTAATT	AATAATATTA	ACGTTTGATT	CGCATGTGTA	300
	ATGTCCCTAG	TTAGCGCTTA	ATCTGAACCA	ACATCATGTT	CTCATTATTA	TTAACTATTT	360
	TTAATTATTT	TAAATAATTA	TTTAATACGA	AAGTTATAGG	ATTCGAACCT	ATGAAATCAT	420
	AAAGATTTAT	AATAGCTCAA	ATATTACACT	TTAAACCAC	CAGTCAAAC	TTCTTAATAT	480
10	ATATACCTTA	TATATGGTTT	GATAATTTAC	TTATAATATA	TAGTATATAA	TTTAATGATA	540
	AACCTCTTATC	ATTTAGGTGC	GTAGGGTTCA	CCCCCCTATT	GCTAGTCAGC	AATATGATGT	600
	ACCTCCTAAA	TGATAAAGAA	GTATAATATA	TAAATATTAA	TATTAAGTA	TTTAATGAAT	660
	ATTATTTTAT	TTTATTTAAT	TATTATTTTT	ATTTAGTAAA	TAAATAAATA	TTTCCACTTA	720
	TTGAAATATA	GGTCTTNGA	TTAGAAATAA	GCNATNATAA	TGTNCCATTG	ACTATTAAAT	780
15	ANTGTGCTCN	CNNGACTTCC	CTATTTNCCN	NNGANAANTC	NGAANATCAG	AANANAGATT	840
	CCNANATNNT	TAATNNNCCC	CCA				

## 1382RP

	GATCTCACAC	GTGACTAAAA	TCACTAACAC	CACGTGACTT	CGTGCACGTG	GCATCGTCCC	60
20	ATTCTGTGCG	TCGCTAGCAT	TCTGCCC GCG	CATCTGTGTC	AGGCCACTGC	GCAGCTGACC	120
	ACGCCGTACC	ACGGCAGGCT	TCACGACAGA	CGGCAAGCTC	AATCGCTATC	TACGGTTTCA	180
	GGTGGAATTT	CTTACCGGCA	TCCGATTAAT	TGCTTTTTTG	GCCTCTTTT	GCCCCCTTT	240
	TTCCAGTGGG	TTGCTTCTCG	AAAACAGGGA	GCTAGCTTCC	CGTAGTACGT	AACAGTCTGA	300
	GAGGGTTAGG	CATCGCTGAG	CTCGAGACCC	GGTGATGCAA	TGTGCACAA	CCTCGTCTGC	360
	GCAAAACGGG	CACGAAGATT	GAAAGTATCC	AGGAGTGCAG	CCCAGGGTCA	TGCGAGACAG	420
25	AATGGGGCCAG	AAAAAGCGAA	AAAATGGACG	ACGCTTTTAT	ATATATATGT	AGCGAGGCCG	480
	GGCGTTCCCA	GAACGGGACC	CGACACAAC	TGTTGTAGAA	TTTCTATCTG	CAAGGAATCA	540
	AATACAAAAT	GGAATCTAGA	TTGGGATGGC	TAACCTGTTT	GAACCTACGAC	ACTGGTTCTG	600
	CATTGAGAAG	AACCTCATCA	TCCGGACAAT	GGTCTTAAGA	CCAACCAACC	AGANACTTNG	660
	TGGANCTTAA	AAAGGNGGGT	TGAACATCCT	GAGAATGAAC	TTCTCGCNCG	GTCTTACAAT	720
	TNCCACCATC	GGTGNTCNAA	NACCCNNAAT	TCGAGATTNT	NCCNGTTAAC	NTTGGCCTTG	780
30	CTTTGAANCC	AAGTNCCTGA	ATNAAATGTN	CCTNTCGAAA	NTTANTACCN	TCCCCTACCC	840
	AAANC						

## 1382UP

35	GATCTATAAC	AGGTGCCAAG	TTGGCAGATT	TGTTTCAGGG	GCTCGACGAT	GTAGAGTCCA	60
	GTAGAATGCT	CTGTAACCCC	AGAGCATACT	TTGCGCGAAA	GTCTTTATCT	GTTGAAATCA	120
	ACTGGGGTAT	CCGCTTTGAT	GCTGTCCCGG	AGGTTGATGC	CTTTCTTGAT	CGCCTTGTC	180
	AGTATCTGGT	TGGTAAGCTC	AATGAGCTCC	GCATGACCAC	GTCCCATATT	GTTTTGAAAA	240
	TAGCACGCAG	AAGCAGGGAT	GCCCCCATCG	AACCCCCCAA	ATACTTGGGC	ATGGGTGACT	300
	GTGACAGTTA	TAGTAAATCG	TGCAGATTAG	GTCTTGCTAC	CAATATTCCT	GGGGTTATAT	360
40	CTGCAGAGAT	AAAGGCAGCT	TTTTCGATGC	TATGCTGCCC	CGCAAAGGAA	CTGCGTGGTA	420
	TAGCCGTTCA	GTTTCTTAAA	CTGAAGGAGG	CATCCATTTT	TCAAATGCCC	CGTCAGCTCA	480
	GGTTTCCATT	TGGTACAATC	AGACCTTTAA	CAACTCCAAA	GAATCGTATC	ACAGCGTCGG	540
	TTACAGAATT	GCCACCTGTA	GTTTATAAAA	GGGCCACTCC	TATTAAGGAT	TTTTTTGACC	600
	GGCACAAGAG	GACTCAGATT	CACCATCACC	TGATTCACTC	ACATGATGTC	TGCGTCAGCC	660
	TTGTGCGAGT	CATTCTGGT	GGATTACCTA	CGATCTTGCG	GAATAATCCN	AAAAAACATT	720
45	GACNATCTNA	AACCAGACTT	CTTTNTTGCN	ATTCCCAAAA	AAATTGGGNN	GNGCCCNNGT	780
	TNNATCCCAN	CATGCCCTTA	AAATTTAGAT	CCTTGACCCT	ACTCCNANTT	GNTNCCCNAA	840
	AAAAAACTA	TCAATGTNTN	CT				

## 1384RP

50	GATCTGCATC	GCGTCCACCG	TGGACTGGGC	GGTGGTGGGC	GGTCACGGAA	AACTCGGCGG	60
	ACTCGGTGAT	GGTGCCGGCA	AGCGTCTCGT	AGCGGATGGG	CACGACCTTC	GCAAAGTAGG	120
	AAAAGAAGTG	GCTATGGCCG	TTCCGGAACCT	CCATGGCGCG	GCCATTGAGC	GGCCCGGGGT	180
	TGCCGGCAAT	TTCCGGGCCA	AAGGAGAGAC	TATGGATCAC	GTGGTTGAAG	GAGAGATGGG	240

55

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	GGTGTTCCTT	GTAGAAGGAA	TCGTGCTGGG	CGTGGCCCTT	GCCAACGTGC	GCAGAGCCCG	300
	GGCCGAAGTG	AATGTTCCCG	TGAACGCGGT	TGAGCTGCGC	GGTGCCAGCG	ACGCGGCATC	360
	CCTCGTTGAT	CTGCTCCTGC	AGGCGCTCCG	TGTAGCCCTC	GCGCTTGAC	TGCTCAAAGC	420
	CTTTGCCATC	GAAAGTGGCC	CAGTTCATCT	CTGCGTACGC	CGCGCGCACC	TCCCCGCACG	480
5	TCTGACAGCA	CACGCGCTCG	CTGCGCGGCA	GGTTCTCGTT	CTGGTCCTGG	TCGCGTGCGC	540
	CATACACGGC	CACAGTAGTC	TTGGTCGTCT	GTAGACGGCA	ACGTCTCGCC	ACTCGGAATT	600
	CCTCCTTCCC	CACGTCCGTC	CNTGTTTGTC	CACCNTTTTT	CCTTGATCCT	CCTCCAACNA	660
	ATTCACTGTG	CTCCCTGTTC	TCTNTANNTC	CATTTCATAC	TCCCCCGGAT	CTTGCAAAC	720
	TATATCNAAC	CCCACTCCNC	TCTGCTGCCG	TCCTTCAANC	ACTGNGCGTC	TCCCTCCCCA	780
10	NTTCCCTCCT	ANCAANACN	CGTTCACAAC	ACCNCNTATN	CCT		
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## 1384UP

	GATCACTTTG	TTTGTGTCTG	CACGATAAAT	GGCCTCGGTA	CAGAGTTTTA	CGAGTGTTC	60
5	TTGGCTGAGA	CCGGACAGGT	CAATCTCAGA	GTTTTTACTA	TTCATTAGTG	AGTAGATTGA	120
	CGCGTAGTTA	TTATCAAAGG	CCACCGGGGA	ATTGTTAAAG	AAGTTGGAAA	CAGATGATTT	180
	CGACATGGTA	TAGTTCTGTA	GCTTAATTAG	AACGGGCAGG	TCTGAGCTCT	CCGCGACGGG	240
	AGTACTGTTT	TGAATGGGTG	GCACAGCCAG	TGGCGGTTGG	GGCGTGACCA	TGCCAAGCTG	300
	TGCGCCCCGCT	GTCAGGCCCCG	CTGGTACTGG	AGCCGGCACG	CTTATCGGCG	GGTCTGCTGG	360
	TGTCGGCGAT	TTGGAATAC	GGTTGTTGCA	CGCTGCTAGG	TATTTTTTCG	GCTCCGCTGG	420
10	GCTCATCTTC	TTCTCGGTCA	AAGCAGGGTC	GAAGTTCAGA	ATACCCTTAC	TCTTCGTCTC	480
	CTCTGCAATC	ATGTGCAACG	TTTGCGCGAT	CTTCCCCAGC	TTGTGGTGAT	AGGGCGCCAG	540
	GTCGCCCCGAG	TTCCGGATCA	GCTGCGCTTT	CATGCCAAAG	TTAACGAAAT	TCTTGTAACA	600
	CGGTTTCGACG	CAGCGCTTCC	CAAGCGGTAC	CGCAGCGCAA	ATCGTTTTTC	TGCTGGTACT	660
	TGTTGTGAT	ATTGAATCNA	ACAGGCCCCC	CAATAANCCT	GTCCACGGG	CCCCGTTCC	720
	GANNAAACCA	GCATCACACC	GCNAAAAAAC	GGGCCCCACN	CGTCGTCAATC	NAACTTACCC	780
15	CTCCAGACTG	NNTATCCANN	GCATNCNCCT	TTTTTNTCCC	GTGTNTCTGA	AANTNCNAAG	840
	CCCCCACCT						

## 1385RP

	GATCGACCTC	GTCATCATGG	GCAAGCAGGC	CACCGACAGC	GACAACAACA	ACACCGGGCA	60
20	GATGCTGGCG	GGCCTTCTCA	ACTGGCCGCA	GGCCACCAAC	GCCGCGCGTG	TTGAGCTGGA	120
	CCGCACTGGC	ACGCGTGCGA	CCGTACGCG	CGAGGTTCGAG	GGCGGCGAGG	AGGTCTGTAG	180
	TGCCGCGCTG	CCACTCGTGG	TCACCACGGA	CCTGCGGCTC	AACACGCCGC	GCTACGTCAC	240
	GCTGCCCAAC	AAGATGAAGG	CGAAGAAAG	GCCGATGGCG	AAGCTCAACC	TGCGCGCGTT	300
	CCCGCGCTC	GACTCGCGG	CCCGCTCAA	TCTGCTGCGC	TTGAGGAGC	CGCCGCGCG	360
25	CGCGCCGGGC	ACCGTCGTCG	CGTCCGTGGA	CGAGCTGCTC	GCCAAACTCA	GGGAGGCCAA	420
	GGCCGTTTAA	CACCTATATA	AACTAACAGC	CCCTATTTCC	TCCGCGGACG	CAGCGTCCCG	480
	TCTTCCAGCA	GCCCCGGCGG	CTGCTTGCGC	AGGTACGTCT	GCTCGTACCA	CGCCTCCAC	540
	TCCCCGCCCT	GCGCCCGCGC	CTGCTGTACG	CTCTTCCAGC	ACGCGCCGGC	ACTCCTCGTC	600
	CCACGCCGCG	AGGTTGCTCC	CCCGGTCGCT	GCCGCCCGCG	CTATCTTGCA	ACNCCGCCAG	660
	CTTGCACTTT	CGCCCCGCCC	CCCCGCATGT	NNCCCNCCAA	CNCNTTTTTA	CACNGGATNT	720
30	TNCCCNNTTG	TTNTCCNTNN	NTTCCNCCCC	GTGGAANTGN	TTTGCCNTTG	CTTGANAATG	780
	CTANCCAAAC	CCCCAATTTG	ATNGNGCCCC	CCCAAAATNA	ACTTTCCACT	TTGCCGAGAC	840
	CCCGCCCTGT	NCCCTTNTTT	AA				

## 1385UP

	GATCCTTGAG	GGCTGGTTCC	TGGGCTTCGA	GCCCGCGGCC	GAGGCCGAGC	TGCGCGCGCG	60
35	GGCCGGGACC	TACGGCGCGG	CCGCGCTGCG	CGAGGTCAAC	GCGGCGCTCG	AGGACTACTC	120
	TGCGTGTCTG	TGGCGCGCGG	CTGGCGTGCC	CTCGGTTCGG	ATCGTGTTCG	ACGCGCAGGT	180
	TCGCGAGTGC	GTGGCCCGCT	GGCGCATCCA	GCAGGAGCAC	GAGCTGCGCG	AGCGCTGCGG	240
40	CGCGGCAATG	ACCGACGCGC	AGGTGCACGC	ATTTCTGGAG	CGCTACCTGG	TGTGCTACGA	300
	CGTCTACTAT	GCGCGTCTGG	TGCGCGAGGG	GCTCGGGAAC	CTGCACCGGC	TGACTGTGGG	360
	GCTGGACGGA	GACCGAAAAG	TTACGTATGT	TAGCCAGAAG	AATATGTAAT	GCCGAGTCTA	420
	TAGTTTCTGG	TCCGAGATGT	CCTCCCAGGG	GATGAGATAG	CGCGTCTGGT	GCGCCTTGTC	480
	GCGCGTGCGC	GCGGCGGGGC	CCGGCGGCGA	CGCGCGCTGG	CGCGGCGCCA	TGCTGGGCGG	540
	CGGCGTCGAC	GGCAGCACGC	TGCCGCCGAG	CTCGTCACGT	GGCGCGCCAG	GAAGGCCTCC	600
	GTCTGCGCCT	GGCGCGCGCT	CAACGCCTGC	AGTCGCGCGA	ACGCTGCCCA	NCACGTTTCT	660
45	CGCGCNGTCC	ACTGCNCGGG	ACTTNTTAAA	CATCCTGCT	TTCTTGGAAT	CCTTGAACNA	720
	NCGCGNGTTC	GCTTNTCNAC	TNTNATGANC	CCCCCAAACC	CCTNTTTGNG	GGCTGCGGGC	780
	NCCCCGCCCC	NNNNCTCTCG	CCNGGTNNNG	TGTCCTTNAC	CCTNCCCCCT	TNCNTTAACC	840
	GTNTANNNTN	N					

## 1386RP

	GATCGCACGT	CATTTTACCT	ACAGGCTGGG	CTTTTGAAGA	AGACGCCTGC	ATGGTACAAT	60
50	GTCTAGCCCA	GGATCCCAAC	TGTGACCAAG	TTCCGCCAGAG	AACCGAAGCT	GCATGACCCA	120
	GTTAGCGGCA	AGTACAAGGG	CGAGCTGGAT	ATAATGACGG	ATAGATTAAA	CAGAAACACA	180
55	GAGACGTACA	AGACACGCGC	TGGGAGTTCC	GACCGGCAGA	CGGCCGCGGT	GCACAAGCCT	240

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	TCTAAGCTGC	GGTTTATCGA	GGACAAGCTG	CGGTCGCTGT	TTTTCCAGCA	GCATCCCTGG	300
	GAGCTGTTCG	GGCCGAAGGT	GCTGGTGGAG	AACATGGGAA	ATGAGCAGTA	CGACTGGTCG	360
	CGGATGTTGC	AGCTAGGCAA	GCCGCTTGAC	GGTGAGTCTG	TGGTGCAGCG	GACGCTGTAT	420
5	CTGCTGAAGT	CGGGCGCGCA	CCGGGAGATG	CTGGCGGCAT	ACGACCAGGC	GCGGTTTGAG	480
	TTCTATCGTC	TGAGGATGCA	GCAGGAGCTG	GAGGAGCAAA	TAGCGTACGA	GGAGGCCACG	540
	ATGGTTGGCG	CTGTGTTCAA	GACAACCGCT	GTGGAGCACG	GTCTGCAGCA	AGAGCAGAAG	600
	GTCTTCGACA	GTGGAAAGAA	GACTTTGTTG	CCGGGTTTGC	CCTGATTTTT	GCNAAAAAAA	660
	ACTCTACAAA	GCAGTCCNTG	GGCCNAACCC	ACCGAAGAAA	AAGAAGAACC	AGGACNNTGC	720
	CGAACCCNAA	GACNCCACCT	GTGNACTCCN	TTGCCAACTT	TGTTATAAAAT	TCTTACNNTT	780
10	TTATTCCCTT	NGTACAATNC	NANNTACTGT	TNTGTGCCAT	CATGTGCCCC	AACAGGTTCC	840
	CCCCNTTGA	NAAANGC					



## 1386UP

	GATCCATGCC	TCGTTATAAC	TGAGCAGAAG	TGTGCATGCG	AACAGAGGCG	TTTCCTTGTT	60
	CCTTGCCAGT	TCCCCCATTC	CCCAAGTTGC	ACTGCAAAAT	GTGAATCATT	GATGTCTTGT	120
5	CGTCGCCATC	GGTGCGCTGA	AAGATGCTGT	TCCGGTAGAC	CGCATTCGT	CAAGCGGAAC	180
	TCTAGGCGGC	GCCGTGAGAG	TCCAGATGAT	GAATCTGAAG	TTGAGGCCCA	GCACGTGTGC	240
	TTAAAAGATT	GTAATCGGGT	GCTGCTTTGT	GGTATCCACA	TGTGCAATTA	CAAATGCCAT	300
	GCAGGCAAAAT	GTCCTCCCTG	CTTAGAATCA	GATTCCAATG	ACCTTATCTG	TCCCTGTGGT	360
	AAGACAATCG	TACCAGCCCC	TGTCCGTTGT	GGAACAAAGC	TCCCTCGCTG	CACTCATCCA	420
	TGTCGAAACT	CGCTGCTGGA	TACTTGGCCC	TGCGGACACA	GTCCACCTTC	GCATAATTGT	480
10	CATCCCTTAG	ATGAACCTTG	CCCCCATGTA	CCATCACAGT	CAAGAAAAC	TGTCGCTGCG	540
	GTAAAAACGA	GATCAGGACA	TTCTGCTACA	ATGATGATGT	TCGTGTTTGA	GACCGTGTA	600
	GAAGCCATGT	CCTATTGCAA	TCACCTCTGC	CAATTNCCTG	TCATTCCGAT	GGCAATGCCA	660
	GCAAACTTGT	TAGCAAGCCT	GTGGTCNACC	ACCGAAAGCC	GCACNTGTTT	GTTAGGGAAA	720
	TGCNTGGCNT	NCGNATGCCT	GAATCCCTGT	NCNAAAAAAA	AANCNCCGTC	CGTTGTCCAT	780
	CNCCACCAAT	NTGCNTGATT	TGCTGGAAGA	GAANGTTCCG	ACACCNCCCC	GTCCTGNAAG	840
15	AATGTGCAAT	CNNCGN					

## 1387RP

	GATCAACCAC	TCGTGTGCCT	ATACATAGGA	ACCAAAAAGC	CTTCTGGCCT	GGTCCTCAAG	60
	TAGTATTGTA	TAAGTTTGGA	ATCCTTGTAC	GCGGTTGCCT	TCCGCGCACC	TTTCATATTT	120
20	TCGGTAAAG	CCTCCACAAG	GTTCCTATCT	TTATCCTTGA	AGTTGTCTCC	ACAGGACTCC	180
	CACAAGAACG	CCCCAGCAAG	CTTCTTATCT	TTACAGTATT	CCTTCTTTAT	TTTCATTGAA	240
	TCCACATTGT	CGTAGACGAC	AAGAGTTTTA	GTATTAGGAT	CGTAGCTATA	TGCAGAGACC	300
	CAAACATTGT	CAAACCTTCT	TGGGCGGTGA	GCTAGCGGCA	ATTGGTTGTA	TAGCCACATA	360
	CCCGGTTCCC	CTTCTGATCC	TCCGCCTACA	CCAGAATATT	TCGGGCCAAT	TAGTTGTTCA	420
25	CCATCGCCCC	GAACGTTGGT	GAAGCCACGG	CCATACGCTG	CCATGCGGAG	TGCAATTTTT	480
	CTTGGGCTGA	CCTTAAATTG	TTCCGTCATC	ATGAGTATCG	CATCATGTGC	ATTCAACTCA	540
	TCAAAGTTGT	CAATACCCAT	ATCTTCATAC	CGACGCTTAT	CTAGGTGCGA	TTGTACGGCG	600
	AATTCGTAGC	ATTGTACAAG	TTGCTATGGT	AGCCTGTTTC	CTCTGACCAT	GCACCGTGGT	660
	ATCGTATGTC	ATCATATCCN	CATGCTGAAA	ACTGTTCACT	CNCAACCGGA	AATGCAATNT	720
	CTGAAGAAGC	NGGCTGCCAG	CTTNATTGAA	CCGTCTCTGN	TCCCGGGGCC	CNANATNTTT	780
30	CCATCTCNNT	GTTNGCAGCG	GTNCTTTTNA	AAACTGGNTC	GNNCNCACCA		

## 1387UP

	GATCACCACA	ACACAGAAGC	ACGCAACGCT	ACAGGACTTC	CCTGTTCTTT	TGCTTGACACA	60
	CGTCCAGCCC	AGAGGACGAT	TACACCGCCG	TCAGGGTTTC	CTAGTCTCCG	GCAGCACAGG	120
	CTCCTTATCA	CATTTTGCAT	TTTTCAGCTC	GCACATGTCA	CAAATAACCA	AATACATCCC	180
	CAAAAGCACG	CTTTTTCTCT	GCCCGTTCTT	TCTCATCGCG	TCAGACTTCG	TACTCGCTAT	240
	GAGCGGCAAG	GGCACGCGCG	CAGGGAGCTC	ATCTACAGGC	ATCGGGTCGC	GGCCACGCG	300
	TCTGCAGCGG	CTGCGGCAGC	TCGTAGCGCA	TCGAGATCCG	GCAAGAGGCC	CGTCAGGTGC	360
40	ACTTACGAGC	ATCGAAGAGT	TTACTAGGAG	ATGACAGCGC	CTGCACGTCC	CTGAGGCTAG	420
	CCTCCCGAGG	CGGGCGGGCC	GCTTGGTATA	GGGTTTACAT	AGCAGAATGG	CACGAATATT	480
	TGCTCTAGGC	AACTGCAGGG	ACGGAAGGGG	CTTCATGCGA	AATCCTTGCA	CCGCCGGGTG	540
	CCGTATATAA	GGTGACGCAG	CTGCGCAGCT	GGGGCGGGCA	TGCTAACCAC	GACAGGATGT	600
	GGAGTGGTGC	GCGATTATAT	ACGACAAGCC	GGCGTGGACG	GTCGGTGCAC	AGGCAGGACA	660
	CCTGGCGGAA	ATCCCAANTC	GTTGAACAAG	GGAACGGGTG	CAGCNGGCGC	AATCTACAAG	720
45	AGTTGTTGAN	GGCGGCCGTC	ACATTTGCCG	TTNCACTGAC	CCTGTCTCGA	TCCANGAAGA	780
	GGNCTGGCAT	NTCCCANAAAC	CTCCCCACAG	CTGTNGACTT	GAATCCNGC	CTACCTTGAT	840
	TTGCANNCCA	GAAAAAN					

## 1388RP

	GATCACCCA	AATTCGTCTG	TGCTGGACCA	GCTTTCCCAA	CAGTCTCCGA	GGTAATCAGG	60
	CTACTGCGTT	CCTATTTTAT	GGCCTTCAAT	AATCTTTTAT	ACTTAATTTA	GACGTTAACT	120
	TCCACATCCG	GTATTTTTC	CATCTGAGAT	ACTGGCAAGC	ACGGCTAGCT	TTAGGAGAAC	180
	TGTATCCCAT	GACTTGTGGA	CAGGGGCTTT	ATGAAAAAAC	GCCTGTCCGT	GTAAGGATAT	240
55	AGAAAAACATA	CTGAGATGGC	TTTTTGTGCT	GAATCAGACA	TTCTTAGGTT	ACATTTTGGG	300

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	CCTGGCTGTA	CAAGGCACTA	ATATGAAGAT	AGAGTTATAG	CGCGTGAGAA	GGAAAGGCTC	360
	CACTGGGTGT	TGCATGGGAT	TTCAGGGTCG	TGATAATAAT	GCCAGGCAAT	CATATAGATT	420
	ACCACGAGGG	AAACATCAAC	GCTATTTAAG	GTCAATCCTT	TTGACATCTG	TCGAGGAAGT	480
5	GCGAATAGCT	GTAAGCGCAA	CTCTACAAGA	TGCCGCCGTC	TCCAAGACCA	ATGCTAAGCA	540
	CCACAACCTCC	AATGACCTGA	TTACTGGGGA	GCAATTCCGT	CCTCGAAAGT	TGGCACGTCG	600
	ACTGACTGGT	TTTCTGCCCC	GAGATCAATC	NATTGATCCN	TNATCCCTTA	CATCNCCGGA	660
	CTTTNGAAAA	CCCAAATTAA	AATTTCGNAN	NCCAAAATCC	NGGGATTTCNC	CACCCTTGAA	720
	CTACCCACNC	GGCCCTATTA	TTTTATAATT	GCNNACAANN	CCCGATCCCC	CGNNAACCGN	780
	GTAAANCGAA	AACCCCCCGG	NNTTCGGACC	NNCNTTTTNC	T		
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## 1388UP

	GATCCAGCGG	CTTGGTAGCA	TGCTGGCCGA	GGAGTTCGGC	TGTTCTGGTT	TTGCGCGCTG	60
5	AGGCTCACCT	ATAGGTGCCG	ACTTCGATTG	CCACTTGTGG	CCAAGACTTG	CTTCTTTACA	120
	TAGCTAAATG	CCACTGATCA	TATAGACTGC	TTATTCTCTG	TTAACTGCCT	CAACGTTCCA	180
	TACCATCTCC	GCGTACTCCT	CTATGCAGCG	GTCACTGCTG	AAGAAGCCAA	CGTTGGCGAC	240
	GGACAGGATC	GACTTCTGGA	GCCAGGCCCG	GCGGTCGCCG	TGGTAGACGC	GGTCAACGAG	300
	AGCCTGGCAG	GCTATGTAGG	AGTCGAAATC	GTCGCTCACC	AGGTAGTAGT	CCCCGTGCTG	360
	GGCGACGGAG	TCCACCAGAG	GTTGGAATTC	ACGCAGGTCC	TGAGGGGAAA	ATGCGCCCGA	420
10	GGAGAGCGTC	TCCAGTACGC	GAGCAATGGG	GGCTGGCAAC	TCTTGGCGGT	GATACCGGTG	480
	CCGGTAGCGG	AGGTCTTTCG	CATCTTCTGC	GAGATTACCA	AAGAGGAAGA	TGTTGTCTTC	540
	GCCGATCTCG	CGTGTGATCT	CGACGTTGGC	GCCATCGACG	GTGCCGATAA	TGAGACACCA	600
	TTCATAACGA	ACTTCATGTT	NGAATTCCCN	GAACCTCAT	ACCCGCTGTC	AAANGTGCTC	660
	ACTAATCGGA	ACNGGGANAA	TATTCGCCCC	GAANATGTAT	CCCGAATGAA	ACCCCTCAGA	720
	AATACNATCC	CTCTCTTANA	CACNGCCCN	TTATTACCTA	TATNGCTGCC	NTTTTACCCG	780
15	GCCCTTNC	CNAAAANACC	TTGAGAAGNC	CCCCNTNTN	GGNNCCCGTN	CCNTTTTA	

## 1389RP

	GATCTTCTTT	TTGAAGCCCA	CAGACACAAA	CTGTGATGGA	GTGCTGGAGA	CGCCAGCTTT	60
20	GGACGACTTC	CTTTTCTTAG	ACCGGCGAGT	CTTTTCTCTA	GGTGATATGC	TTTCTTGGT	120
	GCCGTGTTTG	CTCACAATTG	CCTTTAGCTC	TTCGACGACA	ATCTTTGTGG	ATAACCTTTG	180
	GCCCATCTAAT	GAGCCCTTTT	CAATTGCACC	TTTGATCCAA	CATCTTCCAT	TCCAAACGAT	240
	ATTGGTCACC	ACCAACATAT	TAGTGAGGTT	ATCTTTCCCC	CATGATAAGT	AGAATCTGGT	300
	ATGTATTTC	AACGCACCTC	CCGAGGGTAC	ATCTGGCGTC	TTCTGTTATCT	GCTCCACTAC	360
	TATGTGAGAG	TTTCACATCG	AATGTAGGAT	TTTTTCTTGG	ATCAAGCATC	GCGTCTGCTT	420
25	AGGACCAACA	GGATTGTTTA	ATGGCTTGAT	ATATTCTAT	TCCCTCACAT	TATCTGAGAA	480
	TTGAGACGGT	ATAGCTGAAA	TATTATGATT	AGCCTGTTTT	TCTAATATCT	TTTGCAAGTA	540
	GGACGTGTCC	TCACCAAAAT	ACAGCTTGTA	CACGACACCC	AATGGTGCTG	CGATGGAATC	600
	GAATCATCAA	CAATAACATC	TCTGTGTTGC	TCGTATAGGT	GTTCTTCGTC	GGAGGANGCT	660
	ACTAGGGCGA	TATTNGTAAA	TATTAAGANA	CANTTGTGTA	CTGTTNGAAC	TGCCNCGTAC	720
	TTGATTNTAT	AAAACCTCNN	AATGTTACCG	TTCNACNCTT	TNGAGANTTN	ANCCCTCNA	780
30	TCCNTTCCNC	GTGANTTTNC	ATCTCCCCCT	NTCTATACTG	ATACNT		

## 1389UP

	GATCCGTCGC	ACTTTCACAA	TTGTGAACGA	CTTCACACCG	GAAGAAGAGG	CTGCCATCCG	60
35	CCGTGAGAAC	GAGTGGGCCG	AGGACCGCTA	GCCACGGCCC	GCCTCTATGT	ACCATAGTA	120
	CCGATATCT	ACCGCTGCCG	GCGCGGGCCC	CGCCCGCGCC	ACCGTTGCGT	GCCAGGAGCT	180
	GGTCTGCCGA	CTATCCGTGC	CAACGTACGA	AACGATGCTG	GTTTATGTGG	TCCGCCCGCC	240
	GCTGGTTACA	ATTAACCGCC	CCAGGTTCATC	GGTAGACGGA	GCTAGCTACT	CGTTGTCCCTG	300
	TAAGTGAGTT	AACGCACAAG	GGGAACCTATT	CGTGTGGTCA	GGCAGCAGAG	ACGCTGCAGG	360
	ACATACTACG	AGTTATTTCT	CATAACTAAA	CATTTTGTGA	ACCTTTGTGT	CGGGGGCCAG	420
40	GTCGTTTCGC	AAAAGGCGGC	GGAATAAACA	GGGAGGAGAG	GTAGATGCTC	TTCTCAGGCA	480
	GAGGCTAGCA	AGGATGGCAG	AACAGCGGAA	GCGGTGCGCG	TCGCTCAGAG	AGAGCGCGCG	540
	GGCACTTTTC	AAGAAGCATA	CGGGGGAAGG	GGCGGCGGAA	GGGGCGCGCG	ACAGTGCCAA	600
	AGACGGTTAC	GACCCGAATG	GGGAACCGCG	GANC GGCC	GAGCGGTNAT	TTCAAGTTGG	660
	CGCNGGGGAG	GCCCCGANTTT	NAAACCGGTG	TNTAGACAAA	AACTTGTTCCA	GTTNCNACCC	720
	GTNGTTTACC	AANNNNNNAA	TCTCCNCCCC	NGGGTNGGTG	GCCNGAACCC	CCNCTGGCTT	780
45	ACGGGGNCCA	CATCTCTCCC	CCCCCTCCCA	TTAAANACCC	CGNCNCCTTT	TNTCTGNCC	

## 1390RP

	GATCAAGTAA	TCAATCAGTT	AATAATATTA	AGAATATAAT	ATGTAGACAT	TTAGTCTAGT	60
50	CTATTAAATTA	TTAATTATTT	TGTAATTGTG	TGTTAATTTG	TTGATATTTT	ATTGATTTTG	120
	TTGACATTTT	GTTGACATGT	TGATATGTTA	TAAAATATAA	TTTAATATTA	TTTTATATAA	180
	TTATTATTAT	TATCTAGTCA	TAGACTCATA	TAAATATGAA	TATATTCCAT	TATTAATTGT	240
	TTAGGATAAA	CATAAATTA	TATAATAACT	TATTTTAAAG	TTCAATAAAT	ATGTTTCATAT	300
	TTATATGATT	AATTTCATAAC	GTATTTCGATA	TAAATATCTC	ATACCCTTTT	ATGAATTAAT	360
55	TAAGCGGTAT	TAAATTATTC	TGATTGGATT	AAGTTATTAT	TTAATTTATG	TTCTTAACAA	420

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5	TTAATTGATT	CCATAAATAT	CGATATTTAT	TATTATTTAT	TAAAATATTA	ATGATAATAT	480
	TGTAATACTT	CAATTATTTT	ATCAAAATGGC	AAGTAATCTA	TTAATCNTTT	AATACGATTG	540
	ATAAGAAAGA	AAAGAATATC	ATCTATCGTA	TAATATATTT	CAAGTATGAC	CTCTTCAATA	600
	TAATTAGAAG	TTTAAACTTG	TAGAGAATTA	AGAATTTAAT	ATGAGTCTTA	CATTAAACCT	660
	GATATGAACC	TTTAATCTAC	TTATTTGTTT	AACCGTTGAA	GAGAGAATAG	TTAATCTNAG	720
	TATNACTTAT	ATATTGATAC					

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## 1390UP

	GATCAAACTA	AGAAACCTAA	TAAACTAATA	GAACCTATTA	GATAAATTAT	AGAAATTTCA	60
5	CCAAATACAG	GTTTTTTAGA	ATAAGTTGAT	ACAATATGTG	ATATTATACC	AAATAGTGGT	120
	ACAATTATAA	TATATACTTC	AGGATGACCA	AAGAATCAAA	ATAAATGTTG	ATATAAAATA	180
	GGATCACCAC	CACCTTGCTAC	TTCAAAGAAT	GATGTATTAA	AATTTCTATC	TATTAATAAT	240
	ATAGTAACAC	CAGCTGATAA	TACTGGTAAT	GATATTAATA	ATATAACAGC	AGTAATTTAA	300
	ATTGATCATA	GAAATAAAGG	TATTTTATGT	AAAGTTATAC	CATTAGTTCT	TATATTTAAA	360
	GCTGTAACAA	TAAAATTAAT	AAGTCCTAAT	AATGAAGAAA	TAGTAGTTAA	ATGTAAAGAG	420
10	AAAAAGCTA	AATCAACAGA	AGCACCAGAA	TGTGATTGAA	TAGAAGATAA	AGGAGGATAA	480
	ACAGTTCAAC	CAGTACCTAG	ACCAGATTCA	ACTATAGTAG	ATGTTAATAA	ACAAATTAAT	540
	AGTGGTGGTA	ATAGTCAAAA	TGAAATATTA	TTTAATCTAG	CAAATGATAT	ATCAGAAGCA	600
	CCAATTATTA	ATGGTAAATA	ATAATTACCA	AAACCACCAA	TTAATATAGG	TATTACTAAA	660
	AAGAATACTA	TTAAAAATAAG	ATGTCCAGTA	ACTAATACAT	TAAATAATTG	ATTTTGACCT	720
	TGTAAATATT	GTTGACAGGT	GCTGATAAAT	CTATTCTAAT	AATAAATGAT	ATA	

## 1391RP

	GATCTTTTTG	CTCCAGGTTA	TTCCCTTCTT	GGACACATTT	ACGAAGTGTA	TTTTCAAGAC	60
20	CTGACTCGCG	CATTTAGGTG	TTACGTTAAA	GCCTTTGAGC	TAGATGCCGG	CGACCTCGTC	120
	GCTGCTAAAT	ACATGGTGGA	ATACTATAGT	GACCTGTGCA	ATTGGCAGGC	GGCGGCCAAC	180
	ATCTGTGACC	GTGTAATCAA	GAATGATATG	CATCTCAATT	CCGTCAACTG	GCCGTACAGA	240
	GTTCTGGGTG	TTTATTATTT	GGAGCTTCAA	CAGGAGGCTG	AATCGATCGA	ATGGTTCCAA	300
	TCTGCTTTAC	GGATTGATTG	GTCTGATGTT	GAGGCATGGA	TAGGCCCTGG	ACAGGCGTAC	360
	GCCGCATGTG	GCAGAAATCGA	AGCCTCGATC	AAGGTTTTTG	AAAGGGCATT	AGAGCTGTCT	420
25	CCAGAACATA	AGTATGCAAG	GTTATTCTCT	GCTATATCAT	TATGCCAGCT	TTCAGAATTC	480
	GAAAAAAGTC	TCGAGGCCCT	GAGAAAACCT	GTGAATAAGT	ATCCACAAGA	AGCTATCTTC	540
	AAAGAAAGAC	TAAGTGCAAC	GTTGGTGGAG	CATGCTMTGC	AGTTCTTCGA	CCAAGGTTAC	600
	CTGATAAAAG	CGGCAACTTG	CGCTGCTGAG	GTGATATCGA	TCATAGAAGG	CATTGTATCT	660
	GAACAGGTAG	AATATACAAC	CAATATGTGG	ATTACTTTAT	CAAAGGCTTT	GAATATTTTT	720
	ATTTCCACGC	GTTCTCAGTT	CGACAACCTT				

## 1391UP

	GATCGCCGCG	CAGATTGTGC	AGAACGTGCT	TGCACTAGGG	TCTCTTACGA	CAAAGGACTA	60
35	CATGCAGTCG	TTGGCTTCCG	ATGTTTCTGT	GAATGATGTG	GCGTCCATGT	TTGTGAAGCT	120
	GGTTGAACCTA	GGCTTTCTGG	TCCCGCTTTC	CAACGTGCAC	TACATGCCAC	TGGCCGATCT	180
	ATGGGATGTG	CTCTACAAGA	AGGAATACAA	TGCTATTCCA	AAGAAATCGA	CGTTGTTCGA	240
	TGCCAAGAAA	CGTGCGAGAA	CAAAGGCGAA	GACGAAGGTT	CAGTTCAATA	CGTTGCTGAA	300
	GAATGTCGAA	ATGAGCAACG	TACTAATGAC	TGATATGCAG	ACTTCAATGA	GACGTGTCCA	360
	AGACAATCTT	CCTCTAACAT	TTAACTTCCG	CCGGTACATG	AAGCACCAGC	GTTCTCGGCA	420
	GCTTGATACG	TTTGCACGTT	CCCGTGTGGG	GAGCGTACCA	GCCATGATCT	ATAAGGTGGC	480
40	ACTGAAGATA	ACCGAACCAAT	GTGCCCCTGC	GCCTTTCAGAT	CCGCTATGTG	AGACAGGCCT	540
	AATGCAGGAA	CCTGAGGAGC	AACCTGGCTAT	TCAGGAAGAT	ATGGCGCTAG	ACGATGAGAA	600
	GCTACCGGGC	GTTACATTCA	ATGCGGTGGA	CATATCCAGA	AACCTTACCA	ATAACATGGA	660
	CCTACGTGGC	ACACTGACTT	CTATGCCAAG	AAGATCACCA	GAACGTTGCA	CGCACCAAGG	720
	TCAATCCCAT	AAGCGGNTGA	AGGCTGAAGA	TGGGATGGCT	GTAGCAG		

## 1392RP

	GATCCCCACC	ACCGTCACCC	GCGTGCCCCG	CACCACCCGG	TTCTGTAGGT	ACCGGTTCGCA	60
50	CGTCAGCAGC	AGGTTGCGCG	GCATCTCGCC	GATCGGTACG	GACTCCGGCA	CCTCCTGGAG	120
	CTTCAGGAAC	TGCTGGTCTA	CGAAGCGCGA	GCTCTCGTGA	ACGATCATGT	ACGGGTCTCTG	180
	GCCGCAAGGG	TTCCCCGCGG	CGCTGCCATC	GTCAATTCGAG	TGGTCTGCCA	GGCAGCCCCG	240
	CGGTAGCGCC	ACGTTGCTCC	CCGCAAGCGA	CTGGAAGTTG	TTGAGGTCCA	GCGCCGTCTGT	300
	GTGCCGGCAG	TTGCGGCACA	TCAGCGCAAC	GTGAGTCGCA	CGTGACGTCA	GCACCGGACG	360
	TGACACCACG	ATCCCGCTCA	GCCGCACCAG	CCGCGAAACG	CTCTGTGAGT	CCAGCTGCCG	420
	CAGCCCGCTC	TCAGCCGCGG	CGCTCTGCGC	CTCCACCTGC	ACCGCCGGCA	GCGCGCCCCG	480
55	GTCCTCCGCC	CGGAGCCGCG	CCATCCGCGG	CGCTATTTC	GTCACCCGCT	GCTCAAAGAG	540
	GGGCACCGTC	TCCACAGGCT	CGTCGCGCAC	AGTTTGTACA	GCGCCTCGTT	GTACCAATCA	600

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GATGCTCCGT GTTGACGCGC AGCGCGTACG CCGCACCAGC AGGTTGTTGC GCAACTGCTC  
 GCGATATAAN NAACCGCGCG TCNAACGAAA CTCNGCACA AANCNCNGA AGAGCGCACC  
 NCCTCCGANC GGTCGTTGCG CGCCCGCCTC CTC

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## 1393RP

	GATCACGGAT	TGCCCCAAGT	ANTGCGCAAC	AGTCGTCAAN	TCTGACATAT	CTCTTGCAAA	60
5	TGCTAGCCTC	TGGGGGCTTG	AACTAACCAT	TACTTCTAAT	ACCTGGCTAG	CTGCCCTCAA	120
	ATCCGGATCC	AAAAAAGCAA	TATTTATACA	TAACATATACA	CGAAATCTCA	GTTTCATCGCT	180
	AGCTAGCTCA	TCGTATCCGG	GACTGGGAGA	GGAACCAAT	GCTGTGGAAC	CCTTCGAATA	240
	TGGCAGCGTC	GGCGATGTTG	ACCAAGGACT	CGCCTGGGCC	AAACATGCGG	ATGCCACNTA	300
	GGTGGGTGTC	TTTGCCGTTT	TCGTGGTTAG	TCACGACCTC	GATGCGCAAA	AACTGGCACT	360
	TGAGCAGGCC	GTCGGAGGGT	CGGTGTCTCT	CGAAGGTGAA	CTTGACCCAC	CCATTGACTT	420
10	GCGGACTTCT	AGGGTCTTGT	AGTAGGTTGC	GTCCGAAGGG	CTGTGGCCAG	CGTATATGCG	480
	GAGCGTCTCC	NANGTGTAGG	ACTCATCGAC	GAAGAGCGAG	AAGTACATGG	CAAGCTGGAT	540
	GATGTCAACG	CGCTTGCTGA	AGAAGACGTC	TATGGTGTGT	GGCTGGGAGC	CGTCGCTTTG	600
	CCANAANGTG	GCGGGGTTAT	CATCCNAAGG	CGTTTTCCAT	GGGGTANCCG	GCCTTGAANG	660
	AAGAAGGCTT	CCANTAGGCC	AACNAAGTGA	TATCNACTTA	CCCTGGTTCT	CCAATGTTTG	720
	CAAGCCCNCC	TGTTATTTNG	NCCAGAAAAG	AC			

## 1393UP

	GATCCAGGAT	ATCATGCCCA	AAATCCTTGA	AGCCGCTGCA	AAGCGCCTCG	TGCAAAATCAA	60
20	GAATCTGCAC	ACGGCAGAGA	ACTTACTCTT	CGTATTTTGC	TACCTGACTT	CTATTGATGC	120
	GCGGCAGACA	GTGGACTTTC	TTTCATCAAC	GATCATCGAT	GAAGGCGGCC	GTACCGCCCT	180
	CCAGGCTATC	GTTCCGCGTT	GGCTAGAAGC	ATTTCGAGGT	CTCCGCGGAG	AACATAAAAT	240
	CAGAGAGAAC	ATTTTATCCC	TTTCCAAGCT	TTTCTTCTTT	GAGGATCCCC	GTATAGCGGG	300
	CATCACGGTC	AATGGGGATC	TGATTCCCCA	CGATGGCGAC	ATCATAATCA	CCCGCTCCAT	360
	GGCCAAGAAA	ATGCCTGATA	AGTACACGCA	GATCTCCGCG	GCCGAGAAGA	TAGTCAAGCT	420
	CTTTGTTGCA	GAAGTAGCCT	TCCAGCAAAA	CCAGCCTGAC	CCTGGCCGTT	ACCCTAAAGA	480
25	CGGGTCTGGC	CCTGCTGACC	CACATGAGTC	CGAGGGAGAC	TCAGCTGATG	AAGACTGGGA	540
	GGATGTCGAT	GACATCCTTG	ACTACGAAAA	ATTGCGGGAG	TACGCGGATG	ATAGTGACAT	600
	TGACGACACG	GTGACAGCCT	TTTATTACCA	AGTAACATCG	AAGAGGATGT	AACCACTCTG	660
	CTTACTCAAT	TCTTCAAGGA	AGCGGTTGCC	AGAAATGCCT	CTGGCTTCCA	GGAGATCTAT	720
	AGCAGGCTCA	CTGAACAAGA	GAAGAAGAGC	TATCTGCATG	CATGGTATAG	GAT	

## 1394RP

	GATCTCGACG	ATTACCGCGT	ATGATTATAT	CCCAGCAACA	TGGGCACACG	CCGCACACAC	60
35	AGACATGATA	CTGGTCGGTG	ATTCGCTGGC	AATGTCCACG	CTGGGTCATG	TGTCCACGGT	120
	GGACCTGGAT	CTGCAGGAGT	TCCAATACCA	CGTCCGGTCG	GTGTGTACAG	CACCAGGCTC	180
	GTCTTTTATA	ATTGCAGATA	TGCCATATGG	TAGCTTTTGA	CGAANCATTG	AGCAGGGAGT	240
	AGAGACGGCG	ATCTCGCTTA	TGAAGACATC	CAGCAGGGTG	GGTGCTGTTA	AGCTCGAGGT	300
	TGGCGCGGAA	GAAAACGACT	ACTGTCTTGA	GCTTGCCGCA	GAGCTCTGCA	GGCGCGGGAT	360
	CCCAGTAATG	GGCCATGTCT	GGCTGACCCC	GCAGCGCATG	CATGCATTGG	GCGGGTACAA	420
	GGTTCACGGC	GCAAAGGACT	TGGGCCAGGC	CGTGGCGGCG	TACCACCGGG	CTAAAGATCT	480
	GCAGGCTGCA	GGCTGTTTTT	CCATCGTCAT	CGAATGCATT	CCAACATAAC	TAGCCGGTAT	540
40	CATAACCGAG	AAACTCAGTA	TACCTACTAT	TGGCATTGGC	GCGGGCCCCC	AGACAAGCGG	600
	GCAGGTGCTC	GTACAGTCGG	ATCTGCTGGG	CATGTGCCA	NGGAAGGCC	CAAAATTTTG	660
	TGCNGAATTC	CCCGGACTTC	CNCNCGGACG	CCATANGTTC	CTGTGCCCC	CTATGTTGAA	720
	AANGTGCCCA	NGCNTCTTC	CCNAAAGTNG	GGGCA			

## 1394UP

	GATCGAACTC	CATGAAGGAG	CGTAATGGCC	TCGTGGAGCT	GCACCGCACT	GGGTGCGTAC	60
50	ATAGCGGGAT	GTAGGAATGC	GGGATAACG	ATTTCGAAAA	GCTGACTGGG	CTGCGCCTCT	120
	AGCTTCAGCT	CAAGCTGGCG	CAGCAGCGTT	GCTATAGGCT	GTGTGCGCGA	CAAGGTCGAC	180
	ACTTCAGTTG	CAGTAGGAGC	AGGTAGCATA	CGACTAGTTA	TATCGAACTG	GTGCCGGTAA	240
	TGAGGATGAG	GGTCAATTTC	TGGCTCCGAG	CGCTGGCTAG	CACCACAATT	ATCACCAAGT	300
	CCATACCTCC	ATGCAATTCT	GAGATCTTGG	CTACGTGCGA	CCGGTTTTGC	ACCCCTCCG	360
	GCTAAGTTT	GCACCGTGAC	CTTCGATTCC	TCCTGGGAAA	TGCGAGATT	CTTTACCTCT	420
	TTACGTGTGC	CCTGGAATAT	CCCCGGCAGC	TCCTTCGCAT	ACTGAGTGT	GAGCGTGATG	480
	ACCACCATAT	CCGTATTCCC	TCCCCGCTGT	GCGCCGCGAC	TTTCCGCGCG	GTTATGTGCT	540
55	GCTCCCTGCG	CTGCAAAGAG	CTTTCCAAGT	ACCGATGCAA	AGTCTGTACC	CCCTTGTCT	600

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TCCACCAGAA GCATCTGGCC CATTGGCAAG CCCATATGCC CTAGGAGCCG ATCCATATCT  
GCACAACCCG TGGATGTTGT GGGATGCGAA GTAACCGGCG ACGGACGCAA GCCCGGATGC  
GACTGCCTGC CNCCTCACTG TTGGATGCCA ACCTCTCCAC GCCTCTNGAA ANC

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## 1396RP

	GATCAATCAT	TCTAGAGCTG	GAGCAAAGGA	TACCTATAGG	CTTGCCCTCGT	CATTGGCCCC	60
5	TTTCATTATT	ACATACCCAT	CGTTCCACAG	CGTGTCACAT	TCTGCCATTTC	GAGAGCAGGA	120
	CACCCAAGTT	TTCAAACAGA	ACAGCCTCGT	TCTCTTGSTA	AAAGTTGGAC	CTTCTAACGG	180
	TGTCTCATC	GAAGCCGTCG	TCGCCACTGA	GGACCTTGAG	GGCGTTGGAG	GTGGCTTTGA	240
	TGTAGTCGTT	GAGCATAGGA	ACCGGGTCGT	CGGCAAGCTT	ATTGAAAAAT	TGGTACTTGT	300
	TGGCTGTGGA	GCTGANCTGC	AGGGGAGAGC	AGTTGGGTCT	TCTTTTCGAG	GGTTGCCAGC	360
	TGCGGCTCGA	GCTGGCTGGT	GACTGTGTTG	AATTCTGTGA	GCAGCAGCAT	CCCCTGTTGG	420
10	GCAAGGGAGT	TTTGGGCGGA	CGCCGGTTTCG	GGATCCCTTAA	CCGGGACACG	TGGCACGCGG	480
	ATGTCAAGA	CCAGTTCGCC	GTAGGTGGAG	GTCTTGTCGA	CCTGGATGGT	GTAGTTGATG	540
	CGCACGGGGG	GGATGGGCTT	GATGTGGGCG	TTGACACCTG	GGGCAGCTCG	GTGAGCTTGA	600
	GGTACTTGCG	AGGCTCTGCG	GCGGGCCGCA	GGAACCTAAC	GATCATGGCG	TCCACCTTGA	660
	TGACAACCTG	TCGTGCTTCT	GCGTGCTCTT	GGCGTTGCCG	CTNGGGTCTG	CGACNAAGAA	720
	CTCTTGAACA	GGATTTCTTG	TNAACC				

## 1396UP

	GATCGGTTAC	TTAGAGGGAG	TGCAAGACCT	GGCCTGACTT	ATCTTAGGGT	TATTAGCTAT	60
20	GACGGGTGTG	TTCCGATTTC	TGTCCAAGGG	TTTAGATGCC	ATCAACTCCC	TGAATTCGCA	120
	CTACTTTGCG	TTGTCCGGTG	ATGAACAGAA	GGCCATGACT	TTCGTTGAGC	GTATTAGATA	180
	CTACAATTGG	ACGTTTGAGG	GGATCTGTGT	GGTCCCTGCTC	GGGCTGATGT	ATGCCGTGTA	240
	CGTGGCGGGG	ACCAAACTAA	ACGAGCGGCG	CTCGGACCGT	CTGTTCGAAC	AGCTGAACAA	300
	GTTCTTCTGG	GAGGAGCTGC	AGTTTGCGCG	CGTGGGTTTT	TCGTCCCGGG	ACAAGGGACG	360
	GCTGCCATAC	ATCAGCGATC	GGAATGGCAC	ATGGTGCACC	GCATTGCTA	CGGGGCGCAC	420
	GTGTGTGGAC	CATATTGTGG	TGAAGGCTCA	CTACCCGGCG	CGCTTCAACC	CTGTGGGGCT	480
25	GCTGGTGGAG	AAGCTGCTGG	GGATGTTCTT	CCCGCAGGTG	GTGGACCGCA	CGGCGATGAG	540
	TTTGTGCAGG	TGACGGTGAC	CCCCAACGGG	AAGTGGACGA	AGGACGAGAA	CAGCGCGGTT	600
	CAGGCGACGG	AGGACGGGCT	GAACCGGTTT	CGGTTTCATCG	CGTCGATCGT	CCACAAGAAC	660
	GGGATGAACG	ACTCGCGCGG	CAAGAACTAC	TTCTCTCTCT	TGACTCACNC	GTCCGANGGC	720
	GAACTCTCC	CATGGAANTA	CTCTTCATGT	CCGANAACAA	CCACTGAACA	AC	

## 1397RP

	GATCCCATT	TTCTACAGCA	AATATTACAC	GGCCGGCGGA	CCCTCGACAA	TGCAGAATTC	60
35	GATGCATACA	CAAAACATAT	TACTACAAAG	CTTCAAAAG	GTGTCTCTCC	CACAGACGCA	120
	TTTCTAGGCG	CACTCAAGGT	TTACATTCTC	AATTGCAGTT	TGAAACGTTT	ACGCTTGCAG	180
	AAAGCACACG	TTATACTTCT	TGATAAAATT	GCGATATTCA	TCAATACAAA	TGTGGTCCAT	240
	GTGTCTGTCTG	AATCGATACA	TACGATACTG	AAAAGTTTAG	CTGAATATTT	TATTGATGCC	300
	AAGGAATATA	AGCGACTCAA	CAACGTCGTC	AATATTTTCAT	TCAACGCATA	TGTGATGTAT	360
	AAGCATGAAA	GCCTTATACG	ACTTGCAGCA	GATCTCGAAT	TATTTCTCTT	TATGTCCGTC	420
	AAACAGGACT	GGTCAATGTT	TACCAAGTTC	GAGAAGTTTA	TTTCTGTCTG	TTCAGGAGAC	480
40	ATCTCAGTAT	CGCTCTTTGA	ACAGTGTTC	AATGTTTATG	TTATGTTCTG	GGATCCCTCA	540
	TTGGCCGGCC	TATGGGATGT	CTGCTTGAAC	AAGTCGTTGA	AGTGTTTCAA	GAAATTGGGA	600
	CTAACTAGTT	ACACAGACTT	TAAGGCATCG	TCCGAGCCAA	TGCTAGTGTT	GGTATACAGT	660
	GGATTTGTTT	CTGATATTTT	TACAATACCT	TATAATGGCT	GGGCTCCGCT	ATCGAAAATG	720
	TTATTTCATGG	CATTAAATGG	GGTCTATAAA	TTG			

## 1397UP

	GATCTGAAAT	ATTGCTCACC	CCCACCGTGA	CCTATGTAGA	TGAACGTGCT	GGAGTTCGTG	60
50	ATCATTCTGA	CGAATTTCATC	CTCTTCTGGC	TTTGAGCCAG	TTACTATCCG	TGTTGAACCC	120
	AAGTCGCAAC	AAAGTCTGGT	AAAATGTTCT	TTAAAGCGCA	GTTCAGTCC	GGTCAAGTCC	180
	CCATGCGGGT	TTAAAACAAT	GGAAAGTCTG	CTGTCTAGGT	TAATCTTTGG	AGAGATCTCT	240
	CCTCTGAATT	TAGTTAGTAG	CTCGTGAAGG	AAATTTATGG	ATGGTACGCG	GCTCACAGAA	300
	GCATCGGAAA	ATATACTGAG	AGATTCCCAT	GGAACCAAAC	TGCATTCCGA	GCTTATTACC	360
	AGAAACGTGT	GTCCTAACCT	TGGCGCCTCT	GGTGCCTTGG	CATGATAGTC	GTGAATTAGT	420
	TCCTCAAGTT	GAGATGTAT	GAGATGAACG	TCAATCTCAT	CATAGGCATT	TTCTTCGCCA	480
	TGAAAAAGCA	ATATGTCAAA	GATGAAGTAT	ATCAAGTCCT	CCATGAATTC	CACCTTCTTT	540
55	TCGTGAGGAA	GGGCATCCCA	ATCCACCTTT	AAAAATAACT	CTAATATGAA	ATCGTCCACC	600

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TGTTAGAACA TAGACGGGTT TCCATACTGT CTTCTTGTG GAAGATTTGT TGTA AACCT  
 TTGAAATCCT AATTGAATA NTGCAAAATG GTTTTATCCA ACTGTTTTG GNTGAAGAAA  
 CCGCNGAATC CCATATCCAG ATCTCATGCG GGCNTCNAT CTACATC

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## 1398UP

	GATCGCTCTT	CTTTGAAAGA	ATATGTAGGC	ACCTCTCTCT	ATCTTGCGCC	GGAATTGGTT	60
5	CGCTGCAAAG	ATATGAAGAC	GATGACACCT	GCAGAAGCAG	AAAGAATCCC	AGAGTACGGT	120
	GCAGCAGTCG	ACATATGGGC	TCTTGGTGTC	CTCTGCTACT	TCATGATGAG	TGGCTATATG	180
	CCGTTTCGATT	GCGAAGACGA	TGCCGAAACT	AGTGACTGCA	TCTTGAAGGG	TGACTATTAC	240
	GTTGACGAGG	AAGCTCGTGC	CAACGCCAAT	GAGAGCTATA	ACAGCTGCTG	GAACCTTCATG	300
	CAGCGCTGCT	TTACGATGGA	TGATAATATC	CGGCCGCGC	CACACGAACT	CATGGGGCCAC	360
	GCATTTCATGC	GGGAATACTT	CCAATCGGCT	CGGGCCAATG	ACTTCGCATC	TATCCCGCTA	420
	CTCGAGAGAT	CAAGATCCTC	GAACCTCCCTG	CACCACTTAG	CGCCGCCATC	ACGCGCACCG	480
10	TTTATCTCGT	CTGGCGTGCC	GGTTATTAAC	GAGCGCCCTG	TGCCACGTGT	TGGCTCGCGT	540
	GAGCGCAATT	TGGATAAGTT	GCGGGATACT	TTGCGGAAGA	CCTTTCCCTC	ACTTCGCTTG	600
	AACCTATGCG	CTTTGTTGCT	CAAGCGAATA	CTCCTAATCC	TAATAAGAAG	AACTCTACTT	660
	TTGTTCTTGA	GCCAGCTCCT	CCCACGGGGA	GTCTAATGAA	TGGGTGTTTC	ACGTCACACC	720
	GGAAAGTAAT	CCAACCTCAA	TACGCCAGTC	CTTTCGCGCA	GAAGCTCCGG	CCAA	

## 1399RP

	GATCATTACT	CGCAGAAACT	GAGATGTTAG	GGGGACCAAA	CTCTTTTCTT	TGATGAGATA	60
20	CGGGAGGATG	CCCTCGGAGA	ACCAGAACAA	TGCAGCAAAA	GGCACGAAGA	ATGCCAACGA	120
	GAAAAGCACG	CATCGCTGCA	TATGCAGTCC	CACCCCATAG	TAGTTCCTTG	CGCCATATGC	180
	CTGGGGGCGAG	AGTGTATCTA	AGCTGTGTGA	AATACCCCTCN	AATATTGCGA	AAGTGATATT	240
	GGTGGTCAATG	GAAGCCAGGG	AAACCGCTGC	CAACTCATT	TTTCCCAGGT	GAACCCACAAC	300
	TAATGACAT	ACAACCGGAA	ACATCTGCTC	AAGCAGAAAT	GTAAATATGA	GCGGCACGGA	360
	GTAACACAGA	AGCACCAGAC	TCTCGGACTT	CACGGTGGCT	GGTTCGTCTG	CGAGATCCTC	420
	GGACCCTCGG	AACGCGCTGG	AGGGGCGGCC	CTTGCTGCCA	ATGGAGTAGT	AAGACAGCTT	480
25	TCGGGGCCGT	AGAACACGCA	CTTCTGCCCT	GTCCGACGGC	AGTTGCTGCT	TAACCCGATG	540
	CATGAAGTGA	GTGTAGTGCA	CCATGTCTGG	CGCGGCGCCC	TCCACATCGA	CGGCCACGAT	600
	GTCTCTGGCG	CTGCCGTTAA	CAGTCGAGTA	CCGCCGTTCC	TGCTCCTCCA	ATATCCAGTC	660
	TACATTCACT	GCAGAGGACG	GCCCCGCTCA	CTCGCAAGCG	TCGACGGCAG	CGAGACTGTC	720
	CGCGACAGCT	CTCCTCCGTC	AAGCACGCC	TCCTCC			

## 1399UP

	GATCTTGTAC	GACGGCCGCG	GAAGAATCGG	TGCCATCGTT	TCCAACAGAC	AGTTCCAGTT	60
	TGACGGCCCA	CCACCACAGG	CTGGCTCCAT	CTACGCCAAG	GGTTGGGCCC	TAACCGAGGA	120
	GGGCAACTTG	GCCCTAGGTG	ACAGCGACGT	CTTCTACCAN	TGCTGTGTCG	GCAACTTCTA	180
35	CAACCTATAT	GACCAGAACA	TCGCACCACA	ATGCTCTCCA	ATTAAGCTCC	AGGCAATCAA	240
	ATTGGTCTGAC	AACCTGCTGAA	CAGCCACAAA	GGTATATAGT	GCATATATTG	TATTAGTTAA	300
	ACTAGGAATT	TTTGTGGCA	GCTAGACTGC	CCTACGTGGA	TTTCTCGTTG	CGGATCCTGG	360
	GCTGCCGCTG	GCGCTGACGC	ACAAGAGCAA	CTGCACAAC	ACTGGCGTAC	CGCATGCCTC	420
	CTTGTCATT	TTTGCCGCGG	TGGACGTTCG	TGACGTGAGC	GTGGCACGTG	ATCATAATAT	480
	GTCCCGGGCC	AGGCCCTAT	TGTGGCGGAC	AGGAATGCAT	GCGGAGGTGC	AAAATGGTGC	540
	AAAATGGTGC	CCGATGCAAC	TCTAGGCCCG	AGCTGAAACA	AGATTACCTG	GGCAGCCTAA	600
40	ATTGTCAGCG	GCTGCCTGGC	AGCCCACATG	TGTATTGTGC	TTTTACAGTT	CTTGCTGCGG	660
	CTGTCCAATA	CAGCCGATCG	CGACTTTGCT	GCGCACGGGC	CAC TAGGCCT	GCGCGACAAA	720
	AACTGCAGGC	GCGCCGGCGT	GAATGGCGCC	GGACGATGTG	CTGCCGCGGA	ATTCC	

## 1400RP

	GATCCTGTCA	AATATGGCCA	ATACCAAGCA	GCCGCGTGTT	GTAGAGCATG	TGGTTGAACT	60
	CAAACCCCTCA	AGCAGCCGGG	TTTTGGACTG	TGCACAGGAG	ATATTGTCTC	CATTTCACA	120
	GTCCAAGAAC	AAGCCAGGC	CGGGGGACTG	GAATTGTCCC	TCTTGTGGTT	TTTCTAACTT	180
	CCAACGGCGC	ATTGCTAGCT	TCCGGTGCTC	CTTCCCAGCC	ACTAGTGCAG	TGACGGTCAG	240
50	CAAGCTGTAC	AAGCCATGCT	AGCAACGCCA	TTATCAGAAC	CCACACCACG	TCCCATCGAA	300
	ACAACAGGTG	CAGCACCOCG	AGATTACAGA	CCAAGACACA	CAGCAGCATT	CTCAACATTT	360
	CAACATCCAG	CAGATGCCCG	AGCAACTCCA	AATGCAACAG	CAAGCGCACG	GTACCGTTCA	420
	AGGGGGCAGT	AGCATGCAGC	AGTACAAGCA	CAGGCCTCAG	CACGGCTTAC	AGGCGTATCT	480
	TGGCTGCTAC	CAACAGCAGC	AGGCGAAGTC	ACAGCAGCAG	TACCAGATGA	ATCAGCAACA	540
55	GGTGCAGATG	ATCGCTGGCG	ACGCCAGAGA	CGGTATAACC	GGTACAACAA	AATGGTGACG	600

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GGCAACGGGC AGAACGGTAA TTCTTGACG GAAATGGCTC CCTGGGCAGT AGCAACGTGC  
 CCTTCAGAGC TGGCGACTGG AAGTGCTTGA ACTGTTCCTA CCATAATTTT GCCAAGAATA  
 TTGTTTGTCT GCGTTGTGGT AATCCAAAGA CGGCCAT

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## 1400UP

	GATCGGCGGG	TACTTCAGGT	CATTCTCCTC	CACCACCACC	ACCAGCTGCC	CGGGCCCCGG	60
5	CTCATACAGC	TGGTACGCCA	CGCGAACATG	TCGCTCCGCC	TGCGGCACAT	CCGCCTCGTA	120
	GAAGTATGCC	GCAGCCACCA	GCCGCGTCGC	GCACTCCCCG	CCGCGGCTT	GCGTCAGCGT	180
	CCCCACTAGC	TGCGCGACCG	GTGTGAGCTG	CACCATCTCA	GGGGGCATCA	GCCAGCTCAG	240
	CGTCGATGGC	ACCACCAGTG	CGGCCGAGTA	CCGCTCGCCG	AGCTTCCCGC	TGAAGTCGAC	300
	CTGCGGCTCG	GCCCCCGCGA	GAAGCGAATG	CGGGTCCATA	GGGCCGAGGC	AGTCCAGTTG	360
	GTGTCTGGGA	AGACGCTCAG	ATTGCCATTG	TTTGAAGTGT	CCACAGTTAG	AACTTGCACT	420
10	ATGCTACCTC	CGCGGCGCCT	GCGCGACCCC	ATAGTCACAT	ACTATCATCC	TCACACAAC	480
	CAGTACTTGC	TGCGAGTCCC	AACTCAAGCT	AACGAGTACC	AGACTTGGTT	TTGGCTGTTG	540
	CTGTATGCAT	TCCAATGGTT	TGTATAATCG	AAAAATTGTT	CAGTTGCTCA	GCACATCTCA	600
	TACAAGCAGG	AACAAGAGCG	AGTCGCGAGC	CAAAGACCTC	TTAGGCATTA	GTATCGGTAG	660
	CTAGGATGTC	GGCAGAACAG	TTGCGACAAG	TACACGCAGT	TGCAGGCGGA	ATTGGAGGAG	720
	CTGGTGGTGA	CAGACAGAAG	CTGGAGACGC	AGCTGCAGGA	GAACAAGATC	GTGAA	

## 1401RP

	GATCTTGTGTG	TTGGCAATAC	CCTGTCTTAC	GTTGAAAAGA	AGTGTCTCTG	AGGTGTCCAT	60
20	CAACAAAAAT	ATTACCAAGT	ACAACACCCA	CCCGAACTCT	ATTGGCCAAA	ACATCCAACA	120
	ATGTCGTCTT	ACCTGCACCT	GAATAACCCA	TCAGAGCAGT	CAAAGTCCCA	GGCTTTACCC	180
	AACCATCCAC	GTTGGTTAGG	ATCCTCCTGG	TTTCATTCTT	AATCTGTATA	TCATAGCAGA	240
	CATCTCGCCA	GTGGAATAATG	CTATCAGAAC	CAATTCTCTG	AATAAGTTCG	CGGGATTGGT	300
	CACTTCCTAT	AGTACTAGAT	TCCTTTCTCTG	GTGCATTACC	AAATTCTATG	TCGCAGTTGA	360
	TGGCCTTTT	ATTTTGCTTT	TTTATTTTCT	TCAAAGTTGA	CCTTAGGAAT	ACAGCCATT	420
	CACCTTTTGT	CATCCCACTT	TTATTATACT	CAATTAAGAT	CAGATAAACA	CCTAAGAAGA	480
25	AAAATGCATA	AGCAAGAACG	ATCCCCCAAT	TCATCCACTT	GTTTTTGGTG	TTGTAACCAT	540
	AAGCAAACCTC	TATGTAACGG	GTCCCAATTA	CAAAGCTCTG	ACCAGGAAC	GCTCCCACCG	600
	ACAAGCAGAC	TTTATTTCGAA	ATAGGGAATC	CCTCATAGAA	ACTACCATCG	GGTACCATT	660
	GAGAACATTC	GAATATGCGT	CCGTCAAATT	CATTGCAAC	CATGGCTTCC	ATGATGCGTG	720
	CGA						

## 1401UP

	GATCTGCTGA	GATTAAAGCCT	TCGTTGTCTG	ATTTGTTTTT	TATTTGGAAG	TCTGCAGGAG	60
35	CAGGCTTTGA	AATAGAGTTC	TTATGTTATT	TAACGTCGGG	GTAACGAGTA	TACAAGCATA	120
	TGTTTATGCG	TATGCTAGTT	ATATGCTTTG	AAGAGGTGGT	CTGCAGCTGG	CGGTCTATTT	180
	TATTTTATTT	TTTCATTTCA	CTAAGACTTT	ACATTTTTTT	TTTAAATTAT	TTTTTTTGCG	240
	CTAAGACTGT	GAACAGCGAT	TTTAGAAAAA	AGCGAAAACG	TTCAGGAGGC	CTCAGCTACA	300
	TGATATCCCA	GGCCTTGAT	TTGTGAGACT	GCACTCCCGG	GCTAGGTTGT	GACCAAGAGT	360
	TGACGTGCGG	CGCGGTGCGG	ATTGCAGGGC	TTCACAGTGT	GGTTAATTTA	ACAATTTATA	420
	GAGAATAGAG	ATGCCCCGAGC	TTAATCAACT	GTCGGGCGCG	CCAAATTCTGA	TTTTTTGGAG	480
	TTTGTGATT	TTACAGCAG	ACGAGAAAGC	AGGACAGGCG	GCGCGCGCCA	GGCAGTCCCC	540
40	CCTGCAGGCG	TGAGCGGACA	CAGAGAGAAA	ATACAGGAAG	ATGAATACTG	ATAATCTACA	600
	GATTTTCATTG	ATATCTCATT	GATCCGCTGA	TTATCAATGA	AAGTACCCAA	TGATCCATGA	660
	AGCCAGTAGA	TGTTAGTATA	TTTTATTAAA	TATATGCACC	TTTGTATTAC	AATCTCTGTT	720

## 1402RP

	GATCAGGAGC	CCATCAAGGC	GCCTAAAAAT	CGCATCCCCG	CTGTCGGTTT	TCCCCACTAC	60
50	GCCGCTGTTG	CTTGAAATAC	AATTACTGCT	GTAGTTCCTC	CTGTGATGCT	GGTTGAAATG	120
	TTGCGGCGCG	AAAGGGTCTG	CCTGCTGAAA	GGAGCTGAAA	GGTGGTGACG	TGGTTCCGGG	180
	ACTACTAGCG	TCTGCAACCG	TCTTTGAGCC	CAAAACACGG	AGGCCGATTA	CATTCCCGTC	240
	AGCCGGCCCG	AGGGTAGAAG	ACCTCCCCCTG	ATGGGAGTTC	ATGCTCTTAC	TGCGGGTGTG	300
	GTAATAGTAC	TCACCACCAC	TGCTCGACGA	AAGCGGAGCA	GGGGGTAGCG	CTGCCACTG	360
	TTGTTCCCTC	CTGCGACGTG	CTTCTAACTG	TGCCAAACGC	AGCTGTGCCT	GTTGCTCCTG	420
	GTGCGCGTCC	ACCTTGCCCA	AGAGCTCCGG	ATCATCATGC	AACATCTCCA	GCACCTCCAA	480
	TTTCGCCCTC	AAGCCACGTG	ACTCGGCTTC	CAGGTCGTCC	ATTTCTCGAT	GCTTGATCAT	540
55	GACCTGCAGA	TGGAGCTGCT	CCAGAATCTC	GCGCTTCGCT	ATCTCGTATT	TTATCCGCTC	600

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CGTCTCCTCG CTCTCAGCC CCAGCGGCCC CTCCTCCGCA CGCAGCCCGC TGTATTGTC  
GTCGCCCAGG GAAAGCTCGT GCGGCGACTT CGGTGTCGCC ACCTGGTAAT ATGCCGGCC

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## 1402UP

	GATCAAGTTA	TCGTTGATCA	AAGCGTCAAT	ACCCCTTTTCT	CTAAGCATGT	GCCAGGTTTC	60
	CTTCGCGGCG	CGTAGGTATG	GTTTCCCGTA	CAACGCAATG	AAGCAGTAGG	CATAGTGGTT	120
5	GAAGTACTCT	GCCATCCATT	CAAAGACACC	AACAACGGCA	TCCAAGATTA	ACCACAAGCA	180
	CTGCATCCAC	CCACTGTCCG	ATATCCCGGA	AATAATCCCA	TTGCGAAGCA	GCTGAATAAT	240
	CTGCCGAGT	AGTTGAATCA	GAGACACAA	CAGCGAGCCA	AAGCAAATGG	ACCCAAAGGA	300
	AGTGGTCAAC	GCTCTCTTTA	ATGAGCCAAA	AGCTGGCCAA	CGTGGCATGC	CTTGGTCCGA	360
	CTTCGAAAAA	TAGTACCAGC	AGCCGTAGAT	GCCCCGATG	GTGCAATGAA	TCACATTCCT	420
	GATGACCTCA	GAAATGTAGA	ATCCACAGAA	GAAAACGAGT	ACCAAAATAC	CAATTAACTT	480
10	TCCACGTGAG	CAAGAGCCAC	CAGATACATC	GCAGCCACCA	TTCTCGCTCT	TCGGGTCATA	540
	CTTTATGTAG	GTCGCAACCA	ACACTACAGA	GAATATGACA	GAGAACGCAG	CCGACACAAT	600
	GGTACCTAAT	AATGACACAA	GCCACGTCTG	TGGATGTTTC	TTTATAACTG	ACATGACCGT	660
	ACGCAAGACA	GCGACACTAA	ATGGAATCCT	TGAGCGCATT	AACCAGTAGC	ACACCGCCGT	720
	CAGAAT						

## 1403RP

	GATCCGTTCC	TTGAGAAGCA	CCTAAAGCCT	GAATCCTGG	CAGAAGCGAT	CAAGGGAACC	60
	TCTTGGGAGG	GTAAAGTTAG	TATTAACCTG	GTAGACGGAT	TCGACCACTC	GTATTACTTC	120
20	GTCAGCACGT	TCGTGCCGGA	ACACGCAAAG	TACCATGCAG	AAAAGTTGGG	TCTAGTTTGA	180
	GATTTGACGT	TGCGCCTGTT	AATTGGTATA	TACTTACATA	TTTAGTCATA	TGACGGCTTC	240
	AAGTACTCTG	ATTCTGCATT	ATAAGTGCAG	CCGAATGCCA	GCCTCCGGCA	GTAAATGGCA	300
	CGCAAACGTA	ATTTGCCGGT	AGTTCAACCT	TGGCCGGTTG	CAGCACGCGT	ATGCTCCGAG	360
	CAGACTCAAA	CGTCGCTATT	TGGCGGGTAT	CTACAGCCTC	GTCGGGATCT	CCCTGCCCAA	420
	GACAGCCACA	GATATCACTC	TCCAGCCCCC	AGGAGTAGAG	TTCACCTTTG	TCGGTTAGAG	480
25	CTAGGTTGTG	GTAGTCTCCC	GCAGATACAG	CAATAAACTT	CTGGCCTTGT	TCCAAATTCA	540
	TCTTCATGAA	TGAGTCCTCG	ACGATATCAC	CATTATTTCAC	CTTCAGGGTG	TATGTGCTAT	600
	TCTCGGTACA	TAAAACCAAGT	GTCATGCAAG	ATGCCTCAAT	CTTCGTTTAA	CCGTCCATCA	660
	AATGGCAAAT	CAACGGTTTTT	TGAAACGCCA	TGAGTGTATA	TCCACAGTTT	GCGCCCATTG	720
	TTAGTAATGT	A					

## 1403UP

	GATCTCAATA	TCAACCAACT	TGTGACGTCG	CTTAAACAC	CATATGCGGA	GGACATTATG	60
	TCCATCACCG	TGTACAAGGA	CAATGTTTTT	GCCACGCACA	AGCAGGGCAT	TACGCGGTTT	120
35	CACCAAGGGA	ACGTGAACCT	CTGGAATGCT	CACCAGGGAC	TCGTCTTGAG	TAGCGAAATA	180
	TTGCGCAAGA	GCTGTACCAG	TAATCGTATA	GATCGGATGG	TTACTGGCGG	AAATGATGGG	240
	TCATTAGCGT	TGTGGAATAT	TAACGAATGG	CTGAACGGTA	CAGCGTCCCC	GGGTGGATCA	300
	GCCCCGACCG	AAGAACACTC	GCTTCCCTCT	GGCGAGCGCC	GAAATCTTTG	GACCGAGTAT	360
	CAACAAATCC	AGTTAGATAA	CGATCACATG	ATTGCAACAC	TCGGGGAATT	CATTAGTTAC	420
	CAGACTGTTT	CCCAACTCCC	AGAGCCCCAA	AATATCATCG	ATTTCGCGTAG	GTGTGCGAAC	480
40	TTCTTGCAAA	ATCTCTTCAC	TAAGCTCGGT	GCTAACCAT	GTGGGCTTAT	ACCTGTCAGT	540
	ACAGGCAGCA	ACCCGGTGGT	TCTCGCGCAG	TTCAAGGGCA	ATGCAGCCGC	GCCCAAACGC	600
	ATACTATGGT	ATGGCCACTA	CGATGTGATA	TCCGCGGACC	ACCGTCGCAG	TGGGACAACG	660
	ACCCCTTCACG	CTCACTTGCG	AAAATGGGTA	TCTTAAGGGA	AGAGGCGTGT	TGATAAC	

## 1404RP

	GATCTGCAAC	GTTACTGATT	ATCCTGTAA	CCCTCTTTTG	GGTTAAAAA	TCCTGTGAGT	60
	TAACAGTCGT	GTTGAAGATA	GAAAAATAAAG	CAGTGTATGA	TGATGCTGGA	ACAACCCCTG	120
	ACATAACCAC	CACAAGATCT	AGAAAGTGTG	CACTCATTTT	TGGCTGGCCC	TTACAGGTT	180
	GGCTAGACGC	CTCCTTATCC	ATGGCATCTT	TTAGTAATGC	GCATACGTTA	TCAAACGTGT	240
50	TAGACAGGTT	TTCCGCAGAA	GTAATTTTCA	AGTATGCCTC	GATGGTTTCC	AAAATATAGC	300
	TCCGAGCGTT	GGGTGCAGTC	TGCGTGTAGA	CATTGAAAAAG	AACGGCCAAC	ATATTGGGCG	360
	ATTTCTGGGA	GAGGTATTCT	ATGTTTTTCT	CCGCTTCTGT	CGGCGGGAAT	TGCTGTCCCA	420
	TAATAATGTC	GTCCTTATAC	GCACCATCTC	TGTATAGAAG	ATTACTTGTG	ACCAAGACCT	480
	TCAATCCATT	GCATATGACA	GTACGCAGTT	CAATTCTGGA	ATAAAGTAGG	GACGCTAACT	540
	CTGCAGCAAA	CTCATCCGTG	AATACATCGT	TTAGATCTTT	TGGAAGAACG	CAGAACTGAG	600
55	GGAAGGTAGA	CCACAATTGG	TCAACAACAG	TCTGAAGTAA	TGTGCACTGG	ATAGACTCCT	660

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TATCCAGTTT CTCAATGGTG GACTCGAAAT GACGAATGGT AGGAATAAAT

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## 1404UP

	GATCTTCAGC	AAGATCAGCA	CCACTTGACG	CACTACAAGA	AGTACCGGCA	CTGGCGGTGG	60
5	CAGGCCAAGC	GCAGGCTGGC	CGGCTGCGAG	TCAGGAAAAG	TCGGAGCAGG	TCGTACAGGA	120
	GCCCCAAAAC	GCCGAGCCGC	TGGCGAAGCT	GGGCGACGCG	CTGACGGTGA	CGGCGCTGAC	180
	GGGCAAGATG	AGCTACTACC	GGCAGCTCCA	GGGAAGCGTG	AGCTCGTTGC	TCAGTTCTGT	240
	GTCGCAACTA	ACGACGTCCA	CCCCGGGCGCC	AGAATGCGAC	TTCAGTGAGC	AGTTCATCAC	300
	CTTACTCGTG	AACACCTACC	ACGAGATGTG	TCTGGATGCA	ACCGTCACAC	CGTTCGACAA	360
	GACTAACCCG	CCATCTGCTT	TTCTCAACAA	GGTAGCGCGT	GCTGCGGTGG	AGCGTTCTGA	420
10	GCAGCAGAGC	ATCGCCATCG	GACGTCCGCG	CGATAAATGG	TTGTTGACCT	GCACGCGGAA	480
	GCGGCTTCTA	CAGGAAATAA	AGCGGGAGAC	CGAGGACGTT	CCACAGGGGT	CCGTGCGCTC	540
	GGTGGCCTGT	TCCATGAACC	ACGGCACCCCT	ACAGCGCGAT	CTAAGCTCCG	CTTTTGACAG	600
	GGAGGGCGAT	TTCTTCTACT	GGGATCCGGA	CTTCCAACCTG	TTCCAAGGCA	TCACGGCAAA	660
	ACTTCTAACC	GACACTGGAG	ACATCTCGGG	CAAAAATACC	CCATGTCTTT	GGATC	

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## 1405RP

	GATCTTTCAT	ACTTTCGGGT	TCGTGCTATA	TAACCTAAGAT	TGGACAGAAC	TGCAAGGGCC	60
	ACAGAGGAAG	AGCTGCTGCA	TTGCACATTA	GGCAGGAACA	GCGAATGTCT	ACAAATGCAC	120
20	ACTACACACT	ACCGCTCTCA	GCCGATCCCA	ATCTCAGATG	CGCACAGCAA	GGGACCCAGT	180
	TCTTTGCCCA	TGCCGCTGTA	CTCGCAGCCG	GGCGCAGATG	GGCTGCTAAC	CATTAATGCG	240
	AGCGCTGTGG	GCTCGCCTGT	GGCCCCCGAG	CCGGTGATAC	CTCCACTCAT	GCACCAAGTG	300
	GCGGTGACAA	AGCACGCTCA	TATCATGCCA	GGCTCGTACG	CGCTGCGACA	GAGCTCGCCC	360
	CAGGTCACGG	CGATTATGGG	CGAGTTAGCG	ATGCTGAAGA	AGTCGATATT	CCAGTCGCTG	420
	AACGGCGAGT	TGACGACGGA	GGAATACAAC	AGCATCTACC	AACATTTGAG	TCAACTGCTG	480
	GCGTCCCTCC	CACCGCCCGT	CGAGCCATCT	GCAGCGCAGC	CCCAGCTGCG	ACTGCCGTGG	540
25	ATATCTCAAA	TTATGCCGGG	AACAGAGCCC	CAGGAAGTCC	AACGTACCTT	CATCATAGCA	600
	TCCTCCGAGT	CACAGCAGGG	CCAGCCGTAC	ATCTCGCCGC	CGTTAAGCTC	GACAAATGCT	660
	ACGCACCCGC	TTTCACCGGG	CATGTCGGTA	GCCAAACCGA	ACTACTCCGT	GAGACCAAG	720
	AAGAATGTT						

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## 1405UP

	GATCCAAATA	ACACCACGGT	TTTCATCGGC	GGGTTGTCTT	CGCTCGTGAC	TGAGGATGAG	60
	CTACGGGCTT	ACTTCCAGCC	ATTCCGACAG	ATAGTCTACG	TGAAAATCCC	GGTCGGCAAA	120
	GGATGCGGCT	TTGTCCAGTA	CGTGGATCGC	AGTTCCGCGAG	AGAACGCGAT	CGCCAAGATG	180
35	CAAGGATTTT	CAATTGGTAA	TTCCGAGGGT	CGGCTCTCAT	GGGGCAGGAG	CGCAAAGCAA	240
	ACAGCCGCTA	TGCAGCAGGC	GTTTGCCATA	GCACTACAGC	AGCAGCAGCA	GCAGCAGCAG	300
	CAGCAGCAGC	AAGCCCCGCC	GCAGCATTTT	CAGCAACATC	AGTATCAGCA	TCAACAGCAT	360
	CAACAGCAGC	CTCAACATGT	CATTTCTGCA	CAGCCGTTGC	TGCAGCAGCA	ATTGCAACTA	420
	CAATTTCCTT	ATCAGCATCA	ACCTGCCATG	CCGCGAGGCT	ACGGTTACAC	ATTGGACTCG	480
	TTGAGCGGCA	CCGGTTGCAA	ACATGTTCCA	ATGCAGGGTT	TTCTTTCCGG	TAATATCGGG	540
40	TTCCAACCTT	CTACGGCAAT	TGATAGCTCT	CCAGCAACGA	CCTTGCTTCC	CAACCTTTCT	600
	TCGTTGGACT	ACTCTGGGTT	TCCACCTTCC	ACGTCAGCGT	TCACTTTTC	CCCACGAACT	660
	CTTTAGGCAC	AGCTTTTACA	ACATCGCCTA	GATTCTCAAC	AATGGCAGCG	TGTCC	

## 1406RP

	GATCTCCTTC	CAGTGACGCT	GATGCACAAC	TGCGGACCTC	AGCCCGCGTG	CCTCACGTGA	60
	CCACAGTGGA	CATTTTCTCA	GTTAGCGCTC	GTTTAGCTTA	GCTATACGAG	GGATGGCACC	120
	ACTTAGCGCG	TGCTGCGGAA	CCAGATACGA	TGAAGCCGCC	CAAATTTCGAT	AGAATGCTGC	180
	CTCGCTGAGC	CGCCGTGATA	GGGAAACGAC	CAAAGGTTCC	GTCTGCCGCA	TCGTATGTAT	240
50	GTGCTGTGT	ACGAGGACCG	AAAAGTTGAC	TTTTAACGAA	GTAGATTTTT	TTATTAGATA	300
	TTTAAGCACG	TATGCGTTAA	CGAGCAGCTT	GCAAGGCGTA	TACCAAGGCT	CTGTGCGCTT	360
	ATCATTAGCA	GGGCGACATG	TCAGAAATCCT	TGCTACAGAC	AGTGGTGGCG	TACGTGGAGT	420
	TGGTGCTGCA	CCACTTCATG	GCGTTGTGCT	GGACGACGCA	GCTGTCCATA	GTAATAGTGG	480
	CACCATTCAT	ATACTCGCTG	GTGTGCGAGA	CGTTATATTC	ATTAGGAAG	GATAGAGTAC	540
	CGCTAGTGCC	GTTTATGGTA	CCCTGGGTGG	GTTCCGCGCT	CGCGTATGGG	AGGGCTCCGT	600
55	ACGAGTTTPT	TGCAAGTGTC	AGCAGAAGTA	TGGCGATGTG	TTTGCGTTCA	TGCTGCTGGG	660
	GCGTGTGATG	ACGGTGTATC	TGGGGACGAA	GGGCCACGA			

## 1406UP

	GATCTTCATT	AGAACGCGCG	GATTAGTCAA	AAAGTGCCGG	AATGTTCCAT	CCACTAGGCC	60
5	ATCTGCCCTTC	ACCCACGGAT	TGCAAATGCA	GACAAGGTTT	ATTAGAATTA	TACCGATTGC	120
	CCAAACGTCG	CCTGCAGCAG	TAGGAGCTCG	GAGCTCACGA	CCGAGCGATC	CGCGCTCGGG	180
	TGCCATGTAG	TAAGACGAGC	CTACGCAGAC	ATTGGGGGCG	AGCTCCGGCA	CGGGTGTGGC	240
	CAGCCCGAAA	TCGCATACAT	GTACGTTGTA	CCATTTGTCC	AGAAGAATGT	TCTCCGGCTT	300
	TAGGTCGCAA	TGATAGACGC	CGAGTCGGTG	GCAGTAGAAA	ATAACCTCGC	ACAGCTGCAG	360
	GAAGACCTTC	TTAATCAGTA	GGCCATCCTT	AGCAAAGACT	TGCTCGTTGA	CAATGGCTGA	420
	GAAAAGGTCTG	CACGTGATGT	AATCCATAAC	AATAAATGTT	GCCAGGCTTG	ACTCCATCAC	480
10	CTGATGTATG	GTAACCACAT	GTTTCGTGGGT	GTGCACAGTC	AGGTGCATCA	GCAGCTCCTT	540
	ATAATGTGGC	GCGTGGGCCA	GCTGCTCTTG	GGATAATGTC	CGGATCGATT	CCAGGTCCAC	600
	AGATGGTAGA	TACAGCCGGT	TCTGGAAAGA	TTGAAGAAGT	GGTACAGCTG	CGTGCGCAAA	660
	ATTGTCGACC	GGCCTGACGC	CTCGTCTGCG	CTGCCGCTGT	GCTGCTTCA		

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## 1408RP

	GATCCCGCTT	ACCAAGCAAT	TACAGGAGAC	AGAAAAGAAG	GATAATAATT	TACCACAGAA	60
45	CTCCAAGCCT	GACAGAGCAG	CGATTTACAT	TCTGAGTCAC	ATGACAGCAG	ACTCTCTTTG	120
	CTTTGGAGCT	TCAATAAGCA	CCAATATGAA	TATGAATAGT	TTTAGATGCT	TTGTATAAAT	180
	ACCACTATTA	ACTTTATCTT	GATTAATATT	TATTATTTTG	TTATTTTATT	ATTTTATTAT	240
	TTTATTATTT	TATTATTTTA	TTATTTTATT	ATTTTATTAT	TTTATTATTT	ATTTTATTAT	300
	TTATTTTATT	ATTTATTTTA	TTATTTTATT	TATTATTTAT	TTATTTATTA	TTTATTTATT	360
	TGTTTGTTTG	TTTATTATTT	TTTTATTTAT	TACCTTTTTA	TTTTATGTTA	TTTTATTTTA	420
	TTTTATTTT	ACTTAGTATA	TAATATTATA	TTATATCATA	GTATAGTTAT	ATTATGGTGA	480
50	CTTTATTTCAT	TATATAGATT	GTATTTTGTG	AACATAATAT	ATATGCTATT	TCTATTTCTA	540
	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	600
	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTATTTTA	TTTTCACT	

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## 1408UP

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GATCCGCCTT	CCATCGAAGA	GGGTACTGTT	TGATTATGGT	GATTTCTTGG	TGTGGGTTCCG	60
ACATTCAAGT	GCATAGTTGG	AGGTTACCGA	TAACCTTAGAT	TTTCTTATAA	ACGGTTACCC	120
TACGTCTTCG	CGGTTGGCGG	ATATACTGAT	TAACAGTTGG	AGAGCCTTGG	CGGGATACTG	180
TGAATGCCTT	CTCTTCAACA	TTATTTGAAT	ATGCAAACGT	TATTTAAATT	AAGTAACACA	240
CTTGTGCTTA	TATATTCAAT	TGTTCCAAGC	GCGCCATCCA	ACATGGCGAT	TCTCATCTAG	300
TTTGAGAACT	TGCGTCTATT	CTTATTCTGT	GTACGGCAAC	GGTATTAGGA	GAGACTTCGA	360
GTTTTTGGAA	CTTCAAAGTC	AATACTTCAT	CATCGTAAGT	AGCAGTTACT	TGGCCTAAAC	420
CAGTGCCAC	CTTTGTAGGG	AGCCTGATTTG	TTCCGCCAAA	CTCCGGGTTT	GTGGGTTCTC	480
CAGTAGTCCA	CGCGTCTGTA	TTCTCATCCG	TATTAATGGC	TGGCACGACA	ATAGAAAGAA	540
CTGCATCAAT	CATGTCTCGA	TGCAGGGCAA	TATCTATGTG	GTCTTGAGAC	ATTACGCCAG	600
GAACTCTGAT	GTGGATCTCA	TAGGCGTCCG	AACGCTCCAA	AATTAATAAT	GAAGGAAGAA	660
CGTCAGAATT	TGCGCGCGAG	AGCTTGATTT	CTGAAC TAGC	TGCCACACTC	TCAGCTTTGT	720
GT						

## 1409RP

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GATCCTGGCT	ATCTACCTGC	TGCTGGGCGC	GCTGCACGCC	ATACTAGGGG	GCACATTTCAG	60
CGGATTAATG	TATGTGGAAT	ATGCGCGAGT	AGAAAACGCA	CGTKCATGTG	ACAACAAGGC	120
CACCGGACTA	ACCAATTTAC	AGAACC GCCG	CTATTTACAG	GGCTGCCCTG	ATCGCGATGA	180
GTACTTGGAT	TCCGCTTGCA	TCCGCAGTCG	TACAGGCCCT	GTACCTGCTA	TGCGCAGCAT	240
TTGTGGCACA	ATCCAAGCTG	ATATAGGATA	CAGACATCCA	GCAAGACGCT	GGATGGATCG	300
TGTGTATCCC	TCTGCTGCAT	CAATACGCTA	TCCGCGGCCG	GCAGCTTATT	GTCACGTGAT	360
TCGCTATCTT	GTGGAGCACC	CAGACATATG	TTGCTGAGCC	TCCCTCAGCT	ATATAAGCGT	420
CGAAGAAGGG	CGCGAGTCGA	ATACATGTCT	CTGGCGCTGT	GTGCCTCGTG	CAGTCTCCG	480
CGATGTCGTC	AACTCTCAT	AACCGTTCCCT	TGGCAACTAT	CCGTACAGAG	CTTGCCTTTT	540
TGGTTGATT	CGGGGTCATT	ACGCGGCAGC	AGTCAGAGCA	GATTGAATCT	AATCTTCCAA	600
ACCCTAACGA	AGCCCTCCGT	GGCGCTCCCG	CAAATAACGC	AGGGCCTGTG	GAGTATGTGG	660
AGGCACTTTA	TGCGTTTCAG	GCGCAACAGC	CTGGTTGACC	TAGACTTCAA		

## 1409UP

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GATCGGGGAC	CAGAAAACCA	CACAACTGGT	CCTTGAGGCG	GCGGTGGGCG	TATACGCTGC	60
TACTGTCTCT	TCTTGTCGTA	GCTGTGGCCT	ACGGCTCTGC	GTGCGTAACC	GCTGGCATGT	120
GGCTCATCAC	CAGAAAATAT	GATGTCTCAA	CCGAAGTTGC	AATATTGTCC	TGTTCCCTGG	180
TGGTCTGCGG	CTACGGTGTT	GGACAGCTGG	TTTGGGCGCC	TCTGTCAGAC	CTGTACGGCC	240
GCGGATAAAC	TCTACTTCACA	TCTCTATTCC	TTTACGTGGT	ATTTAATATT	CCATGTGCGG	300
TGGCTCCCAA	CATCCAGACG	CTTTTGGTTT	GCAGGTTTAT	TTGCGGCGTC	CTGTCTGTCG	360
CTGGACTATG	CTTAGTCCGG	GGCTCTCTCG	CCGATATGTT	TCCAGCCGAC	CTGCGTGGGT	420
TGACCATCGC	GTTCTTTGCA	TTTGCACCAT	ATGGAGGTCC	GGTATTTCGG	CCACTTATAA	480
ACGGAATTCAT	CGCTGTCCGA	ACAGAGAGGC	TTGACCTTAT	CTTTTGGGTC	AACATGGCGT	540
TAGCCGGAGC	TGTTTGGCTG	TTAGTCGCAC	TGGTGCCCGA	AACATATGCG	CCAATTATTT	600
TGAAACGGCG	CGCAGAGAAG	CTGAGGAAAC	TAACAGGCAA	CCAGAATATA	ATGACAGAAC	660
AGGAAGCACA	GGGACTCTCC	CTGTCCGCAT	GGTGCAGACT	TGTCTACTGA	GACCG	

## 1410RP

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GATCAATTTCG	TCACATTTTCG	CGTATGCAAT	TTCTACCATC	TCCTCTTTGG	TAGCCTTTAA	60
TTCCACTCCT	GGTGTAACAT	CACATAATGCC	AATAGAAAAG	CCTCTATTTC	CCAGATAGCG	120
CGCACAAAGC	TTTGCCATCC	TATTCATAGC	CTGCGTTGCT	TCTTGTTGCC	CGAAATCTCT	180
CAGAAATAGTA	TAGAATACGG	AATGTTTCTT	ACCATCACCA	AGCACAGACT	TATCCATGAC	240
ACCAGACAGA	ATATTAGAGC	CTCTGATAAC	TACATAACCA	TCATTAGCAG	ACATCTCATT	300
TGGATAGGCC	TTATTCTTAG	GCGCAATATA	AACCTTATTC	TTTGCAATCCA	AATTAATAAT	360
AACGGGAGAT	TTCTTGTTTCG	GTTTTATCAA	TAGAGAGAAG	AGCTGTTTTC	CAGTCCATAA	420
GTAGTGTGGT	CGCATAATTCG	CAGGCGGCGG	TATGTCAAAC	TGCAGGTTGC	CGTCAGACAT	480
CATAGAAAGC	ATTTGGACAA	AAGTTGCGCG	GTCGAAGAAG	GAGTCTTTGT	GAGAAATCAA	540
ATATGATCCA	GTGATGAAAT	CCTGGGTAGC	TGCAATGATC	GGTTCAACCG	ATTTCCGAGT	600
CAATAAATTG	TTTTTGACAC	CCATAAGGTT	GATTGCTTCC	GGGCGAGCCT	CTTCCGTTTG	660
AGGAACATGC	AAGTTCAATTT	CGTCAACCATC	AAAATCGGCG	TTGTAGGGG		

## 1410UP

	GATCTGAGCC	CTAGCATCTT	CGGTGGAAG	CGGGAAGTCT	ATTTTCCTAT	CCAAACGACC	60
	GGAACGCAGA	AGCGCTGGAT	CAAGGACATC	GACTCTATTC	GTAGCAGCCA	AGACTTTTAC	120
5	CCTATCGTCA	GAACCAAAGC	CATCTAGTTG	GTTTAGCAAC	TCAAGCATGG	TTCTCTGCAC	180
	CTCTCTATCA	CCGGACTTCT	CCGAGTCAAA	ACGCTTAGTT	CCAATAGCAT	CCAACTCATC	240
	GATGAAGATA	ATGGTAGGTG	CCTTTTCCTT	CGCCAAGGCA	AAGGCGTCGC	GGACCAGCTT	300
	CGCACCTTCA	CCTATGAACA	TCTGGACCAA	CTGCGGAGCG	GCCAGCTTCA	AAAAAGTCGC	360
	ATTGGTCTGA	GCGGCACAGG	CTCTTGCCAG	AAGCGTCTTG	CCGGTACCCG	GTGGACCATA	420
	CATCAGAGCA	CCTTTCGGTG	CCCTAATACC	CATATCCTTG	AACTTGCTTG	CCTGCTTCAT	480
10	GGGTAACACG	ATTGCTTCGA	CTAGTTCCTC	GATCTGCTTG	TCTAGCCAC	CAACGTCGGA	540
	GTATGTTTCC	GTAGGCTTGT	CATCCACTTC	CATAGCTTTC	ACTCTAGAGT	CAAACCTCCGA	600
	AGGAAGCGTA	TCCAAGATCA	GGTACGAGTC	CTTGTTTACA	CCCACCAGGT	CGTTCGGCTT	660
	CAACTGCTTA	AGGGTCCACT	AGCCCAACCA	TGGGGAGAAA	AACGGTTTGT	CGCGACGAAG	720
	TTTCACA						

## 1412RP

	GATCTGGAAC	CAGGATGACT	GTCTGGCAGT	TAAGTCGGGC	GACCAGATTG	GCTTCCTACA	60
	CAACTTCTGC	TCCGGTGGCC	ACGGTATTTT	CATCGGGTCT	GTTGGCCACA	AGAAGGGCGA	120
	CTCAGTCACC	AAC TTCTCTG	CACAGGACAA	CCAGGTCTGC	GAGTCGGACA	ACGGTCTAAG	180
	AATCAAGACT	TTCGTGGGCG	CCATTGGCAA	GGTCGACAAC	ATCAAGTTCA	TCAACAACAA	240
	GGTCAAGAAC	ATCCGCAAGT	TCGCTATCGT	CATCCAGGGC	GACTACAAGG	ACGGCACCAC	300
50	CACCGGCACC	CCAACCGGCG	GCTGCCCAAT	CACCAACCTA	GAGGTCAGAG	GCAACACCGG	360
	TAACACCGTC	GGCAAGGGCA	GCAAGCTCAA	GATTCTCGTC	AAGAATGCGT	CTAAGTGGAC	420
	CTTCGCCGAC	AACAACATTT	TGGGCAAGAC	CTTCCCAGGC	TGCTCTGGCG	CACCTAACGG	480
	CATCAAGTGC	TAAGCGCCTT	TTTTTTTTTT	GGCTGCGCCT	CGAAACTATT	ACTATGAACA	540
	TTGGCGTCCA	CCGCCACTAC	AAAAGCATCG	GGTCTATCCC	ATTATAACAT	TAAATCTCA	600
55	GTTGATATTA	TATTTTACAT	TCGAATGTCC	TTAGGGCTTT	TTTATATTAT	ATAAACTTTA	660

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GATTAAAAA ACGAGGTACA AGCAGATCAA CGAAGCTTTT CGGCCAGCCA

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## 1412UP

	GATCGAACGA	GATAAACAGA	GGTATTGGTT	GTTATCACAA	ACATATAATC	CTGGGGATAC	60
	AACGCTGTCA	AACTCTGGGC	CTTCTGCTTT	GTGTCTAGAT	TCCTTTTGCA	GGCTTGAGAA	120
5	TAACCTGTAC	AATTTTMTGA	TGTGGTTAGT	AAGAGACGCA	TCAACGATAT	CATCGCACAA	180
	AGTTCGGTTT	CTTTCCCTTG	CAAGCGGGAA	TGCGCCTTCA	TTACTTCCCG	AATCTTCTCC	240
	ATGAGTCGAT	GGTCTCGGCG	TTGAAGCTTG	TAGTGTCAAA	GGTCTATTC	TTGGAGAAGG	300
	TTCTATCTCT	ATTTTTTGTC	CCCAGAAAGA	ATCATTGAC	ATCCAATATC	TTGTAACTTC	360
	CCTGGGATGT	AATCTTTGAA	TAGCGGGTT	TCGGTACAAG	CTGCTACCTG	CCAGATTATT	420
	ATTTAACGAT	TCTTCTGGTC	CGTGAAGGTG	ACGTATAAGG	TGGACGCTAT	TGGGTTTCTT	480
10	TTCCAACATA	GGTTGTTCAT	CAAATGAGAG	GTAAAAATGGT	TCCTGCTGGG	AACGCGACGA	540
	AGGCTCCTTT	ACTTTAAGTC	TTAACAAGGC	GTCAACATAT	TCTTTTGTAA	TCGTTCTAGA	600
	AGTGGTTACA	AAATCCATAT	TGCGTCTTAG	ATCTGACTCC	TGAACGCCTT	TGTCTAGTTT	660
	CTCATCCCCC	AGTGGTAAAT	CTGAACGAGG	GACAAAGTAC	ATGCAACTGT	CCTCATCATT	720
	GTAAGTCA						

## 1413RP

	GATCTGCTGG	GAGTGACTION	GGAAGCTTTG	TCAGTACCTG	GAATGAAAAA	ACAGTCTCTG	60
	ACAGAGCGGG	GAAGCTGGGC	CTGATGGTCG	TTACAGCGGA	CCAGTTCAAA	GAATATGAAC	120
20	AATTGAAGAC	TGTCAGCCCC	AAGGATCAAC	TTGCTCAGCA	GGCGAAGGAG	CTAGATATGG	180
	TGCTAATTGA	TGCTGCTGAA	CTATACGAAT	TAAGAAGCAA	AGTTTCCGAT	GGACTGTCTG	240
	GCGATTTGAA	CTCTGACTTT	GTCTTGAGCA	AGGAGATCAT	TCTTGAGAAT	GCTCATAGTT	300
	ATGGTTTAAAC	GGTTCTTCAA	ACGGAAGAGT	ATCTTCAATT	ACAGAGTAGT	TTGGAGAGAG	360
	AACAGGTAAC	GTCCTACAAC	ATTGCCGAGA	AAGCAACTAC	AATTGGCTAC	GTTGCACTTC	420
	CAAGAACCGA	GTACGATGAA	CTTGTAGCTT	CGCAAGCTTC	TACGAAAGAA	CAGAATTTTG	480
25	AGGTATACGC	GGCGGAAAAT	GGCAAGGTCA	TAGTGGATAA	ATCTGAGTAT	CACGATTTGA	540
	AGATCAAAGC	TATCCCAGTG	ATTTCAACCAT	TGCCTCAAAT	GAGCAAAGAG	CAGATGGTTG	600
	AAAAGGCCAA	GGAACCTGGA	ATGGTAGCTT	TGCTCATTGA	CGAGTATGAG	AAGTTAAAGA	660
	GCCCTATTTT	CGATAACGCT	TTGAATGCAA	CAGCGAAGGG	ACCGTGGAAA	GTTTGTCTC	720
	CTAAAGGAGA	GT					

## 1413UP

	GATCCAGTTT	TAGGTCCACT	TCAAACCTGGA	TTTTCGGGTA	CTCCCCGCAC	ACCACCGTCA	60
	AGTCATCGGC	ATAGATGGAC	TCAAGCACTT	CCAGCTCCTG	CTTTTGCTCC	TCCTGATAGT	120
35	CCATACCTAT	CCGCTCGACC	AACATGAGC	CCACGCGCAG	CTTAGGGCTA	GACCGTTACA	180
	GCTGCAGGTG	ACCGTCCGGG	GGACGATGCG	CTATCGCTGG	CGAAATTTTT	CGCCTATACC	240
	ACCACTTATG	TTACCCGGTC	TATAGTGCTG	CTCTCCGACC	TCACTGATGG	TGCTGTCCCG	300
	CGGGGACTGC	TGCCTCGTGC	GGCCAAATCC	CCACCGCTCT	GAACGCTCGT	TCCATCTGCG	360
	TCACGGGTTG	ACCGAACGGG	AATTGCGCGC	GCCGAGAAAT	CTTGCGCAAC	CATGCTGCAC	420
	GTAGCCTTAC	TGCCAAAATT	AAGCCGTCAA	ATGGCTGGCT	ATCCTTCCAC	GCACGCCCAT	480
40	AGTCACCTGA	AGCTGGCTGG	AACAGTGGTC	ACGCAGCTTT	CTGACGCATA	CCAGGAACAG	540
	GTGGCCGAGC	CCGAGGCCAA	CGGTGGGTGA	TTATGTCAGC	GACTTTTGGT	GGATTACGTA	600
	AATCTGGGTG	CATGCCTGGC	ACGACAGCGC	GCATCGCACC	CCAAGACAAA	CGTGCCACAC	660
	CCATTCAATA	TTAGAGGACT	TTGCTGCACA	CCCTAATCAT	CCGTTGGGTT	GTGAGATACG	720
	C						

## 1414RP

	GATCCGTAAT	CGAGTTTAGC	TTCCGTGTG	CATCATCGAC	AGGTGGAAAT	GCTCGCTTGT	60
	CGGCCGTCTG	AAAACGAGTC	AGATGTGCAG	AGAGGCTGAA	GTCCAACATT	TTAACCACCG	120
50	CTGAAGACCG	GGAATAGTAG	GGCAACGTAG	TTCCGCGAAC	TTTCAGTTTG	TTTTCTTTTA	180
	ATTTAATGGA	CTACACCAAA	AAAAGCTCAA	CAACAGTCCC	AATTAGTTCT	GCTAGAAGAT	240
	GCAAACACGT	TAGTGATCAG	TAAGTATGTG	TACTCGTGTA	CTCGTCTGTC	ACTGCAAAAT	300
	TCGCGTCACA	ACTAGCTGTG	AACCATGGTT	TGAAAAAATA	TAATGATAAT	GATTCCGCCC	360
	AGGATCGAAC	TGGGGACGTT	CTGCGTGTTA	AGCAGATGCC	ATAACCGACT	AGACCACGGA	420
	ACCACCTATA	AGCCCTTAAT	TATACTCAGA	TACTAGTGAC	CATTTTCTAG	TCACATGATG	480
55	CTAGTTTCTT	GAATAAAAGA	TGCACGTGAT	TACCAAATCT	GTATTTACTA	GGTAAAAATG	540
	CTTGGTGAAT	AAGTACGTAG	ATATTATATA	TGTATACATA	TGCATTTTAG	ATGCAATAAA	600

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AGCTCTATTA TGTATGCGCG CGGAGCTTTA AGCCAGTGTG TTTTCCGATT GTTTGTGGA  
TGCAATGGTC TTTGCATAAA AGCCTGACTT TCATCTTTTT CGTGCTTGGA TGTAACTTC  
CAACTCTGA

660  
720

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## 1414UP

	GATCTGGCCC	CGCGGGCGCA	CCGCGGCCAG	GGGCCAAAAA	GGAGAGCGCC	CGCGGTGGCG	60
	GCCGCCACTG	CGGCGGTTGC	ACAAGACATA	TATGTCGGTA	TATAAGACCG	CGGGTGCCGC	120
5	GTGGCTGCCG	TGCAGAACCC	GCCGTGCGCG	CGCGGGCAGA	GATTTCTAAT	ACTCTGCGTT	180
	TTCTTTTTGC	AGCGCCTGGT	ATATAAGTTC	GGGCTGTGTC	GCGGGCCGTC	GGCGCCGTTT	240
	GCCAGGGAGA	TAGGGGAGCA	TTCCGCAGCA	GCCGTCTGTA	GCCGGACCAG	TACGACAGGG	300
	ACGCAGGACA	CAAAGCAGGC	GACGGCGAGT	GCGCGGGATC	AGCAGCGCAC	AGCGAGCCAG	360
	GGGTATAAGA	GCCGCGGTAC	GAGGCGGCTG	GTAGGTATAG	GGCCAGATGG	AGGTGGGTGC	420
	TAACGGGATT	TTTCTGCACC	AGAACGACTC	TGCGGAGACG	ATCAAGCTGG	AGATGTCCGC	480
10	TGTCGGCGGT	TCGGGGAGCG	CAGGCAGCGG	CATCGCGATG	GGCAGCGCGG	ACGACGAGCT	540
	GACGAAGTGC	ATCAGCGACC	TGAACATCTT	CGATCTGCTG	CACAACAACC	CGCCGTCGAG	600
	TTCGGACGAC	AACAAGGAGG	GTGGGCGGCG	GGCGGCTGC			

## 1415RP

	GATCGTGGTT	CTGTTATCGA	AACGTTGGTT	GCTAGAACAT	TGCGCCAGGT	TGAAAGTAGC	60
	CAGAGCATGA	TACGAATTCT	GGGATTATCG	GCTACATTAC	CTAACTTCTT	CGACGTCGCA	120
	GACTTTTTGG	GGGTAAACAG	ACATGTGGGA	ATGTTTTATT	TTGATCAATC	GTTCCGTCCA	180
	AAACCCTTAG	AACAGCAGCT	GCTTGGTTGC	AGAGGCAAGG	CGGGCAGCAA	ACAAGGAAGG	240
20	GAAAATATTG	ATAAGGTTTC	ATATGAAAAG	CTTTATGAAC	ATGTCTTAAA	TGGCTCCCAG	300
	GTCATGGTTT	TTGTGCACTC	AAGGAAGGAT	ACTGTGCGCA	CTGCGCGGAA	TTACATTTCT	360
	TTTGCCCAAG	CCAACCAACA	GTCCGATGTT	TTCTTAAGTA	GCGATCAAAG	CGTTACCAAG	420
	TTTCCCGAG	ACATCTCCAA	ACATAAGGAT	AGAGATATGA	AGGAGCTCTT	CCAACATGGG	480
	TTTGGTATAC	ATCATGCTGG	TATGTCTCGA	TCTGATAGAA	ATCTAACAGA	AAAGATGTTT	540
	AAAGAGGGAG	CTATTAATGT	GCTTATCTGT	ACAGCGACGC	TGGCCTGGGG	TGTGAACCTA	600
25	CCGGCTGATG	TTGTCTTGAT	AAAGGGAACT	CAGATATMTG	ACTCTAAAAA	AGGTGGTTTT	660
	ATAGATTTGG	GGATTCTGAT	GTGATACA				

## 1415UP

	GATCATCAGG	AGTTCGTCAC	CTTGGAACCC	AATTGCGAAC	CACAATTCCCT	TCTGAGCCTT	60
	TGGAATTTTG	TCACACCAAA	CTCTGAAACC	GTCTTTGTAA	CTTTCATTAT	GGCGGAATGC	120
	TACAAGTGTC	AACTTATCAG	GGTTGGATTG	GTCCCTAAAA	TGTACCTTAT	CCAGAACAGG	180
	AAGCATCGAG	GCTTACGTA	TAAACTTATC	TTTCGCCGCT	CCTTGAATGT	TATGCACGCG	240
	GCACACTGAG	CACAACGCAG	CATAGCCCAT	CCGACCTAGC	TTCTCCAACG	TCAGCATCTC	300
	GCCACTATAC	TCATAGGGAA	AGCCATCATC	CCCGAATAAT	TGCGGGTCTA	AGCGTTGTAG	360
35	CGTAATTCCA	GGCAAAGCAG	TCACCGGGTT	GTCCCTCATA	CATGTTCCCT	GCTTAATGCA	420
	CTGCATGGCT	TTAATCATAG	TCATAACTGT	CCTGAGGTAC	CCAGATTCGC	TTGCAATATC	480
	GATATAGGCC	TGTAGAATAC	GTAGCGCCTG	GTCGAGAACT	GAGATCGTAT	CTTGGAATAA	540
	ATCTGCAATT	GCTAAGTCAG	CTCTACTTAG	GTAAGCTTGT	AAAAGCAAAA	AGGCTTTGAC	600
	ATGGGGGTCC	CATATTGGTA	ACTCTTGTTT	TCCTGTAAAA	GTACTTTCAA	CGGAATATCT	660
40	AAGAGTTTCT	GACATTTCAA	CATTTCATGAT	AGTCTCGCCC	CCC		

## 1416RP

	GATCATCATT	ATTTCCCTGCG	TTCGTGCCGA	CGATTCTGAAG	GGCGGGGTCG	GTTTCTTGAA	60
45	GGATTTTCAGG	CGTATGAATG	TTGCTCTCAC	CAGAGCAAAG	GCCAGTCTCT	GGATCCTGGG	120
	TCACCATAAA	TCTTTATACA	AGAACAAGCT	ATGGATGCAT	TTGATTTTCAG	ATGCGAAAGG	180
	GCGTGACTGC	CTCCAAATGG	CATGTCCGGG	CTTCCTTGAT	CCACGGAACA	GAGCCGCCCA	240
	GGATGCTCTT	CATAGGTTCA	AAAATCACCA	TAATTATATC	GAGAACGCAG	ATGATTATGG	300
	GCCTGAACCG	GTGATGACTA	AATCAAGAGG	ACGCAATAGA	TCATCCAGAA	AACGCAAACA	360
	TATGGAAGAT	AATCCAGATG	ATAACTACGA	TCCCGTTGCT	GAATTCAAGA	AGGAAAATCA	420
50	AAGAGAAAGC	AACACAGGCA	CCGGTGGTTA	CCGTGCGGAT	ACATCTAACC	ACAGATTGGC	480
	ACCTGCTAGG	AACGATAGCA	AGAAGGCCAA	GACGTGCTCC	AATGCCGCCG	GTATTTCCGA	540
	GGCTACTTCA	GAGGATGGTG	ATCGAGGTCA	GAAAGGACAT	GGAACTAAGA	AGAAGTCTTC	600
	CATATTCGGG	AATTTTATGC	CCCCAGTTGA	TGACGCGACC	CCTGCTGCCC	ATGTGTACGA	660
	CCCTAAGGAA	CGCAAGCCCA	AGAATGCTGC	ATCCGCTTAA	GCGGCTGGCC	TTGGGAAC	



## 1416UP

	GATCTTGCCC	GGCAAGACCA	GGAAGTCGTT	GTACGTCAAC	CCGCCCCGCG	TCTTGAGTCT	60
	CATCAACTGC	TCCACGGGAC	AGCCCGTCCT	TCTCGGCGTA	CGTCGCCAGG	TGCTCCAGTG	120
5	CCGTGGCTGC	GTCTCTGTAA	GTCAATTGCGC	TTTGTTCCGGC	GTGCTATGAA	GAGAAGGAGT	180
	CAACACTAAA	CCCAAGCTCT	CAAGTTGACC	CATCCATCAA	GTAACATATCC	CGAACAGACG	240
	CCGGTAAACC	CAGCTGGGAT	TTGGCGCATC	TAGAAAACCT	ATTTATACTG	CAGCTCATCG	300
	CTGCAAACTT	TTCACGTAAA	AGAAACGATG	ATCCAGCGGG	GGCCAAAAAG	CAATGGGCCCT	360
	GCGCCGCACG	ATGCGAGCCC	TACCGGCGGC	CAGCACCAGG	TAGGAGCTGT	CAGGGGCCTA	420
	GAACGCGCGC	ACGCTAGACG	GGCTCCTCGG	GGGCCGCGGC	AGGCGTCCGA	CGGGCGCCTC	480
10	GCAGCAGCAG	GCGTGCCAGG	CGGACCAAAA	GACCGACCAG	CCAGCGCAGC	AGTCTGTAGA	540
	CGGCGCGGAG	CAGGCGAACG	GCCAGGAATA	CAGTCCAGAG	CACGGCGGAG	AGCAGCAGGA	600
	AGTTGAACAC	GCCGTCCATG	CCCACGCGCG	CACAAACGGG	AACAGCGCCA	GCGCGCGCTC	660
	GCAGAGCGGC	TGCAGGAATG	CGACGACGGA	CAGGAACGGC	AGGATAGGAC	TA	

## 1417RP

	GATCCCCCTTG	GCGTCGTCGT	TGACCAGGTA	GCGGCGCTGT	AGCCCGAAGA	AGCCGGACAT	60
	CGGGTCTGAC	GCGGTCTGTA	GCGGACGCGC	CATCATGCGC	GCGCTACTGG	AGATCACGCG	120
	CCGGTACAGG	GGCCAGTCCT	TGTCGATTCC	GACGCCGGGC	GCGTAGCGCG	TGCCCAGCAC	180
20	GAACGGATGT	GTGCGTAGTG	AGTCCAGAAG	CACCGGTACG	CTCTCTGGCG	GATGCTGCAG	240
	GTCGCGCTCC	ATGCACACCA	GGTACTCGCC	CTTGGCCTCG	TAGAAGCCCT	TGAGCACCGC	300
	ACTCGACAGC	CCGCGCTCGT	CCGTGCGCAC	GATGATCCGC	ACGTTGTAGC	CCTGCTTGGC	360
	CAGGGCCTCC	ACCTCTTCCA	CAGACCCGTC	CTGGGAGTTG	TCGTCGACAA	AGATCAGCTC	420
	AGTCTTCTTG	GAGTCCGCGT	TACCGAGCGC	GGCAAACAGC	CGCGTGGCAA	GGGGCTTGAT	480
	GTTGGGCCTT	TCGTGGTAGG	CCGGCACGAC	CACAGAGTCT	CGATGCTCAT	GGCGCTCGTA	540
25	TGGTCCTTAA	TGTAGTGAGT	AGCGAACGTC	GGTAGCTGTT	TCGCAAATAA	GTGAGGCCTG	600
	CGCGCCTAAT	GTCGTGTCTT	TATCGTTGCT	TTTTGGTTCTG	TGTCACGGGG	TTACCCGGCC	660
	ACCAGGCTAG	ACAGCGAGAC	CCGCGGTGAG	CAGCCACGA	CCAAGAAGCG	CTGTA	

## 1417UP

	GATCTGCGTA	GGTAGTAGAT	GAATTGAGGG	TATAGGGA	AGTTTGGTGC	CAAGCGGAAG	60
	GAGCGGGGGT	CGCCCTTGTT	GTAGTCGGCG	TACTTCTGGC	AAAGCTTGAT	CAAAGTTCTA	120
	TCGATCCACC	GGATGACGTC	AGCGCCATCA	TCGGAATCTG	CCTTATCGAC	TGCAACACGC	180
	GCCATTAGTA	CAGCAGCGGC	CTCCTGGTCA	AAGGAAGCAG	CGATTGCCGG	GTTACCGAAT	240
35	GGCAACATCT	GGTTAGCAAC	TGTAGTCACT	CTGACACGGT	TGGTACCAGA	TGCATGCTGG	300
	TATGCAGTAA	TGAATTGGGT	GTATGCCAAT	TTTGGTCTGT	CCCCATGAG	GCTGGCAGTT	360
	GCAGCGGTAT	TTGCAATCTC	GAAAAAGATA	GCGTAAGAGT	GGTGAGGGCT	CAAGGACGCC	420
	ATTTTCCATG	TAGAAGTGCC	CCCAATACCG	ATTTCTGAAT	CGCTCACGTT	CTGTGCATCA	480
	ACGTTAACCG	GCGAAGCATG	GCCAATCAGT	CCCTGCAGCT	TTAGATCTGC	ACTGGTTTTC	540
	ATGCACATGG	AAGCATTGAA	CGCCATGGTT	AGGTACCCTC	CTCATCTTTA	GAAAAACAGTC	600
40	TGATGAAAGA	TTGCTTGAAG	ATGGCCGTCG	AGAATGCGTC	AGTCAACAAC	AAAAACACCAC	660
	CAGTGGAGTC	GGTCAACTTC	TTCATCTCAG	ACATACAACC	TGGTCGTAGC	ATCCA	

## 1418RP

45	GATCCGCGAG	ATTCATCGTG	GACCCGCCAC	AGGCAATTAC	TATAACAACA	TCCTGCGGTG	60
	TTAAAGGACC	TAACTCACGC	TCAAGTATTT	CAGGATGATA	TCCTAGATGA	AGAGCTGCGC	120
	CACACGCTGG	TTCCGGTTACA	ATATTGCTCT	CTTCCGCAAA	ATTTAAACAT	GTCTGTACTA	180
	CAGCGAGCTG	GTCAAGCACA	ACAGATTTTG	TCCTGTATTT	TTGGGCCTAA	CTCAGAGTAA	240
	GATATCCATC	CATAAGATGT	CATAAGAAG	TAGCAACGCT	TTTAGGATTC	ATCGAAACGT	300
	TCCTGCCAG	CAGCAAGAT	CTGTGCAAAA	CCTCGACCC	CTCTGTTTCC	ACTGCTACAA	360
50	CAGGGATAGA	GTCTGCCAAA	CCATGTTTCT	CCAGCCCAT	TACAATCCCA	TTATATAACC	420
	CCCCGCCACC	TACGCTGCAG	ACGATACCTT	TCACGCTCTC	CAATTGCACG	CCTTGAGAT	480
	GCACTGCTTC	TACTACTTCA	TCTACCATTG	TTGCATGCCC	TTCCAGATG	AGTGGGTGT	540
	CGAATGGATG	TGCATATATC	GGAGCGACTT	TTTCTAAATT	CACATTCCTC	ATCAACTCGG	600
	AACGTAAGTA	GTCATCGCTC	TCTTTCAATA	CACTTCCCAT	TGATATCACA	TCTGCCCCCG	660
55	TTGACCGTAT	CCGCTCTACC	ATCCGCCGTC	GAGTAGTTTC	AGGCACTACC	ACTGTGCAAG	720
	GTATCCTA						

## 1418UP

	GATCATCTGC	GTGCGATACT	GGCAAAAAAT	GAGAGACAGC	ATGATGAAAA	TATAGTTAAT	60
	AAGATATTGC	ATGATATAAG	CACAGGCGGG	TTTCGTCGAA	GAGGAAAGGG	TGCACTTGAT	120
5	CTGGAAATGA	GTGAAAATGA	AGACCAAGAG	TTACAACAGT	TTAGACAGAA	AAGACGAGAA	180
	CTTTTGAAC	AAAAGATATT	GGAAAAATGGT	GATACTAGCA	AGCTCGTATC	TAACCCCAAG	240
	TCATACGCCT	TTTTTCAGAC	GATGGTGGAC	GATGTTACTG	AAGCATCATT	TGGAAATACA	300
	TTTGATGCCA	ATATAGATGA	AAAAACAGAT	CCATCTGCTG	CAGGTCGGAA	AATTGTCATA	360
	TCAGAACAAT	TTGTAAAGGA	AACCTGTGCA	TTCTTGTCGA	GCAAGAGTGG	CGACTCAGAA	420
	ATCCCTGCAG	AAACTAAATC	TATTTTCATCC	AGCACAGTTG	AACGTGAAGA	AATTCAAGAC	480
10	CTTCCATACA	TTGAAGCAAA	ATAGTAACAT	TAAACATTTG	AAAGGAATCT	AGAACTTCCT	540
	GCTCAGATGG	CTGAACTCAG	CAGTGGAGAT	GAAGGTGATT	ACGGCTTTTC	TTTAGATAGA	600
	TTGCTCTGTC	GGCAAAAAGT	TTAATAATGG	AACTAACGTC	GACGATAAGT	TTAAAAGTGG	660
	CACCAAGGCA	GTGCGAATCT	TAAAGGCAAT	AAGACAATTG	GCGGTCAAAA	GCC	

## 1419RP

	GATCTGGGGA	GTCTCATCGA	AACGTATTCTG	ATGAGGCTTG	GTGGTGGCAG	GCGGCTCCTC	60
	GCTCGATTGG	CGAGCTGGTG	ATGACTTCGC	ACTTCTCCGG	GCCGGAAAAT	TCGTGTCAGA	120
	CAGTCGGCGT	TGGCGTTGAA	GCTGCCGCTG	TTGCTGCACA	CGTGGTGGCG	CCCTTAGCTG	180
20	AATACGTAAC	GCTGGCGCGG	TGTCCCGCGC	ATCCAGGTAT	TCCTCGAGGC	TTTCTCTCTC	240
	GGCGATGTCT	GAGATATCTG	GAGCACCGCG	AGCATTCCTGA	TACACGTGGC	CCGAAGATGT	300
	TTGCTTCGCG	GTGAAGTCTC	CCTCAAACCC	GTAGAAGTCA	TCGGGGTATT	CTCCATCCGG	360
	CATTGTCAAT	GTAGTAGTGG	TCTCCACATA	GCGTACGCCA	TTGATGTGCT	TCACCGTCTG	420
	GCGAGTCACG	GTCCTGTGAT	GGCCCTGGAG	GTCCTTCGTT	TCCGTCGTCT	TCACCGTTAT	480
	CGTATTGCCA	GCTGCGACAG	CAGGAGGGCC	AAAGCCGTTG	TTGCTGCGTA	GCGAATTTCGC	540
25	GCGTCGTTGC	GAGCTCATAC	TGTAAGTCCG	CGGAGGCGCA	CCGAGGTAGC	TGGGCCGAGC	600
	AGCTCCTAGC	GACCGCGTCC	GCCCGTACCC	AGTCAGTGAC	TGAGTCCGCC	CCATCCCAAC	660
	CCCTGGTCTT	CGGAGTGACG	CAACCGACGC	CGCCGCAGAC	GACAAGCCGC	TGCCTGTTGA	720
	ATA						

## 1419UP

	GATCCGTCCG	CGCCTGCGTA	CCCATAGGGG	CGAGGTCGCC	GCCGGCCCGC	CAGGTCACTG	60
	CGCCCCAAACC	GCACCTGCAC	CTGAACCGAG	CCTGCAGCCC	ACGAAGGAAC	GCCACGCTAC	120
	ATGTGCCCGT	GCAGAGCACC	GCCCTTGCTT	TGCGGGGCTG	AAGTGACTGT	GGCAGCTCC	180
35	GCAGGACATA	TCTTTTTAAT	GAGCTGTGTC	ATGCGCACAT	TCTCACCGTC	GCGCTACCGT	240
	AGCGTCGCCC	TCTGTCAACG	TGTGAGCTGC	TGCCAAAACA	AACAAATCGG	GACGGGCCCG	300
	CATGCAGTAA	TTACCTCCTC	CCGAAGGCAA	CGCCTTGCTT	TTGTTTACGT	TGGCCAGAGA	360
	TTTTCTCTTT	GGGGTGGATT	AGCTCACGCG	TCATCCGCGT	GGCAGAGGTG	CCTGCCCTGA	420
	CAGTTCTTCG	AATATTAGAT	GCTGGTATGC	GGGCACGCC	AGCGCAACCG	ATTGTAGTTT	480
	ATTGTTTCGT	CACACCCGCG	TAGAGGGCCG	AGCTACAGGA	TCGCCGATGT	GGCGTGACGG	540
40	ACAGCGTCAA	CGTTACGATC	TCAACGGTCG	CTCGTGCGGG	CCCGTCTGTG	GTAGGCGTTG	600
	AGATACGCTT	AGGATGAAAG	CACGAAAATT	AAGGTTGTCT	TAAAAACACA	AAGTCAACTG	660
	GGGTTTCCGA	ATGGGTTAGA	GTGCCATCGT	AATGGCGGAC	GGAGAGTGTC	CATGGTGCGA	720
	G						

## 1420RP

	GATCAATTCA	AGGTTGCTTT	CCCAGACATC	TACGCTGTTT	TCCAAAAGAT	CGCTCAGCAG	60
	CACCCCGACT	ACGAAGTGAC	TGTCACGGGT	CACTCACTGG	GTGGCGGTTA	TGCCTACTTG	120
	ATGGGCTTGG	AGCTCCAGCT	ACTTGGCCAC	AAGCCACATG	TGATCACCTA	CGCCGGCCTG	180
	CGTATGGGTA	ACGCTGACCT	CAACAAATGG	TACGACAAGG	TGTTTCGACAA	CGTCAAGAAG	240
50	GTCGAGGACT	TGAAAAACGG	CGGAAACCCA	AGAAACGCCT	ACATCCGTGT	GGTTCAGAGC	300
	CGTGACATTG	TTCTATGGT	TCCAATGGC	CCTATCTACA	CGCACGCGGG	TATCCTATTT	360
	ACCATCACTG	ACGTGGACAG	CGAAGTACCT	CTACAATCGG	GCGTCAGACT	TGATGGCTGT	420
	AACACCAAGC	TAAAGGAGTT	GGTCGGCGAC	ATCCTCTTCA	GCGGGAAGTT	GCTAAGCTTG	480
	GTGCGTCTCC	TGAACCACAA	CAAATTTTTC	AGAAGAATGG	CTTTGCCATG	CACTGATAAT	540
	TCCTTGAAGC	TATAATTCCG	AGGAAGTAAT	GAATTTTAAG	TACGGAACGT	GCAGTCGCTG	600
55	CAGTCTTCTG	CCTCTTCCTT	ATGCCCTATA	TAGTTAATTT	GATGTTCTGT	TCTATTTTTT	660

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TACATTTTCC AAACACTGGG AATGCCACCT TGTAGATGTT GTTCCCAAGA TGGATATTTA  
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720

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## 1420UP

	GATCCGTCGC	GAGGCGCGCA	CCAAGCGCAA	GTGCATGGTG	GTGTGCGCCG	GCCTGGAGGT	60
	CTTCGAGATT	GACATGAAGA	AGCTGGCGAA	GACCTTCGCG	TCCAAGTTTC	CGACGGGTTG	120
5	CTCTGTGTCC	AAGAACGTCG	AGAAGAAAGA	GGAGGTCTGT	GTTCAGGCG	ACATCGCGGA	180
	CGAGGTCGAG	GCCTACATCC	ACGCGCTGCT	AGAGGAGAAG	GGGATGAAGG	GTGTCAAGGT	240
	CGAGCAGATA	GACGCTGCCA	AGAAGAAGAA	GAAGACGCCG	ACGACGACGA	CGCCGCCGCC	300
	GTCGTGAAGA	GCGGGTCCGG	ACATGTGTAT	CAGATTTCGT	TGTAGTGATT	AATGATTGCC	360
	GCGATTTCCA	GTGTCTTACC	AGTCCAAGAG	GACAGGTGTC	TGGCATGCTT	GCACATTGCT	420
	GGCGTCTGCG	TGGGGACCAT	GAGCCTGGAG	ATGGATCTAA	TTGAATGGGC	GCTTAACCTG	480
10	CGTGCTGCGG	GAGGCGGGGT	ATTTGGCAGT	GGCAGCGAGG	AATTGGACAG	AGTGCTAAAA	540
	CTGCACTACC	GAGTGACATA	CCATGCGTTT	GACCGGGGCA	CCAAGCGGTC	GGTGTGGGAA	600
	GTCTGCTGGC	GGAGGCCGAG	AAGATC				

## 1421RP

	GATCCCTCAG	TTCCCCATCT	TGCCCTCACA	GCCAGGATGG	ACCATCCGTA	ACTGGGAGTT	60
	ATGCGGTTTC	ATTTGTCTTT	TTAGTACAGT	ATTATCTCTC	TGGTTTTACA	TCCTACTTGT	120
	TTTATCGTTA	CTTGGGTATG	TATGGCATCT	TAAATTTTAT	CGACTCTAGT	ATTTTTATGA	180
	CTGTGTAAAC	TAATGAAAAA	TAATGAATCG	AAGTCTCGTT	TACCTAGAGC	TGATTATGCC	240
	ACATGCGTAC	TATCGGCGTG	CCACCGCAAT	TATGTATCTA	TCCTACAGAT	AATCCTTTCT	300
20	ATTAGCAGTT	CTCACGAAAC	GTCTCAGTTG	CCACTCGACG	TCAGCATCCT	TGTTCTCCAA	360
	GGTGCCCACT	GTCAGCTCGT	AGAGCTTCAT	TTGCAACCGT	GGTCCCACCT	CGGCCAATTC	420
	AACCTCATCT	CTCGTCTTGA	CGTATACGTG	CTGCCGCACA	CTAATGAAAT	CGCCGCGGTT	480
	CGCAAATGTG	ATGACCCTAG	GGCTGTCTTT	CTTGACTCCG	GGCGGGAACA	TGTGCTTCAG	540
	TATTTTAACG	ACCCGTTGCC	CCAATGGAGT	ATTGAAATTA	TC		

## 1421UP

	GATCATCATA	CCGTGTCCAA	CATCGCCAC	GGAACCACCA	GTCACCTGAA	GTGGAACGCA	60
	GGTAACATAC	GCGATGGCCT	CCACGACGAC	TTGGCCAGCT	TCAAGGACGC	AGTCGTGCAC	120
30	TGCTCAGCT	TCCGACGCG	CCAGTCCCG	GACTACCGCC	ACCAGTCGTC	CATGTTCCGG	180
	AACGGTTCTG	CTGGCAGTGC	CAAGTCCGGG	TCGTGGTTTC	GTGGCGCGAC	TGACTCGCGC	240
	GATGGACTAC	TGCAGCGCGG	GCGCGAGGCC	GGGCGCGAGG	CCGGTCGCGA	GGCCAGCTCG	300
	TGGTTCCGCG	GCGACAGCCG	CACCGAGGAT	TCCGGCCGGT	CGTGGTTTGG	GCGCGACGCC	360
	CGCGACACCC	GCGACACTCG	CTCGGACCGC	TCGTGGTTTG	GCCGCGACGC	ACCGGAGGCC	420
	GCGACCGACG	GCACCTGGCT	CAACGGAGAG	CGCGACCGCT	CGTGGTTTCG	TCGCGAGAAA	480
35	CACGCCACCC	TGCACGAGTC	CGACCGTGTC	TTCCGGAATG	GCGGCCGTCT	CGGCGTCGAC	540
	ACCACGCGCT	AGGCGCCGAC	GCCCGCGGCA	AGGTCGACGA	CATcAagcaG	GCAGGTGCAG	600
	ACCTCGGCGG	CTCCGCGCAG	GCCAAGGTCG	ACGACTTCAA	GCAGGCCGCG	GCTGACCTCG	660
	GTCGCTCTGC	CCAGGACCGC	CTCCAGCGCG	GCGTTGCCGA	CGCCAAGCAG	ACGCTCTCAG	720
	GCGCCGCGCT	CACCGTCTCC	GGCGCCGCGG	CCTCCGCTGC	TGGCGCCTCT	CGCGACGCGG	780
	CCTCGTCCGC	CGCCGACAAG	ACCCAGTCCC	TCTTCAACTG	GGGCTACAAC	AAGGCCGAAA	840
40	AGTCGAAGGC	CATCGCCATC	GGCGAGTACG	ACAAGGCCAA	CAAGGACTAC	CAGCAGGCCG	900
	TCGACGCCTA	CAACCGCTCC	AAGCGCCTGC	TCGCCGACGG	CGACCAGCAC	CTTCGCACCG	960
	GCCTCGAGAG	CGCCAGGCC	CAGCTGCGTG	ACTGTGCGGA	CAAGCTCGAC	GCCATCTcCG	1020
	CGGAGTTTGA	CCACTACGCC	CGCGAGAACA	TcTcCGACAT	CTNCCGGCGN	CTGGACCACG	1080
	AGGACCGcGA	TTCCGCGGcT	TCCGGcCTCT	TTAGCTGGTT	CCGcTTCAAG	GCCCgGcTGT	1140
	cGAAATCGAC	CT					

## 1422RP

	GATCCGTGTC	CTGGGGCTGG	TCGAGAACAT	GAGCGGCTTT	GTGTGCCCAT	CGTGCGAAAA	60
	CGAGTCGACC	ATCTTCAAGC	CAACAACAGG	TGGTGGTCTG	GCCTTGTGCG	AGGAGCTGGG	120
50	GATAAAGTTT	CTTGGAGCCG	TGCCGATTGA	TCCGCGAATT	GGAAGATGCT	GCGACTCTGG	180
	CGAAAGCTTT	TTGGACGCCT	ATCCGGACAG	TCCAGCGTCG	ACCGCCATCA	TGCATGTGGT	240
	AGAGGCTCTC	CGTGACGCCG	TCGGCGACGT	ATAACGCGCC	TAGCAGTTCC	TGCCAGTGAC	300
	AGACTGATAC	CAGTTTATAC	ATACATACAT	ATTTGTAAAA	AAGACGCTTA	GTGTTACGTG	360
	GATGCGAGCG	CCCGTTTCAG	GTAGATAGTT	TCCGGCTGTC	CCAGCGGCAA	TGCAAGTAAT	420
	CTGTCTTTAA	AAGACGGGGT	CTCCAACGCT	TGTCGATAAT	TCTCAAGGAT	GATATGACAG	480

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ACAAGTTTGG	ACATGACACA	GCAAACGACG	GAGAGTTCTC	GGTGGGAGCC	GAAATCCGTG	540
GCCAGGACGG	GCAGAACCCG	GACCAGATCG	GAAAGCAGCT	CTTGGTTGTG	GTTGTTGTCA	600
AGTGCTATCT	GGAGGTACTT	CTCAAATACC	CCCAGGCCGT	GAGTCCAAGT	TTCCATCTGT	660
TGTGCGGGGA	AAGTCTCCAA	TAATTGACGC	AGTGTCTGCA	AGTTAGCAGC	TGA	

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## 1422UP

	GATCTCCTAG	GCGCCAAGTC	GACGACTACA	GGCGGGCTTT	TTGGGCCAAA	GACGGAACAG	60
	AAGCCCGCAG	GCGGCCTTTT	CGGACAGAGT	AGTGCCGCTC	CCAATGGCAC	TGGCGGCGGT	120
5	GGTCTCTTCG	CTAGCACGGG	CAACAGCGGC	AGCACCCAAT	TGGGTGGGCT	GTTTCGCAAC	180
	AGTGCTGCGG	GCGGTGGTGG	GAGTCTTTTT	GGCGCCGGCT	CGGCCGCGAA	CAACAACGCA	240
	TCCACCTCGT	TGGGAAATCT	CTTTGGGAAA	CCTAATGACA	CGGCACCGGC	AGCTGGTGGA	300
	GGTCTTTTCA	GCAATCGGCC	GAACACAGCC	ACCACAAATA	CCGTTTCTTC	CACTAACAGT	360
	CTTTTTCAGCA	ATAATCAGGG	AAATGGTGCG	CAGAATAATG	GGGGGCTCTT	TGGTGCGAAA	420
	CCTACCGGGG	GGCTCTTTGG	AAACAGCACC	GCTCAGCCAC	AGTGCTCGCT	TTTTCGAGCT	480
10	TCCTCCTCAC	AGAATAATCA	GCAGCAGCAG	CAGCAAACAC	AGCAACTGTC	CCTTCTGGGT	540
	TCCAATCCAT	ATGGCCTGAA	TCTGACTGGT	GTTCTGTGTA	CTACCATGCC	GGAATCTATA	600
	ACGGCAGCAA	TTACGTCTAA	GAAGAAGACG	AAGCCTACCG	CT		

## 1423RP

	GATCGAACAC	AAATTCATCT	ACGAACACAA	ACTTGGAGCG	GTTCTGTGTG	GTTATATTGG	60
	ACAGGAACAT	TGACCTACCT	TCAATGTTTG	CGCATTTCGTG	GATCTACCAA	TGTTTAGTAT	120
	TTGACGTATT	CAATCTCTCC	AGAAATACGA	TTTCAGTACC	GAATACTGAT	GAAAAGGGAC	180
	AACCCACATA	TAAGAAGATG	GATATTGAGC	CTAAAGACTT	CTTTTGGACG	ACAAATGCGC	240
20	ACTTGCCGTT	CCCAGACGCA	GTGGAGAATG	TGCAAAATGC	ATTGGCAGAC	TATAAGGCCG	300
	AGGCGGAAGC	GATAACCAGG	AAGACAGGCG	TTGACAATAT	AGGCGATTTA	GATCCTAACT	360
	CTCAAAATGA	TACTTTGCAA	ATTACAGGAG	CAGTGAACAA	GTTCGCCGAA	CTGACTGCTA	420
	GGAAGAATAT	CATTGATACA	CATATGAATG	TTCTGGCTGC	GTTGTTGAAA	GAGCTAGAAA	480
	ATAAAGGGTT	GGATTTCGTT	TTTGAAATGG	AGCAACAAAG	TGACTCTGCT	AAGGTGAGGC	540
	AAGCATTCAT	GGACGTTTTG	AAAGATGGCA	AGACCAATAA	CCTCAAGGAC	AAGTTAAGGA	600
25	CATACATAAT	CATCTATTTG	ACTAGTTCGG	AGAAGCTTCC	CGATCAATTC	GTCCAACATG	660
	TTGAGAGTTA	CTTCCAAGAT	AATAATTTTCG	AAACGCCAGC	GTTGAAGTAC	TCTATAAGT	

## 1423UP

	GATCATCCTG	TTGAACTGCA	TGCTCATGTC	GTCCGATGAG	TACACATGAT	TGAAGTCAAA	60
	CAAATGTTTG	CCCGACTTGA	CCTTGCCGCC	ACGCAACGTC	GCAAACAATC	CGTCGCTGGA	120
	CCGAAAGTCT	GGGATGCCTG	CAGCCACAGA	GATCCCCGCA	CCCGTGACCA	CCACGATGTC	180
	CCGACTGTGC	TGGAGCGCAT	ACCGAATGAA	GTCCGGCGTCC	CGCGCGCTCA	CCAGCTCCGG	240
	GTCACGTACG	TAATGCGCTA	GCTGAAATAC	CGAGTTCGTC	GCAGGCCTGT	ACGTACGCCG	300
35	CGGCTTCCTC	CGCACCGGAG	CCCGCGCCTT	GCGCAGCGCC	GGTAACAGCT	CCTTCGGTGT	360
	GACCTCCTCG	GACACGCTCG	GCCCCGCTGT	GCAGGCCTCT	GTCTGCTTCT	TTTTGACGCT	420
	CGACGGCGGC	GTGATCGGCA	GCTTCACCTT	CATCGGCGAC	CGGTACCGCT	TCACACCGAT	480
	ACCACCGATA	GCCCTCCGTA	TCCCGCACGT	TCCACAAACC	TCTGCCGCTT	GCTGCATCG	540
	TGGTTGCCCC	GCTGCGTGCC	GTGTAGCGGA	CATGAAATGA	GTGACGGCGG	GCCCAATTTT	600
	GCCGGCGTTC	GCTTTCGACC	AATCCGGAAA	ACTTATCCCC	CGTAAAACAA	AGGCAGGACT	660
40	TCCGGTGTGG	CGATAGCGGC	TTTTGTGCGA	TGGGCTCCTG	GTCCCGTTAC	GCCTACATT	

## 1424RP

	GATCTCATCT	GTATTTGGAA	GGGAACGCAC	CAGACGGGGG	TGACTCGCAG	AAGCTGCCAG	60
	AGGAGAGAGA	AAACATAGAA	AATATATTTA	TATTATCTAT	ATTCAAGTTA	CATAAGAATG	120
	TGTCTAATTT	TTATTGTTTT	TAGATTTTCA	CTTGCGAGTG	CCCTGCATAT	GACTATCCTT	180
	TTATTCTAGA	TTTCAGTGCTA	GCTAGTCGCA	AGGAAATCGA	TATCGTAATT	CCCATTTAGA	240
	ACAAGATACA	AATTAGCGAA	TTTCCCAGAA	AAACCGGTCT	TATAATACAG	CATCATTGCC	300
	GAATCCATAC	CAGTCCTTCA	ATTAACTTTC	CGAATCAAAA	AAGGCCCGGC	GCGGTCTCAA	360
	GAATCTTTTC	GCCAGTACTC	GAATGGTGAC	TATCAGCAAG	CGACTCTTCA	CTACCCGAAA	420
50	CGACAGTAT	ATTTGTGTGC	AGCAAAATGAT	TTAAGGCTCT	CGAGACACCT	CTTATTGGCG	480
	TCCTATGTGT	TCTGTGCACG	CCCTGGCCCC	GATAAAGAAT	GCAGGTGCGC	TAATAGTAAT	540
	TACTAACCGT	TTTTTAAATC	GCCGTCTTGG	TTGAGACCTG	TGAAACGATA	ATCCCATTTA	600
	TACCAGATGA	ACTCGCCGCA	CTATAGTGTC	CGTAATTTCAG	CACTGTGGAT	TCCGAGTTAG	660
	GGTGCGCGAA	GTAGCAAAAT	TGTGTATCCT	CCATAATAAG	GATATCCAAT	GCCAGTATAA	720
55	TAGT						

## 1424UP

	GATCATCGTA	TGCACTCAGT	TGTATTCTAG	CATAGCCCGT	GCGATTGCCG	TGATTTTCGAA	60
	CGATGATGAC	AGGCAAATCA	CCATGAGGAG	CCGAGGATTC	TCCGCTAAAT	TCAGCTGCAT	120
5	TTGCAACAAA	GATGGCGTGT	TTCTATGCGA	GCCCCCTCAC	ACGGGCGTAA	AACATGTTTCG	180
	AAATGCTGCT	CGCTCTGCCT	TGCGCTGCGT	GTGCCCTCAG	CCAGACGGTC	TGTTTGCTTC	240
	TAATGTGGGG	GAGAGTCGTT	CTACTCACGT	GTTTCAGCGTG	CTGAATAACT	TGCCTATCCT	300
	TACAGCTGCT	GACCTGAGGC	AATGCACGTT	TCCAAGTCCA	ATAGTCTACG	GGCCCCGAAGG	360
	TTGTGCGGAA	TGCACAGTGA	TGGTAATCT	ATTACTACAG	CCCACTGCAA	GCGTACAGAC	420
	AACCTACAAT	GACGGCGCGT	TGTACAATAA	AATCAATTCC	GCTTGCTCGA	CCGTAAACCC	480
10	AAAGCTATAC	CGTACCTTGT	GTCTTCCCT	GTTTCCATTA	GCCGTTGCAT	GTGCTTTTTT	540
	ACTGTGATTA	CAGAGCCTTT	CTGTAGAATG	TGTACGTGAA	TTTAATACTA	GAGAGCTATA	600
	AAGCTCTCTT	GTTCTTGTA	TGTCTGTTTC	AGAAGATAAA	AGGTAACACC	AGAAAACGAG	660
	GTACGACCCA	ACGGCTATTG	GACTACGAAC	TGGACAAAAA	CTAAGAGTCG	TAAGTAAGAA	720

## 1425RP

	GATCAGCTCC	CACTTGGTTG	CAACAGTATT	GCTGAGACTA	TCATTCTTGT	AGAGCGATTTC	60
	TTGTGAAGCA	GTTGGCCCGG	TGTATGAAAC	CGCGTGTTTA	CCAAGTGGAG	GCCTTTGTTC	120
20	AGAAATTTTA	GTTCTTTCTC	GAACGTATTC	GTGGTCCCTG	AGAAATAAGT	TTTGTGTGCTC	180
	GACATAGTCA	GGGTCAAAAA	CATTACAGG	TGTGTCAATCA	TATGGCGGCC	GGCTGCCGGA	240
	GGTTGTGGGA	TCAGCCTTTC	TGTTGGCTTC	CGAGTCTCCA	ACCCTCGAGA	TAGCTTTTGA	300
	TAAGTTGTAG	AAGTCGTCCA	AAATATCGTC	TTCGCCGAGA	GGAGCAACGC	TCGAGCCCCCT	360
	GAACAGTGAT	CCACTAGAAC	TTCTTGCAGT	AGCCTCGCCG	TCAGCATTAT	TGCTATTGTG	420
	TGTACTGCTC	GAGTTGCGCA	GATTAGATAT	ATCAAACGTG	TTCGATTGTG	TGGAACCTTT	480
25	ATATTCAATC	TATGCTCCAA	AAGAATCTCT	GCTTTGCGGA	GAGCCTCGCG	CTGCATGAGG	540
	AGGAGGAGCC	ATAAAAGATG	AATCCCTGCC	AGGAGAGTTG	TGTAACCGCC	CAAAATGGTGA	600
	TGCAGCGTAG	TTGTCATAAA	TTTGAACCAG	ATCTGCACGC	GACTTGTACA	GGTCCCTGGG	660
	GTTGTATCCT	GCCTTGGGGT	CGCCAACCTC	TTTAATGGAC	CCGAAGAAGC		

## 1425UP

	GATCATACAC	GCGCTGCGCA	TACAGTTGGC	CAGCACCAGC	ACCCGCGACA	GCCTCCAACG	60
	GCTAGAGACG	GACACCGCAG	GCCTTGTCGC	CCACGACCTT	TCCCGCTGGG	CCGACAGCAC	120
	CAATGCATAC	ATAAACGGCA	CAGAGGCCCTC	CGTAAATGCC	GGCCTCCTCG	GCTGGGTTAC	180
35	CACAGCAACT	ACAGCCCTCA	ATACCACCGT	CGCCGCCCTG	CTCGCCGACA	TCGATTCCAC	240
	CGTCGACCGC	GCGTTGCGAG	ACACGCCACT	TCACCGCCCC	ATGGTGACCG	TTGTCTCCTG	300
	TGTAATCGGG	AACAAGTTGC	GCGCCATCGA	GGCAGGCCCTC	ACCTGGACCC	ACGACCACGT	360
	ACGCATCGCG	CTGCCGCGCA	TCCATACCGC	CCGCCTTCCG	CACGCTGTCC	CAGAACCAGA	420
	CCTTCCAACC	CATCCCGCCT	ACACAGCCGT	GCTCCAGTCC	CTCAGTGACC	GCCTACGTCA	480
	TTCCGGTTGAC	CGTGTGCTAC	ATCAGTGCTG	TGCCCGGGTC	CGCATTGAAC	TCTACGTATC	540
40	GCTTGCCCTG	CTCGGCCCTC	GGATTCTGCA	GACACCTCTC	GGCTTGGCAA	TGCTGCTATT	600
	CAAGTCGCAC	TGCCGTCGCA	GGAACCTGCG	CCGCAGAATG	CCTTGAGCCT	AATTCTTACA	660
	TAATCTTAAT	TCGCCATTCT	GCTGCTCGAA	CACGAACCTC	GCGTTAGCCG	G	

## 1426RP

	GATCTTCTCT	CCGCTCGACG	TCACTGGCGG	CATGCACGAC	GCCATGAACT	GCTGCTGCCG	60
	CTCCTGATCG	CCCTCGTGCA	CTGCTAGCCG	CGACTGGCCC	TCCAGAAACC	GGCCCATCTT	120
	GTTGCGATCC	TGCAGCAGCA	CCACCACATG	CGGAACCACC	GGCTGCCTGG	CTGCTTTTCGC	180
	TAGCTGAAAC	GAAAGAAGAC	GCCCTATAGG	CGCGCTGCCT	AGCATATACA	CCCACGGGAC	240
	ACCCATAACA	GCCCTTCTAA	CCCTCAACCG	AGTCACTGAG	AACTGGCGTA	GTGCGCATCA	300
50	TCCAGCTCGC	GATTTTTCAT	TCTAGTTAAAT	AATCCTTACA	CCGCCAACAC	AAAGGACGAT	360
	TCACCACCAT	TCTGGCTCAA	CTAGGAGGCG	TGTCGGGCGA	ACCAGGAACG	CGTTACTCGG	420
	TAAGCGGGCA	TCTAGTCAAG	TGGGCAGTTG	CAGGCGACTT	CTTTTTGTGT	GTTATTTCAGG	480
	GTGTAGGATG	CTTGTTATAG	GGTTGACAGG	AGGTATTGCA	TGCGGCAAGT	CGACGGTGTG	540
	GCGGAGACTG	CACGAGCATG	ACCGGATCCC	GGTGATCGAT	GCGGATGCGA	TTGCGCCGGA	600
	GATTATGCGG	CCGGGGGAGC	GGGCGTACCA	CGGGTGGTGG	AACGGTTTGA	GCAACGGGTG	660
55	CCGCAACTGG	TGCAGGCGAA	CGGGGAGCTG	AACCGCGCGG	CGCTGGGGGC	GTGGATCTTC	720

CA

5 1426UP

GATCTGCTCC	AGCGCCTGCT	TGAACCAATC	TCCAGAAGAG	TGTCCGCCTC	GTCAAGAACC	60
TTGAAGTCAA	CCTCGGTAAA	GTACTTTGGA	CCGCAAGCCT	CGAGCATGTC	GATCAACCGG	120
CCGGGCGTGG	CAACCACGAT	ATTGGGCCTC	CTGCGCTCTA	GGGATCTGAA	AGTTTCAGTC	180
CGCGAGGAGC	CGCCCATCAT	GACAACCGCA	TTGAAACGGC	GAAGCTTCCT	GTTGGCGTTG	240
CGCATCTCGT	TGATCTCGTT	GAAGATCTGC	GCGGCCAAGT	CCCTGGTTGG	TGCAATCACA	300
ACAGCCTTGA	CATTTTCCGA	AGGAGGCCCC	TCCAAGAGCC	GCTGGAACAG	CGGCATCAGA	360
AACGCAAGTG	TC'TTACCTGT	TCCAGTTTTC	GCCCGTGCCA	CCACATCGTG	CTCCGTCTGC	420
AGGATCGGCT	TCAGCGTCTT	CTGCTGCACC	GGTGTTAGTT	TATCGAAGCC	GCGTGACTGC	480
AGCATCTCGT	ACAGCTCGTT	GCTGAGCAGC	CCCTCCTCCA	CCAAGGTCCG	CGGTGTGCTT	540
TCGACCCCGG	CAGCTTCGTC	GGCCACACGC	ACCACCTCGG	TGTTGGGGCC	GAGGCTGAAT	600
CCCTCGCGCG	CCGCGCCGTC	TGTACGGCCG	CGTCTGCCCT	GTGGCTTCCG	CCACATGCCG	660
CCGCGGGGAC	CACGCTCACC	ATCCTCCCCTG	TCGCTGCCCCG	GCT		

1427RP

GATCTTTCTA	TCCGGGAAAAG	AGTCCATCGA	ATACAAGGTG	CTTCTAGAAG	GGCCCTATGG	60
AAACACCATT	CCGCGGCTTG	CTGCTCCTGA	CCGGCGCTAC	GTGGGCGCCA	GCGCAGGTCT	120
TGGCGTAGCA	GCGGTCTACC	CACACTTCGT	CTCTCTGTGTG	GACAAGGAAA	GCCAGTTCAC	180
CCATTCAATC	TACTGGATTA	TAAATGACCT	TTCATATCTG	CATTGGTTTT	CGCATGAGCT	240
GAGGTAACTG	GCGGACCGGA	ACTGCGACAT	CAAAATTATT	TACACGAGGA	GCAATGAGTC	300
GGCTAAAGAA	CTGACCCGAG	ATGTTGCCGA	TTCCGCCTCT	GCGAAGTTTCG	TGGATTTCGT	360
GGATATCTGC	AGGCTCCTCC	TGCGCCGAGA	TCTCAAAGAG	ATCGTGGAAG	AGCAGATCCT	420
GCTCTCGTCT	AACCAGGCAC	AGGACGTCAC	GTTTATTAGC	AGCGGCCCTT	CGACCTTTAA	480
TGACCATTTT	CGCTATGCTG	TGAAATCTAG	CATCACGGGC	AAACTCCAGT	GTGATGTCGA	540
CCTAGAGGAG	GAAAGCTACA	CCTGGTAGAT	AGATAACATC	TTATTAGTTA	ATTGTACTTA	600
TTTATTCCTC	TTCTGTATC	TTAAGCAAAT	CCCGCCATGT	CTCAACCAGC	TTCTGCATGC	660
TTTGCGGATT	GAGCCCTGCC	TCGACCACGT	CCAGAGGTAC	CTGGTTTTTC	G	

1427UP

GATCATCTTG	TCCATGCCCT	TGGGGCCCAG	CGACGTTCTG	ATCGCATCCG	CGACTGCTCT	60
GGCAGCAATA	ATGTTTCGCC	TTCTCACTTC	CTGCGGCTTC	TCGCGGTTTT	TGAACGTCCG	120
ATTGCTGGCA	CTGACCTTCG	GTGGCATCTT	AATATACTTC	CTGATTCCGC	GCCCCAGAAG	180
CCTTACTTGC	TGCTAGAGAA	GTTAAGGTTG	TTTGTTTATG	CTGACAACGC	CTAAGTTACC	240
GTCAAACGAT	CAGATTTTTG	CCACTGGAAT	TTCCCTTCGT	ACAAACGGAT	ACTTGATCCT	300
TTGATCTCCA	AGAGCTGTTC	CATCGGGATG	GCCTGCTGAG	TAGTGCCGGG	TTGAAGGGAA	360
AATCGGGGCT	CGACAACCTG	GGAAATGTCT	ACGGAGGACG	CGGCGTTAAC	AGGGATCGCG	420
GTGACGGCAG	AGCTCAAAAA	AAAATGCCCG	TTTTCCAGCT	GGTATGAGGC	GTTCAAGGGC	480
CACACTCCGC	GGGCCGAGGT	GATTCGGCCG	CTGCCCGAGG	AGTTCTGTAG	CTACGTGGAT	540
CAGCGCGGGA	TCAGGCTGGC	GCGCGAAGAA	GGCTCGAAGT	ATTTCTACGG	CCAGGAATGG	600
AGCCTACGAC	GGACGGAGAG	TACAGCGACT	GGGAAGGCGG	CGACAGCGCG	AGTGAGCGGT	660
CGTTCGTGCC	GCTGGACCGG	TGGCGGACTT	CCCGGAAGTG	CACGCGCGGG	TGAAGCAG	

1428RP

GATCATACAC	GCATTGCAGG	TATACATTAT	AGTGCTCATA	ATTATCGGAT	TGCAAAATAGA	60
ATGGGGCCCT	TACCGTAGTA	CTGTCTTGGT	AATGCAGCGA	CGCTCAGGCT	TAAGAAGCTT	120
TTTGTCTCTC	GTGTATTACT	AACAAAATAA	TTTCCTCGAG	CACAGGGAGT	AGAGATGAAT	180
TACATAATCC	ATATGGACAC	CTCGTCACCT	TCCAGCGACA	TTAACATTTT	CTTATGAATG	240
CCCAATAATG	GTGCCTAAAT	GATGTGCTTG	GTGTAATGCG	CATTATAAAA	TGTATGTGGA	300
TTATATATTG	CTAGTAGAAT	CATGGTAGCG	AGGTCTTTGG	CCATACCCTT	CCATACCCTT	360
CTGAAGAGAG	ACATAGCAAC	AGTGTCTTGT	GCAGACAGTC	TGCCGTCGAA	TGTTGCCTTG	420
AAGTAACCAT	GAGTACCAAG	ACTCTCCTTA	ATGAAGCCAG	AGCGTCCAGA	TTTCGTGAAT	480
AGTGGGATCG	ACTTGAACCA	CTCGACATCT	TCTGGCCTAA	AGAACATATA	GCGCACTGTG	540
ACGACGCGCT	TGTGGAACCT	GAATGGATGG	CCAGTTAATA	TGATTCTCTT	GGCCAATATC	600
CGTGTGTGGT	CTGCGTTTCA	GAACGTGCCG	TGGCCACGGA	ACGTGAGGCC	CTTTGGATCA	660
GAGGGGTTTT	CTTTGAAGTA	GAATGGCCGT	GACTGGGTCA	GGTCCAAGGG	AAGCATGCAT	720
GTC						



## 1428UP

	GATCAAACCA	GAGTGCAGG	CGCACACGCG	GCACTGGCGG	GAGCCCTTAC	CGTAGTTTCT	60
	TGGGTGGGAG	AACCAAACGT	TTTCGTGAGC	CATCTTGTCT	GCAATGCGTT	AGTACTCTGT	120
5	CTGACCGCTT	GGAAGCGCTC	CGGCCCTCGT	GAGCTGCCCA	CACGCTCGGC	GTCTGCGGCG	180
	TCCTCATTTGC	CCGCACCGTA	TTCTGTCTGC	ACCGACAGCT	CTAGACCACA	CTTCGCCCCA	240
	TCCTGTGCAC	ATACGATTAT	GCTTTGTCTC	TTGGTATTAT	CCTTAGATTTC	GCTAGACTTC	300
	GACACTATGG	TTATCACCAC	TGTTGAAGTC	TGCTTCGGTT	GGCACCACAA	GTCTCGGGAC	360
	TGTAGTTGGA	AAGCGCAGTT	CGCGGC AAAA	CAAGCATCTC	ATAATGTGTG	GGTGCAACCG	420
	TTGAATGTGT	GGGTGCAACA	GTCAATTGTA	ATTTCTTTT	TTGATCGAGA	GATGGGATGC	480
10	GATGAGCTAG	TTGAAAAATT	TTAGTATGGC	AAAACTGGCA	TGCATATCTG	AGATGGGCCA	540
	TCAATTGCGG	CAGCTTAGTG	TTAGACGACC	AATCCAGAGG	TGGTAATTGG	GCTATGGCAG	600
	GTAAGTCGCA	CAGGTCTGTC	GTA AAAAAGG	GCCACAAAAC	GTTCAAGTCG	AAGCATGCGA	660
	GCAAGGGCGC	GTTGAAACGG	CTGCACAAGG	GCAAAGTGGA	ACAGGAGACC	GCTGCTGGGG	720
	TGAAGG						

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## 1429RP

	GATCAAAGTT	TAGCATGTAA	ATGTGCAACA	AACTATTTAT	TACCTCTGCA	CTGCCCATGT	60
	CGCTTTGAAAC	CGCCGAGGAT	CCAAACCCAGT	GCTTTCATAA	TGGAATTGCA	AAATTGAGTG	120
20	CAGTAATTGA	TAAGTATCTT	GAGAAAAGCC	CTCCCGACTT	TACCCTAGAT	GATTGCTTAA	180
	TATGTTTCAAA	AGCCTCCGAG	TTAATAAAAA	GGCTTGCTAC	ATCCAAGGTG	CATATAGATG	240
	TGATAGATGA	GACTAACAGC	ACCATTCATA	AAAAGCGGAA	CGGCAATTTT	CGAATCCACAT	300
	CACCCAGAGC	AGTATACACA	TCCATTGGA	ATGTCGTATT	AAGAAAGTTG	GATAGCGTTG	360
	TCGACCAAGG	AAAGGTAGAA	ACCGTCCAAT	CCTTTGATCA	GATACTTGAG	AATTTCCCTTA	420
	TTAACTTGAA	AGAAGTCGAC	TTTACTCTAT	CTGGGGTTGC	TCTGATGTAT	AGCACTATTG	480
	ACTACTGGAA	CCCCACATG	ATCCCAGGCT	ACGGCAAAGT	TACGACTGTA	GAGCATTTCC	540
25	TGGTGCAGTA	TATCTTACAT	CGATATGAGG	TATTATATGT	GGCCGGCGAT	GAAAGCCTAC	600
	TAGATAGTCT	GGTTGGTGCC	ACTATTTCGGA	AGCTATTTGA	ATGCATGCAG	TCACAGCATG	660
	ACCACCAGAG	CCTGGTAGCG	AATAGCCAGG	CTGATACCGC	ACGAAGAGAT	AT	

## 30 1429UP

	GATCAACCGA	TAGCGGAAGG	CGGACGAGCC	TCGGAAATAG	TACTAGGCAG	TGGTTGGCTT	60
	TTGTTTTTAG	CTGTGTTTCA	AGATGTCAGC	GAGAACAAGC	AGGGAGGCAG	GCGCCTCCAG	120
	GGTGATGGGA	GGTCGGAGTA	GTATGGATGG	AAAGTCCGGG	ACAGGAACAG	GGTATTTGGA	180
35	ACAGCTGAAC	TCGCCAAGCA	TTCAGAAGCT	CATGCACTCG	GACGCTTCCA	CGACAGCACT	240
	ATTGGAGAGG	TTGAAGATGT	CCCTAGTGAC	TTGCGTGGAG	TTACAGAAAT	TCATAAGAAA	300
	GAAATACTTG	CTAGAAGAGG	GCCATGCGCA	GGAGATGGGC	AAGGCTTATA	AGAACTTCTT	360
	TCCGGAGGGC	GCTTGCAAGT	GCTTGCAAGT	TAGCATACAT	AAGGTTTTTG	AGTATGACGG	420
	AAAACCTTGC	CAGGTGAAAC	TTTCATATGT	TGCTGCGTTG	CAGAAGATGT	ACGATGAGTT	480
	AACGTCGCTT	CTTGCAATCCA	TGACTAAAAT	GCGCAAATCC	CTCAAGGAGA	GCAGTCGGCG	540
	GTTGGAAAAA	GAAGTCGCAG	ATGCTATACA	TAGCGCCGAA	AAGGCAAAGG	CAAGATATAT	600
40	GTCCTTGTGC	ATGGATTGGG	AGAAGCTCAA	GCTTGTAGAT	CCTGCAAAGA	CGAAGTTGAC	660
	ATTGCGGGGC	TCAAAGACCA	CTCGAGAGCA	GGAAGAGGAC	TTATTAGAAA	GATTGATA	

## 1430RP

45	GATCGCAGAG	AGACACAATG	TCCCTGTGCC	CACTTTGTCT	ATGCTTTATC	ATTTATTGAT	60
	TCTTGTGCAG	GGGAAAACCTG	AAGGCCCAAC	AGGGAATTGT	CAACCATGTT	TAAACTTTTC	120
	CATGTGCATG	GAGCTCCGTA	TGTAGCAATA	TATTCTCATA	GCTAGAGATC	TCACTATATA	180
	TTAGCTTGGC	ACATTTATGT	CATATCGACG	TTGCTTTTTC	TACACCTTTG	TGTCAGGTAG	240
	CAGGGGCGCG	ACATAACTAG	TTATAAAAAA	GATGCGCGCG	GAGAACGAGA	TCTACTATCT	300
50	CTCTGAGTAG	GCACAGTTTC	CAACGTATTA	GTCCTTAATG	AGCAAGCGAA	TCATTCAACT	360
	CATACTTCTC	TCTGCCTTTG	CGCGAGCTAA	TTACGTGGAG	CCCTTCAAAT	CAAATCCATA	420
	CATTGCTTGC	TCAGAGGCAA	GCCATTGCCC	AAAGGAATGG	CCATGCTGCT	CGCAATATGG	480
	ACAATGCGGG	AGTGGGCGCG	TATGCATTAG	TGGCTGCAAC	CCAAAATTCT	CGCATAGCCC	540
	TGAGAGCTGC	GTGCCAGTGC	CGGCGCTACT	ACCGCAATTG	GAGATAGTGG	CCAGCGATGA	600
	TAAAGGAGTA	TACCTAGAGA	TGTCGGGTCA	GCCTGCCTTG	GTCACAAAGT	TCCAGCGCAA	660
55	GAGCTCGGCG	CAGTTGTTGG	AGGTACATCA	CGAGGAACAG	CAGTATGGTG	TGTCGGCATT	720

EP 0 866 129 A2

AGAGCAGGAC

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## 1430UP

	GATCGATTTG	GTTACCTTGT	TGTCCAACCC	ACGTACTTCA	AGAGATTCCG	ACGCAGAGTT	60
	GTAGACAGCG	TACCTATTCC	GAGCGACAAA	AGTCGCAAAG	CTTCCCTTAT	CCTCAACTAT	120
5	ATTTGTGGCA	TCAACAGCAC	CGCTAGCCTG	TTTTGGAAGC	AGGCAAAGAG	CATACCTATC	180
	GCCATCCCTG	CTACTTGAGT	TCACGAGGAG	AGAGTGTTCG	GAGGGATTAT	AAGAGATGGA	240
	CTTGAACACG	TTATATGGCT	TTCCAAAGTT	TTTTAGAGAA	ACAAATGGCA	GAGAGGACAC	300
	CTTCTTTTCA	TAGTCAAACA	TTTGGACCTG	CTTCTCTTTG	TTGACAAAGT	AAAGCTGGTT	360
	CTGGTTTACA	GCCACAGGTG	GTCTCTCACG	GTCCAGTTTA	AAGACCATGA	TACCCGAGTC	420
	ATGCGCCGCG	CCAAAGAGGT	TCACATTAGG	GTGCGCCCTA	ATCGACCAGA	ATCTGTCTCTG	480
10	TTCTCTTTTG	AACTGTTTTA	CAGGAGTGGC	CTTGCTTAGA	TCCCAGACCC	TAATGGGTAGA	540
	ATCCTCGCCG	ACAGAGATAA	TTAGGTTTTG	AAATGGGTGA	AATATTACAC	TGTCGACGTT	600
	GTTCGTATGA	CCCTGCACTT	GTCGACCTCC	CACGCTTTGG	TGGAGCTCAT	ACGCCACAAC	660
	TTGACCTGTC	TGTCTTCAGA	ACCGGAGACA	ATCAAGGGCA	GAATCGGATG	GAACGAAGG	

## 1431RP

	GATCATGTTA	TACAGACCTT	CAAAGTTGAT	ACCAAAACCC	TCAATGGACT	CGCTGACCAT	60
	ACTTGGTACT	TCCTGTTTAG	AGGCCCTGCG	GCACACTTAC	TGCCTCTACA	AGAAAAAACT	120
	GTTCCTCTCG	AATTGGATCA	CCCTTTTTCG	GACACTAACC	ATTTGCAATA	CAATGCTATA	180
20	TTGCCTCTAT	CAATGGTCTA	TTGACCTTGT	TGAATCCAAG	CTCGAAATCC	AGCAATGTGT	240
	AGAGATACTG	CAGCATTTTCG	GTGAGAAATG	GGTTMTTGCC	AAGGAGTGTG	CGGTCTGTCTT	300
	TCAAAATATT	GGAAATGCGA	TACTAGATAT	AAGTCTCTCC	CGAGGACAGG	TAGAAAACGT	360
	TGATAAATTG	ACTAGGGAGC	TATTTGGAGC	TAGCAATGAA	TACCAAGATA	TATTGGACGA	420
	AAATAACGTA	GATATATCCT	GGATTGACCT	GGCTATCTAA	TTTCTGAAAC	CATTGAGAAC	480
	CTGTPTTAAAC	TATTTGGCAG	TAATTCATAA	TGTATTGGTT	GTTCCATAGC	TGAATTGCTA	540
25	TTGCCGCTAT	GGAGTTGCTT	ATGCAATACA	CGGGTTAGTG	GGTGATTGTC	GTGTTCTTAT	600
	ACCCAAACTA	ACCGAATCCG	GTCTTAATCG	ACTCCGGTAG	ACTTTGTCAT	CCAGTAAGAC	660
	ATGTCCTTACA	CGCCCGATTA	ATGGTTGTAA	TCTTTAATCG	ATGAATGAGA	AATGGTATAT	720
	GTATGTGACT						

## 1431UP

	GATCTCCTGT	ACCATCATGA	AAGTCTTTTT	ATCACGGGAA	AACCCGTTTC	TCAGGCACAT	60
	CTGACGCAGT	GCTTGTCGCA	CATCAAAGGT	CAAGTTCCGA	TCCCTTGTGA	GCGCTTCCAA	120
	CTCCAGAAC	TCTTCTGCA	GATTTTTTAC	TGGGCGCGGC	ACAACCTCTG	CCTGCCCTCTG	180
35	GGGCACATAT	TTCTTTAACA	CCTCCTTCGG	AATCTTAAAG	TCCCTCACAT	TATAGCGACT	240
	TACGAGACCT	TCGAATAAGA	AGAGGCACCT	TATATATACG	TTTGACATAT	CCAGTTTCAT	300
	CTCGCACCCC	CGCACGATCA	GGTCCCGGTA	GTCCAAGTGC	GCTTTCTTTC	TTGAATTTCGT	360
	AGAGCTCGCC	CCCAGGGATG	AGCCTCGCTG	ATCAGAGGTG	CCTGTCTTCA	GCGAGAGCTG	420
	TGGCATACTC	GGCTGTGTGG	CAAGCTCCAC	CTTCACCTGC	TTGGCAAAGT	TCACATTTAG	480
	GCCCTGCGCA	AACGCGTCCA	GTCGAGCGAA	GATATGGTTC	ACCAGCTCGA	GTGGCATCGC	540
	CATCTTGTTT	ACGTCCAGTG	ACACGTTCCC	TTGGCCTAGC	TGGTGCACTA	GGGCCGCGCT	600
40	CTGTGTGAGT	TGTCGCTGCC	ACACAGAGTC	CAATTCCACT	CGCATCATGC	GCATCGCGTG	660
	CTTCAACGCA	CGCTCACTGA	TCTCCCCCTG	CTCAGGCATC	TGTGGAGCCT	CTTCTCGGCT	720
	TC						

## 1432RP

	GATCCAGGAC	TGCCGTGCTT	GGTTGCGCTC	AAGGGAGACT	TAGAAATGAG	GTGTTGGGCC	60
	GCATTCTGCG	CTGCAGATAG	AAACGAAGAC	AAGATGCCAC	CGTTACCCAA	TTCTCAGGCC	120
	CCAGAGAAAA	AATTCCCGTA	CCGGTGCTTC	CCAGTACCAT	CCTGGTCAAA	GGGTGTGATA	180
	TCCGAAAAAT	TATCCTCAGT	GTCTCTCTTG	TATCCTGCAT	CCGAGCGCGT	GCTTTGGCCC	240
50	GCCCCCGCGG	GCTCGCCGCC	CGCGCCAGAC	CGCACATGCG	AGTGCCGCGC	GCTCATCTCA	300
	ATTGGCATGC	TGAGCGACGA	CGAATTGCTG	TGCCCCCGCG	TATGCCAGCT	GGCGGCGTCC	360
	CGGCCACCCC	ACCCAGGCG	GAGCGACGAG	TTTGTGCTGT	TCGCGTAAAC	CACCGGTCCG	420
	GACATGAGCC	ACGATTCTGC	TCCTGACACC	CGGCTCTCCA	CATCCGAGCC	CTCCCCCGCC	480
	GCCACCTCGA	CATCACCCGC	CTCCGGCCCC	GTCCGCGCGT	CCCCATTCCG	CGTCGCTACC	540
	CGTCTTTTGG	CACTGCTCGC	GCGCCCCCTC	CGCCGCCCCT	CCCCCGTATG	CTTCTTGAAA	600
55	AGTGCCGCGC	GCTCTCTCTG	AGCGACCGCG	ACCGCTTCCG	CTGCTCTGCC	ATCCTTGCTA	660

GCCTCTGCCT GAGAAGAGCA TCTACCTCTC CTCCCTGTTT ATTCCGCCGC CTTTTTGCGA  
AACA

720

## 1432UP

GATCCCGGTC	GGCCGCTCCT	CCTCGAACAT	GTCTGTACC	CCGCGCAGCG	GCTGGAACAT	60
CCCCCCCACC	CCACCGTACT	GCCCCGGGAA	GAACGTGTGT	TCCACCAGCT	GTTCGTGGCG	120
CGCCTGGTCC	GGCGGCCGCA	TATTCTCCTC	CTCCTGGTAA	GCCTCCTGCT	GCAGAGACTC	180
CGCCAACTTC	TCGTCTGTCG	ACTCCGCGGC	CGGCCGCGCG	CTTGCAGGCC	CACTGCGTGC	240
GCCAGCCTGC	GTGTGCGCCG	CGTGCTCGAA	GTACAGCGAG	ATTGCCGTTT	CCACGTCGCC	300
ACCTGCCATA	TCCAGGAACT	GCCGCGCCAG	CTCCGCGTTC	GCCACACCGC	AGATGCTTTG	360
GAATACGCCG	AGCTGCTTTG	CTGAACATCAT	GCTCCTACTT	TCTGGCGCTG	CCGTGCTGTG	420
TGGCACACTC	AGGAGTTTGT	CTGACGTTGT	CGCTGGCTCC	AGCCTTTTAT	ACCGGCGCGT	480
GCCACACATC	CGCCGCGCCC	AAACGCTTAT	ACATATACAT	GCTACTTAGT	CCGCCGCTTG	540
GTACCCCGCC	CGTCTCTGAA	GCGCGTGTGC	GTGCCCTGGA	AGTGACACCG	CTGATCGCCG	600
CGCGCTCGGG	CGCCG					

## 1433RP

GATCGATGCG	GACCACCGTG	CGGAGGAGGC	CGCAGGTGGA	TATGCAGTTT	GCGGCGCTGA	60
GCGCGCCGAT	TTCGAGAGCT	CGCGCGTCCG	CTGGCGTGCC	CGCTTCGCGC	AGCCACGGAA	120
CCAGCTGACG	CGAGGTGTCT	CCCCCGCGGC	TGGCCGTTTG	CCCGACAGTG	CTCGCCGCTT	180
GGTAGTTCTG	TAGCCACGCG	GGCCCGTTAA	TCTCGCCAT	TACGTAGCCG	AGCATCTGCA	240
CGAGCAGCGG	CGACTCGCGC	ATCTTCTGTA	TTTGTAGCAG	CTCGCGCTCG	ACCTTCTCGT	300
CTGGGTGCGC	CATGTCCGCG	CCCAGCCGGT	ACTGTTCTTG	CAGTCCAGCG	TCTGTACAGT	360
ACCGTGCTAT	TTGCCGCTCG	TTTACGACTT	CGTCATTCTC	AGCCACCGGT	ATTCCCAGGA	420
GCTTGCCATG	TGCCCGCCGT	TTCTGTAGGA	GAACGTGGTA	GCGCCGGATG	ACCTTACGTG	480
CTTTGGATGG	TTTGATTGCC	GGCGTATGTT	TGACGGCGCT	CTTGCCCGTA	ATGCTTCTTC	540
GCTTCCCTGG	CAGCATGTAT	GAAAGTTAAA	CCGCAGTTAC	TACTGGTACT	AGATATGCCC	600
TCGGAATGCC	ACCCGATGAC	CTGCTGGTGT	ACCTTGCTTT	TGTCATCACG	ATGCTTCGAG	660
CTGAATCGTT	GAAGAATTTT	GAGTGAAA				

## 1433UP

GATCACGGAA	GAAGGCAAGG	TCAAGAAGGT	TACATTTGAT	ATCGAGCCGT	ACAAGCCCAT	60
CAACACTAAG	CTATACAAGT	GTGACAATAA	GTTCCGGACG	GAGGTGCTCT	CGGAGCTGCT	120
GGAGGCTGAC	GAGAAGTTTC	GGTTTATTGT	GATGGATGGT	CAGGGGTGTC	TTTTCCGTAT	180
GTTGTCCGGT	AACACCCGGA	CTGTTCTACA	AAAGTTCACT	GTGGACTTGC	CGAAGAAGCA	240
CGGTAGAGGT	GGTCAATCCG	CGGTGCGTTT	CGCCCCGTTT	AGAGAGGAGA	AGAGACACAA	300
CTATGTGCGC	AAGGTCCGTC	AGGTGGCAGT	CGAGAACTTC	ATCACAAACG	ACAAAGTTAA	360
TGTTAAGGGG	CTAATTTTGG	CTGGTTCTGC	GGACTTCAAG	ACGGACTTGG	CCAAGTCTGA	420
ACTGTTTGAC	CTGAGGTTGG	CAGCCAAGAT	TGTGAAGATT	GTAGATGTAT	CGTACGGTAG	480
TGAAAATGGT	TTCAACCAGG	CTATTGAGCT	GTCCGCCGAG	GCGCTGGCCA	ACGTTAAGTT	540
CATTCAAGGAG	AAGAAGTTGC	TCACCGAGTA	CTTTGATGAA	ATTCCCGAGG	ATTCGGGCAA	600
ATTCTGCTAC	GGTGTGACG	ATACTCTGAA	AGCGCTAGAT	TGGGTGCGGT	GGAGAAATTG	660
ATTGTGTTTG	AAAATCTAGA	GATTGTTCCG	GTACGTGTTT	AAGACTTCTG	AA	

## 1434RP

GATCAGATGC	TTCTGTGGTC	CTAGAGAAGA	CTGCTATTCT	TAACCCCTCG	TCAACGAATA	60
TAGCCGAGGA	CGAGTTTGTC	GATGCCATAG	CGGAACCTCC	ATCGGCGTCC	GTGGATAGTA	120
CGCCTTATGT	GACCGCGGCG	CGCGATTATT	CCTCGGAAGA	CACCGGGGAA	CGTTCTGAAC	180
CTACAATAAC	GGAATACAAA	ACTGAATTG	AATCACCATC	CACCTTTGGC	GACGATAACG	240
AGAGTGATAT	TCTTGTAAC	TCTGCGGACC	TGCATCCATC	GGTGTCTCTT	GCGAGTCAAA	300
CATTAACAAC	GGAAGAGCTT	CAAGCCGTTG	CGAACAGCCA	CCAATATAAG	ACCGAGGTGC	360
AGATTGTAAA	ACAAGACGAA	GATGAAGTGA	AGGATGTTCT	AGAAATTGGAC	TCGCCACCAG	420
CATCTCTGTA	TGATGGTGAT	GTTTTGAAGG	AGGCAGAGAA	AAATGATAGT	AGCAATGTTA	480
TTCTGTATGA	TTCATAGAT	ATCGATGAAT	ACCTCGATGA	AAACTTGGTT	AAAAACTTCA	540
CATTGGAAAA	CGCTCTTTCT	TTAGATGAAA	TCTTCGACGA	TGATAATGTA	GTTTTTGGAG	600
AAGAGAAAGCT	GCTTGTGGAT	CCAGACCTAG	AATTCCCGGA	ATTAACCTGA	ATGGAACAAG	660
ATATGGAATC	TGACTATCTG	CCGCTGATTG	AAAATGGTAC	GGAGGCTGTT	CTACAA	

## 1434UP

	GATCAGGTTT	TCCGGTACGT	GAGAACGTAT	CTAAGGCACA	AAGGGCTTTG	GGCGACTGTG	60
5	CGGACGCTTG	AGTTGCGAGA	TACAGGACAA	AGCTGTTACG	GCGGCAACTG	GTGCAGCACG	120
	AGCAGCCGAG	GAGCGATTCT	GCGCGAAGCG	ACGGTGAATT	CGAGCCAGCT	GGTAGCAGGA	180
	GTGCCGGATC	GTCTATTTAG	TTGCGACGGG	CGTCGGAACA	GGATGCACGT	AAACGTTGCG	240
	GTAACACGCG	ACGCTGACGC	GACGCTGCT	ACGCCGATAG	CACGGGAGCG	CAAACGACGG	300
	CAGCCGCTGT	CGCCAGAGAT	GTCTTCACCA	CTGCGCGGTA	GCAAGCTGCA	GCGGCGGAAG	360
	CAGACACTTG	AGGCCGGTCC	GGGTGCGCGC	AGTGGGACAC	ACACGGTGGA	CGAGCTGGCC	420
10	GCGCAGCTGG	AGCGCGGCTG	CGAGCAGGCG	TCCGAGCGGA	AGCCGCCGTA	CTCGTATGCG	480
	GTGCTGATCG	GCGTTGCGAT	CCTACAGTCG	CAGGAGGGCA	AGCTGACCTG	TCCGAGATAT	540
	ACCGGTGGAT	CTCGTCTTTC	TTCCCTTACT	ACCGGCTGTG	TGACGCGGGG	TGGCAGAACAA	600
	GCATCCGGCA	CAACTTGTCT	CTGAACGAAG	CGTTTGTCAA	GCGCGGCAAA	TCCGCTCATG	660
	GCAAGGGCCA	CTTCTGGGAG	ATCAAGGCAC	TGTGAAGGCG	CTTCTCCGCG	ATGGG	

## 1435UP

	GATCCGATGC	TACCCGTCGC	CCTGCCAACC	CGTTGCGCTA	GCGTTGACGC	CTAGGTCTGA	60
	AACTGAACAA	CAGGTGGCAT	TGTGGGCGGG	CCAGCAGGCC	CTGGGCGCGAC	CATGCCGCCA	120
20	TGGGCGGCGA	ATAATACCAC	CAGTTGTGAA	GCCCAGGTGT	CTGTAACTCTG	CACCGAACAT	180
	CTTTATCTAC	CAAGGAGGAG	CCTTGAAAAT	TATATATCTA	CCCCTCCCCC	TAATATATTT	240
	GACCAATTTC	CTCTCCGGAA	ACCGAATGAT	CGAAGACGCC	ATCAGGGCAG	CGGACAGCAC	300
	AGGAAGTGAG	GAGTGATCTC	GCAGGTACGA	TGGAAGCACA	GTCTATACAG	TCTATTCCGGT	360
	CGAACCAAAG	CGTACGGAGC	ATCSCGAGCA	CGAGCGGAAC	CGCAGACGAG	TCCGTAATCT	420
	TTGAACGGAG	CGTTGAGGAT	CGTTTGCCCC	CGTGAAGGAC	GCGAAGGGTT	GCAGCCTGTG	480
25	TGGTGTCTCC	CAGGCAGGGT	CTCTGCACGC	CGGGGTATCG	GCGACTGGGG	GCGCGTCT	

## 1436RP

	GATCAACCTC	GGAAACGTAT	TTAAAAGCTT	GTACTCGACA	TCATTAAGTC	TTCTCCTCGT	60
30	TTCTTTTGGT	AAAGTATWAG	CATCCAGTAA	AGTAACAACG	AAATGCAATG	CTGAAAGATC	120
	GTATACCCTA	GACGACCTAA	ATGGGGTATT	TTGATCATCC	ATACTAGCTT	GAAGATCAAT	180
	GAAGTCAATA	ATAGTGTTGA	CAGACTCAGG	GGAGAGTTTG	GACTTGATGT	ATTCTCATAA	240
	GCCAGTCCAT	CCCACCTTCC	TAGCACTAGG	AGTAATCTTC	AGCGATTCTT	TAAACGGAAAT	300
	ACTTCTGATA	AAATCCTCCA	GCTTTTTTTC	CTCGTAAAGG	ATCTGTACAA	AATTAGCAAG	360
	CGGGGTGGTA	TCCTTGTTAA	TTATGATTCT	TCCAACTTCA	ATGACCTTGT	GGTTGGGGAT	420
	TTTCTTGATA	AGCTCACCAA	ATACCATCGG	AGATTTTTTCA	AATACTTGGA	CCATTAGAGT	480
35	GACCAATAGT	TCGTTAATAA	TCGCCTTATT	TTCAACCATA	AGACTGAAAT	GCTTCGTTTC	540
	TGAGATCAAA	GTCAAGGCCA	AATATTCCGG	AACAATATTG	TAATCATCGA	AGAAACAATC	600
	ATGGAATAAT	TGGAACATAG	GACTGGAGCC	AAACTCCTCT	CTTGATAAGA	ACAGTTCAAT	660
	ATCGAGCTTC	GATACCGATG	TGAGATATAA	CAAGGAGTTC	TTTGAGTTTG	GGAGTACTTT	720
	AGAGACTT						

## 1436UP

	GATCCAGAAG	ATTATCCGAC	AATATTAGTG	ATATCAAGGC	ACAGATCGCT	GCCAACACTA	60
45	GAGGTATTCA	ATTGCTTAAC	CAACTGGTTG	ACGTTTTTCGG	TCTAGGGACT	GTTACAAGGT	120
	ACATGGACGC	AATTCAGGAA	AATGCAGCTC	TTACTGTAAA	GAATGTCTTG	CGAAAGATTA	180
	CCAAGCATTT	TGGCAAAACC	GTCTATTTCGG	CCGAGGATTA	TATGGATGAT	GGCTCTGTTA	240
	TAAAATCTAG	GGTGGAGCTA	AATGCTAAGG	AAGATAAGTA	TATTTTTGAT	TTTACGGGGA	300
	CTTCTCCACA	GGTCCACGGT	AACCTCAATG	CACCTGTTGC	TATTACCAAC	TCTGCCATCT	360
	TATACTGCTT	ACGTTGTTTT	GTAGACGAAG	AGATTCCGCT	CAACCAGGGC	TGCCTAAAGC	420
	CCATTACTGT	TATTATTCCA	GAGAGCTCTA	TCCTATGGCC	GACCAAGGGT	GTGCGGGTAG	480
50	TGGGAGGTAA	GTTCATGACG	TCTCAGCGTG	TAAC TGACGT	AATTCTCAA	ACTTTTAAAG	540
	TCATGGCGGA	CTCCCAAGGA	GACTGCAATA	ACTTTACTTT	TGGGACAGGT	GGGAACGACG	600
	CTTCTACCGG	TGAATATACT	CAGGGTTTTG	GATATTATGA	AACCATATGT	GGCGGGCATG	660
	GTGCAGGTGG	AGATCATGGC	GTGGTCCGGG	GTGGCATGGA	ACACATCCTG	TTT	

## 1437RP

	GATCGCGCGC	GAGCTATCGC	TTCCGCGGGT	CAAGCTGCAC	TGTAGTATGC	TCGCGGAGGA	60
5	CGCCATCAAG	GCCGCCATCA	AGGACTACCG	CAGCAAGCGC	AAGGCGACCG	AGCTGCGCTG	120
	AGCGCAGGCC	GCCGCAGCCT	GTCCGCGGCC	GGCCGCGGCC	AGCCGCAGAG	GGACGTCCGC	180
	GGGCCGCGCA	GAGCCGCCCG	TTTTCTATGT	AGCGACTCKA	GCATCTAATA	GACATGGTAA	240
	TAGCTTCTCG	TTTTCTACGT	TTGCACACAG	TATACAAAAT	TTTCACGCAG	CTCATCGCCA	300
	CTTCCACTTG	CTGAAGCGCA	GGTACGGCAC	CAAGACCTCG	GCTATGTCCT	CGACTCTCTT	360
	TGACGACATC	TTACCGATCC	AGGAAGTGGA	CCAGGGACGG	TACAATAAAG	TATCGCGGAT	420
10	TGAGGCCATC	TCCACGTCCG	AGGACACGTG	CAAGCTGACG	CTGGATGTGA	ACACAGAGCT	480
	CTTCCCGCTG	CAACCACAA	AGCAGCTAAC	GGTGATGCTG	GCGACGACAC	TCAACCTCGA	540
	CGGAACGAG	GACAGCCACG	GGTCCTGGCG	GCCTCCGGCC	CCTGGGG		

## 1437UP

	GATCCGGCGG	GACCGCTACA	ATATTCCCAT	ATGTATTAYA	GGCAACTTTA	TACCCATCTC	60
15	CTAAGTGCGA	TACGTACTGT	TTGTCACTCT	AGCGTCTCGC	TCGCGGTGAG	CCCCGTGTTG	120
	CGGTCCACCA	GCGCGCCGAC	CGCGCGCCCG	GGCCCGACGT	GCAGCGCGGC	CGTCGCGCCC	180
	GCCTGCACCG	CCGTGCGGCA	GGCTGCGACG	AACTCGACCA	CGTTCGTGCT	CGAGCGCACG	240
20	AACTTCTCCA	CGGCCACGTC					

## 1438RP

	GATCTCTTTT	TAACGGCTGT	TACCAATAAC	GATACCGCAG	CTACATCTGG	AGAATAGTCT	60
25	GCATCCCATG	CCTCCAAGTT	CCTGTGAACA	TACTCCTGGG	GATCGACCTC	GAAGCTCTCC	120
	AAGGTCTCTT	CGCTAGGACA	AAGAAGCGGG	AAGATAACAT	GTTCCTAAAT	GGTTGCATAA	180
	TGTGGGTCAA	CTATCGGCCA	AGTAGACTTT	TGGACCACTG	TTTGTTCAAT	GAACCTCCAAT	240
	ATGTAATATA	GCGACTCCTT	GCTTAACCAC	AATTCGCCCTG	CACCCACCT	TTCAATCTGC	300
	TGGAATGCA	ACTGCAATAG	TTGCGGCAGA	AACTGCTCCA	CATACAGCAT	TTTAAATTCA	360
	GTGTACTCAA	ACTTTTTGCT	GAGAGATTCT	GAGGCATAAC	GTGGAATAA	TCGATACATG	420
30	TTAGCATATG	CCCACTTTTT	GGCTCTGACC	CATGGATGCG	CCCGCCTATC	ATCGACCGCC	480
	AGCGCCATCA	CATGCTCCGG	CAGCTGGCTT	TGTATCACAG	AAACATGGAA	GTGCGCCAC	540
	GGAAATGAAGT	TTTCCGACCG	TTGGAGAGTG	AACGGCAGGT	CATTATATGT	CACAACTTG	600
	TAGATCTTCA	GCACAAGCTT	CAACATATTC	CCCACGATCT	CGTTGTGCTT	TCCTCGCTGT	660
	ACAAAAGCGC	GTTTGCGTAG	TGCAGCAAGT	CTGGGAAATA	TCTCATGATC	AGCATCTCCA	720
	GCTCCTGA						

## 1438UP

	GATCGGCAAA	CCTAATGCGT	CTGGACGTAA	TGTAATCCAA	CAGCGACTGT	AGAGCTGCCT	60
40	GCGGTTCTCC	GACAGAAATC	AGCTCATCTG	CCCGCTTCAA	GGCGTTTTCA	GGGCGCAAAA	120
	CAGGTGGAGC	CATGCTGAAT	TAGAGCTATT	TGGTGACCTG	TTTGAGTAGT	GTGGACTTCC	180
	TTTGAATGTG	GTGAACCTTG	AAGTAGGTTA	TTCAACTAGA	AAATTTTTTCA	CCCAGAAGGA	240
	TGCCCTCTAT	CAGCGGCCGT	GTCTGACGAT	GATCTCAACC	GCGTAAAGGA	CGAGAAGTCG	300
	TAGGTCGAGT	CTAATCTACT	ATTGGTACTG	ATGAACGGGA	CTGGCCAGCT	AACGTGAAGG	360
	CACTGTCTGC	GGGATGAGGC	CCCAGCGCCA	GCGCACGGGC	CCTGCGATGA	GCACAGGTTG	420
	CCTCGAGACG	ATTGCGATCG	GCTGACGGGA	AGCCAGGTTT	CCACAGCGTT	GGCGGACTCG	480
45	CGTCGTCAGG	CTGGAACTGT	AGAAGGGTTG	TCTTGAGCTC	CGCGCACGCC	GCACGCTGCC	540
	CAGGTAGCTG	GCGGGCCGTG	TTTCATCGCGC	ACAGCGGTGG	GCTCGCTGTC	ACGTGGCATC	600
	GAATATGTCA	CGTGATTACA	CGCAGCAGGG	CATCGCAGAC	AATGCGCAAG	CAGCAACAGG	660
	AGGAGGGTGT	GATCGGTGGT	GTGCGTTTAA	GAGTATGTGA	GCTGTGCAGC	TGGCTCCCCA	720
	TCTCTGGGTT	TACTCGTACC	TGTGCGCTTA	TATAGGCATT	GCCAAAAGGT	TTCC	

## 1439RP

5	GATCCTGTTG	GACGTCCTGC	AAAGTCGTGG	TCACCCCGAC	CAACTTCTCC	TCTGTAATAC	60
	CGCTGTACTT	CGTTAAGTAG	TCCACAATGG	GCTCATCTGG	CTTGACAAAC	TTGTCATAAA	120
	CTAAGTTACA	ATCAAAATCG	ACGACGCTCA	CACGCGTCAA	CACGTATCCG	TTTTTTGAAA	180
	GGCACATCTC	ACAGTCGATG	GCAAACGTGT	GAGAACCGTC	GTGTTGGAAA	CTGACAGTGT	240
	CCACCCACCC	ACTGTACTTC	TCCTTATTCT	GATACTTTAG	CAACAAAGCC	TTTTGGTACT	300
	CCTCCGATAA	GCCAGGTGTG	TTTAGATGGA	TGGGGTACTC	ATTATGCAAT	AAGTCATCAA	360
	CGGTCATTAG	CAAAATCAAGC	AAAGTGATTT	CCTTTTTGTT	CAATTGTTCC	ACCTTTGCGA	420
10	TCTTCTCCTT	TTTTGACAAG	CCTACATTGA	CAAAAGAATT	GTATGCAGAA	AATAGGGAAT	480
	TCTTTGATCC	CGGCGCTGAT	AACGGCAAGA	TACACATTTG	CTTGACATC	TGTTCAATTT	540
	CACTAATCGA	GTTTAGATGT	GCGTCTTGCA	ATTTTCGGAAT	ATTTTTATGA	AACAATGAAT	600
	CCTTCGGTAG	ACTGAAGTCC	TCGGGTAAAA	GGCCTGGAGT	GAATAAGACG	ACCACCTTCT	660
	TCAAAGAGGC	CTATTTTCTA	TCGTAATCCA	GTTGGGAGAG	TTGTTCTGAT	CGTGGAATAT	720
	GTACTGGA						

## 1440RP

35	GATCTATTCT	TCATTTCAGCA	ATCAACAAGA	GCTGGTGAAA	CTTGGGCAAG	AAGCTGAGCA	60
	AAGCGGTAAA	TACAACCTGG	CATTCAATGC	ATACTGGATT	GCAGGAGATA	TCAACAAGGC	120
	CAGGGACGTG	CTTTCGAAGA	GCGGACGCCA	TTCCGAGGCT	GTGCTTCTGG	CATCCACATA	180
	CACCTCAGAC	AATGACGCCA	TCAACGCTGC	TGTAGAAAAA	TGGAAGGAAC	AACTGAACTC	240
	AGCTGGAAGA	GTATCTATCG	CAGAAAGAAT	TATACTTTCC	GGAGAAGACG	ACTTCCCTGC	300
	AGCTCCCCAG	ACTTTGGTCG	AAATGGATGA	CGGATCAGAG	TCCGCGTCTA	AATAAACTAT	360
	AATTTTAAAG	ATAACAGCAG	GAATAAATTA	ATTACCACGA	AGGAAATTTG	TATGTACATT	420
	CTAACTAGAC	CCAATGGTAG	AATTTCAATG	CGTAAACACG	GCAACCTTAT	CAATATCTTT	480
40	CCGTTTGTCC	AGTCCGACAA	AGTAAAGTTC	TTTGGATTCA	GATCGGCATG	CTTCCGGCTT	540
	AAAACGCCGC	ACTTTGGTGA	ATACCTTTCTG	CAGACGCCGT	TCTAATAGCT	GGTCTTCCTT	600
	GCCAGTGTAT	AACTTGCAAA	CGAATGAGCC	ACCGGGCCTC	AACAATGCAA	TTGCACATAG	660
	CAGTGCTGCG	TTACACACAAG	TCCATCGACA	TGTA			

## 1440UP

45	GATCCTACAG	AAATAATCCA	GTACAAGGTA	CCTCTAATCT	ACTGTGTTAA	CATGGAAGAA	60
	ATTTTCGCCCTT	TAGGCTTTTTT	CTTTTCACCG	AAAAGGTAAC	GTGTTTCGAAA	CATATATCAC	120
	GGGTTTCGAAA	CTGACTAAGG	TTGCTCATGC	CTAAACCAGA	TAGGCAGCAA	TGGCAAGGGG	180
	CTTGAGGTGG	TACCAGAAAA	GCTGCCACCT	CCTGCTGCGT	GCTTACTCTC	GCAAACGGTG	240
50	TATACTATTA	GTGTTGGAGT	ATTTATTGCT	TATTAATAA	CCGAATTGTG	GGCCTAGAAG	300
	TGGCGATTAT	CACGTAGCAG	CAGCGGCTGG	CAGCGCAGAC	TGCTCGCGAA	GCCGAGCAG	360
	TGCGTTTGAG	GCAGCGTTTA	GAGCTGCAGC	CGTGACCATC	AAACCTTCGC	CGCGGAGGAC	420
	GAGTATGAGG	GCTAGCTCGA	GGCGCATCAA	GAGCTTCTTC	GATATGCCGC	AGACCTTGCT	480
	GAAATACTCG	TGGGAGTGCA	CGGTGTCTTC	CACAATCTTG	GTTGAGACAC	GTATCAAGGC	540
	CACTATGAAG	CGATGCACAT	ACCTCTCGGC	GATGGGCCAG	CGGATCTGCA	CCGGACCGGT	600
55	TTCCGAAGGA	GGCCATTTTA	GCGTGAGGCG	GAGTAACAAG	CAGCCCGCGG	TCTGGTAGAC	660

TATGGGCGCA AACATGCATT TGGCGTTGAT GCCGTCTAGG TACTGCGTAT AC

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## 1442RP

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GATCAATTGC	GTCTTCATCC	GATGAGACAT	TTTGA AAAATT	GTTGGAATAT	TGGGCAACAT	60
CAGGGTATGG	TAACACCTCC	GGTTCTAAAC	TTCTAATCGG	TAGCCTCGTC	GCGCGTGTA	120
CGCATGGATC	ATCAATGGAC	GGTGCTGGGG	GCGATCTAGA	CACGCCCCGAA	TTGGGGCTTG	180
GTGTGAGGTT	TTCTGTCGGA	CTTCTCACTT	TATCAGGTAT	GACTATCACT	TGATGATTCA	240
TTAGATTCCG	TGTATCCACA	ACATGGACGT	GGCTTTGGTG	TTCCGAGATA	AATAGTAGGT	300
CATCAAACGA	GCGGCTAAAC	TTGCACACCC	TAAAGGACCC	GTTCTGTGCA	TGTCTTCGAG	360
TTGAAGGTAT	CTCCGCAAGA	GGCGTGTCCA	TTTTTCTCAT	ATCGTACACC	AGACAGAGGC	420
CGTTTTGGAA	TATCGTAGCC	ATGTGCACGT	CGTTTTTCGCT	ATAGCTTGTG	TAAAAGCCGT	480
TATCACCACC	AGGCGAATCG	TAAATACGAT	CTAGGACTTC	GGATCTATCG	ACCGCGGCAT	540
ACCTTGGAAC	GCACTTTGTG	CGCGACCATT	TTGAACCCCA	CTCAGGAGCG	GCGTCATATT	600
GTAATGAAAA	ACAACCGCTT	AGTTCATCTG	TCTATAGACC	GCAAACCTGC	TGGAATCTCC	660
CGAAACCACC	ATCGTCTTCC	CATCGTGTGA	TATTGCCGAG	CAGTTTAAAG	CAAATTTTAA	720

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## 1442UP

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GATCAAGGCT	GGGAAGTTGG	CGTTGACTGG	CTTGCCCTGC	GCAGGCTCTC	TGTTGCCGCT	60
CTTGCCGCCCT	CTGTTGCCGC	CCTTGCCGCC	TCTTTTGTG	TCTCTCTGGT	CGCGAGACTT	120
AGGAGCAAAG	GACTCGGTGC	CATCAAACCTC	TAGGAACCTGC	TTGGCCTTCA	AGTGCTTCGT	180
CTTGACGTTT	TTGACCTTGG	TAGCCTCCAT	GAAGACCTCC	TGCTTCTTAA	CGAACAACTC	240
AGCGTCGTCG	AACCTTCTCGA	CCTTTCTGGC	GACAGGGGCC	TTGTTTCAGGT	CGGAGTTCTG	300
CTGCTCCAAG	TACGCCCTCCA	AGGTGACGGC	AGCTGCAGTG	GCTTGCTCCT	CCTCGGCAGC	360
GTCGGCGGCC	AACCTCCGCCT	CGGCAACAGC	GGCACCAGCC	TCCTCATCGG	CCTGCTCCTT	420
CTCGTTGTGCG	CCCCACGCCT	GCTTGATCTT	CTTGCCAGAG	TCAGTCTTGC	CGGTTCTCGA	480
GTGGCGGTCA	AAGGTCTTTC	TGCTGTCTCT	GGCTGGCTTG	CCTGGCGCAA	GAGCGTCCTT	540
GGACTTGTTC	TGCGAACGGC	CGGCCTGCTT	GTCTCTGAAC	GCAGCCTCGT	TGCCGGTTGG	600
CTTTGGTCTG	TTGTTCTTGG	CACGCGATGG	GTCGGCAGAT	GGAGGAGGCA	CGTCCGCCCT	660
CTTGGAAGAG	GTGGTCTTCT	TCACAAGCTC	CTTTGGAGGA	GACACAACAA	CGGTGGCGTC	720

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## 1443RP

	GATCTATGCG	GTGCTGTGCG	CGTGCATCGA	CCAGCACAAG	AGCTTCGAAT	TCGATAGCGG	60
	GAGCTTCTTC	TTTCAGTACG	TCGAAGGCAT	CTACTCGTAC	AGGACTGCGA	GCCTTCTTGC	120
5	GGGCTATCTG	CGGACGCACT	CCGTGCCGAC	GGCCAGCCAG	TACGCCAAGG	TCTTCCTAGA	180
	CCGCGCGCCC	TCGCCACGTC	AGGCCGAGGT	GCTGCTGCTG	GGCATAGTTG	CGGATGCCGA	240
	CGCCATGCAG	CGGCTAGTGC	AGGAGTGCAA	AACGAGTGGA	GCCGTGACAT	CTGCGAGCTT	300
	CTCGCTTCTC	ACAGAGTGCC	TCGACATATA	CCTGTCTGAT	GTGAACGATA	CCGTTTTGCT	360
	GGGGCCCCAAG	AGCAACTTCC	CGCTTGAAGA	TCTCGTGGTG	TTTTGCAACT	TGGTGCGTGA	420
	CGCGATATCT	CAGGCTTTGC	GTGCTGAGCA	TGATTATGAG	GTGAACAAGA	TGCGCCGCGC	480
10	GCTCTCCTTA	CTCCAAAAGC	TGTATATTAG	GGATAGAAGG	ACCAATTTCC	TCTCCGCGGC	540
	CAAGGGGGAC	GACTTCTGGG	TCATTGCGGA	TACCACGGTG	AAAAACTGCG	ACATTACATC	600
	TCTCTCTCTT	TACTTTGATG	AGTTCTACAG	AGAACAGTTG	GATTTGTTCC	TGGCGCAGGG	660
	CCGTGCTCGG	CACGAGGTCC	CAGCGCGCAT	CTCGTAGCGT	GGGAAAACGA	TATAAA	

## 1443UP

	GATCCGGCAT	TTACATCTGA	CATGTAACCG	GGTGGTTCTG	TAGGTAGGGT	GTTCAATGTA	60
	AAGTGGTCCG	AGTTCGAAGT	TGGGGTAGTA	CTAAATTCTGA	ACCCCGGTGG	CGGTGGTAGA	120
	AGATGGCCAT	CGTGAAGGTG	TTCCACAAAA	CTATTTCGTTT	CACCCCTCGGA	TACTTCATCT	180
20	TCATAACTGC	TTTCTAACAA	TACATCTCGG	TCATAGTCTT	CGTAGGCTGG	TGGAGGCAGC	240
	TTCATGCCGT	TCAGCTTTGC	ATATCCCCAT	TTCTTTACGT	TTGCTTCAAT	GTAGACGAAT	300
	CCGTAGGTCC	CGAAATTAAC	GTGTATCTTG	CATGGGACAT	TCGCACCAAC	AATCGGGTAA	360
	AGATACTTAA	TTTTCCAGCC	CTTTATGTGG	CCACCAATGC	GTTTCTCATT	TAACCTTCTG	420
	CCATTGCGCG	TGAAGAAAAC	TGTGCCGCTC	CGAGTTCTGT	AGCCAATCCC	GATGACGTCG	480
	CCCTTTTTCG	AGCGGGGGAA	TAGTGAAGAG	AGTTCTTGCG	GGAGCTTAA	CGAGTTGTTT	540
25	AACCTACGTG	CTCCATTAGA	GTCATATGCA	ACTGAGTGAT	GGTGTCTGCC	GGGAAGCCTA	600
	AAATAGGGAT	ACGGCGATGT	AGCAAGACCA	AAGGAACTA	TTTGGTTTTT	TGAGAGATGG	660
	CTGACCGGGC	GGCCAAGCCT	GTCACAGAGT	CGAAGATCTT	GCACTCGAAG	T	

## 1444RP

	GATCTGGTTT	TATAGGTTCA	CGAAGGGACT	CTGGACGCGG	ACCCTGCTGA	AGTGTGCCAA	60
	CATGCTGTAC	TTCGTGGCCG	TGATGCATTT	CTACGACGAC	TACGAGCACG	CGCCGGTACT	120
	GAGAAGCATT	GGGTACTCGA	TCTTTATTCT	GAGCATTGGG	ATGAATCAGG	CACTGCATCA	180
	CGGCGGGCGG	CTATTACAGG	GGCGACGCCG	CGCGCGGTCC	TGGTGGTGGC	GGTCCGACAC	240
	ATTGTGTCTG	CAGCCCGCAC	TATATATCAG	CCAGTTCTAC	CTGCTGCTAC	TGAATGTACA	300
35	GAACCCGAGC	TTTCATTCTGA	CGCCGAAGCT	TGACATAATT	AATCGCACGG	TGCTGGTGGC	360
	CTACGTGCC	CTGGCGCTTC	AGTGCTTTTC	TCGGCAGCTG	ACGAGCTAAG	TCACTCGGGC	420
	AGGAGTGCT	CGTGTAGCTC	GTGTGCTATG	CGTGCGGCTG	ATTGCTCAGC	GGCATGAACA	480
	TCTGTTATCT	CTAAATAGCG	TTCTCTAGCT	TGCTTAATCC	TGGTTACCAC	ACTGTGAGAC	540
	GGTATATCTG	CCTGCAAGGG	ATCCAGCTCT	GCGAAGGCTG	CAGCGGTCTGA	CGCGTGCATA	600
	CGCAGCATA	GCTCGCTCCA	GGGGATGGAT	ATCCAGCAGC	TCGCGCACAC	TTCCCGCCCC	660
40	TGCTGTTCCC	CCAGCTCGTT	TGTGCCGCGC	TCGCGCCATC	TGAGAAGCGC	ACGTCGTGCA	720
	CTTCGAGGGC	ACGCTC					

## 1444UP

	GATCCAAATA	CATCCGGTAT	ATATGCTACT	TGTGCCAGAA	GACATGAAAA	GCAAGCATCA	60
	AGGGAGCTAA	TGAGCATTCT	ACAGGAAAAAG	GCGGAAGAAT	ACTACGTTGA	TGAACTCAAA	120
	GCTATCGCAG	AGACTGAACT	CTTGAGCGAC	AAAGAAGATG	AAGAAGAACT	ATCTGTGGAA	180
	GAGCAGGTGC	AGAAAGAGCT	AGAGCAATTG	AAGAAAGGCA	GTGGTCTCTG	GGATACCAAA	240
	AAGAAACCGG	TCCTGCAAGA	GATTCAGTTG	GGATGTGAAT	GTATGGTCTT	CATCAAGACT	300
	AGAAGACCAA	TCAAGCCGGA	ATGCTTTGTC	AAACGCCTAG	TACAGGAACT	TGCATCGTCA	360
50	GAAAATACTA	CCAAGGTTTC	GCGGTACGTC	CAGAGATGTA	CACCCATCAC	TGATTCCTGC	420
	AATGCTAGTC	TAAACAGAAAT	GGAAAACTC	TGCAGAAGGG	TGCTTGCTCC	TCATTTCCAT	480
	ACTGACAAAG	AGATAAAGTA	CAAGTTCGCG	GTCGAGGTGG	TAAAACGTAA	CTTCAACACG	540
	ATAGACAAAA	TGGATATCAT	TAAACTTGTC	GCGAAGGAGG	TCGGTAAGAG	TGGGGATTGG	600
	GGGCACTCTG	TGGACCTAAA	GGACTACGAC	AAGCTGGTCA	TCGTGCAGTG	CTATAAGAAC	660
	3172700000	7000000000	0000000000	0000000000	0000000000	0000000000	

## 1445RP

	GATCATCTTC	CGAACATACT	CGAGGGAGTT	CGCGTTCGGG	AAGTTCTTGT	ATCGTTGCAT	60
	GTAGTGGAAT	TGCTCGTAAT	CGTCTGTAAA	TAGAAAATMG	GCGTCAATCA	TGTTGTCCCC	120
5	GTGGACGCG	CCGGAAATGA	ACATGAACGG	TGGCAGCCCC	TAGCGCACCT	TCTGGCCCCG	180
	GCACGCGCG	AGAATCGCAT	CGTTGGTGCG	CAAAATATCG	CTGTACGCGA	CCGGCATCTT	240
	CTCTCTTCG	ATGGGCTCCA	ACACCGCCAT	CTTCAACAAC	TCGCGCCCAT	AGCTCATCTC	300
	CATCTCCCG	GAGAGGAGAT	TGTAGTGCGC	CTGCGGGGCG	CGACTCGTGC	CCGACTGCTC	360
	CGAACGCGC	AACGTCGACG	TGCTATTCAA	GCTAGTGTTC	GAAAAGTGCA	CATGCTCGTC	420
	ATACGAGGAA	CAGCTGAGCG	CCATCTCGGT	CACGCTGAGA	AGGTACTGTT	CTTCCCGCGT	480
10	GTACAAAGAC	CCCGCCTTGT	ATGTCGAGCC	TCTGGTGTCAT	TCCATTGGTG	TCGCCATTGC	540
	TCTGGCGCAG	CCTGATACAC	TCGCCGTGCA	AATACTACCG	CACCACCGCA	CGAACGACCT	600
	TTCCGCCATT	CTTTTGGTTT	ATAAAACCCG	ACTACGCATA	TATTTTCATCC	TGCTCTGGCA	660
	TGTCCTCGATG	CCGTCTCCG	TGTGACATAG	CTGCTTATTC	ATCCTGGGCG	TTCATTT	

## 1445UP

	GATCCTTACT	GACGAGGAAG	AATCGAGCAA	TAAAGTTGAC	GCCGCTTCGA	GCTCTAATAG	60
	CGGTAAGAGC	ACCGCTAGTA	AACGTCCAGC	CAAAACTAGG	AAGCCTAAGG	CTGACACTGC	120
	GGCTACGAAA	AKCGGAACCA	CCTCCCGGAT	GCCCAAGACT	GCTGCTTTGC	AGGCGCTGCT	180
20	GAACAAGAAA	AGGGGGGCTT	CGGCAGAATA	GACTACTGGT	AAACGTAAGT	AATAGTATAA	240
	ACTTGGTTTT	TTAATCCCTG	GCTATCTCAG	ACTGCTAAAG	CATGGCCGTT	TAGGTGTGGC	300
	CTCCTCGGTA	GATGGTTTGC	ACCACGCAAG	GTGAAAAAAA	GATCACCAAC	CCTGAAAAAC	360
	GTTTAACACT	TGTCAATCTC	TAAAGGCGCT	GCAATCAAGG	CATATTACCA	TTGTGGAGCC	420
	ATGAATCTTG	CCAATGAACC	GAAGTTCCAA	ATACAAGTTG	ATGAAACAGA	GGATACAGAG	480
	TGGAACGATA	TTTTGAGGCA	GCATGGTGTC	ATCCCAGAAC	GGCCACCTTC	ACCGACCGCA	540
	CAGCTCGAGG	AAGCGCTCGA	GGAAGTGCTA	CNGAGACCAC	ACGAGAATAG	ATTAGAGAAC	600
25	AAAGACTCTC	TGAACCTGGAG	GACTGGAAGA	TGAAGAAGAT	GATGAATTTT	TGGAGTTTTA	660
	CCAACGTAAG	AGAATGGCAG	AAATGCAGAA	GCAACAAAGA	AGCGCAAGTA	TGGGGAC	

## 1446RP

	GATCTGCAGG	CTGCTACGGA	GGAACTCGTT	TCCGAGGTTG	CTCGCCTGAG	TAAAGACCCA	60
	AACTTTCCTA	GCATTTTTCG	GCAGGAGCTA	CAGAAGCTTA	CTGGTGAGCC	CCATATAGGC	120
	GGCAAGGTGG	ATGATATAAC	GGTAGTGATG	GTGAAGGTAG	ACTAGTAGAT	TGCACATATG	180
	TAGAATTACT	AATATCATTC	GAATTTCTGG	CTTAAGACAA	TGTTCTTAAT	CCGCTCTCTC	240
	TCGCTCTTCA	ATCTCTGCTC	GCCTTCTAGT	ACGTCATGAA	CAAACTTGAC	GTCGGTCCGC	300
35	AGGCATATCG	GGCGGAGTTG	AGTCCGCTTT	CCTGATTGTC	TGAGAAACGT	AAAGGGCACC	360
	TTACCCGCTT	CGACTTTTGA	TGACAGATTG	CTGTTGACCT	GTGTGCTGGT	CCCAGATCCA	420
	ACGATAGGAA	TGTTGTTCAT	GGGGATTTTC	TCATTCTTGC	GGGATTCTAA	AGATTGTTGC	480
	ATCACAGCTT	GGTACACTTT	TTCCATTTCA	TCTTCTGCTC	TCCGCTCCTC	CTCCGACTTT	540
	AGCTTTCTTT	CGTATCTTTC	GTTTATCTTT	TTGCGCTCTA	GATCTCTGTC	AATAGTAAAC	600
	ACGTCGTGTG	CGTCGTCAGT	ATCTTCTTCA	CTTTCACCTG	TTGACGGGGA	ATCACTATCG	660
40	TCGTCATCCT	CATCGTTATC	TTCTCTGTAT	AAGTGCTATT	AACGTCCTCT	TCTTCTACCT	720
	CGCTGGAGTC	GGCACTGTCT	CCACTACTAG	ACTCGTAGCC	ACTATCTTCG	TCCTC	

## 1446UP

	GATCAATTAC	ACTACTAGCA	ATCTACTTTT	CAACAATCTG	ACTGTCCGCG	AGGTAAACT	60
	CTACCGTGAA	CAGCTGATGG	TACTCAAAGA	GCAGAGGTTT	ATAGTGGAGG	GCATGCTCGA	120
	GAACGCCAAG	AAACAGCGGC	GTTTTGAAGA	GGTTAATACG	TTAAAGGAAA	ATACCAAAGA	180
	GCTAGACAAT	CAGATAGCCC	AGCTCGAAGA	AACCCTAGGC	GACCAGGGTT	TTGTTTAGTA	240
	TCTAGCATGG	AGTTTPTTGC	TTAACTATAA	TTACTGTGTA	GATGCCGCGAG	ATAGCATGTC	300
	GTAGCATAAT	TGCGAATTTT	CACCAACATG	AAAAAGTGTA	TGTGTATAAG	GCATCCAGTG	360
	AACTCCTAAC	ATGCTGATGA	GGTTTTAAGT	AAAGATATCA	CTAGCAATGA	ACGTAAGTGC	420
50	AGTTTTTGAG	CTTTATGTCC	TCTGTAGAAC	ATAATATTAA	CGACAGGGGG	ATAGGATGAA	480
	AGAAGACAGC	AGTTATTGGA	GCTGAACAGT	GAAGCCTGGT	CTGGAATTGA	TGCGTTCCCG	540
	AATAAAACCA	GCAAGCTTGA	CTCAAGCATC	AAGAGAAACA	CAGGGTTTAT	CAAAAAGCTG	600
	AAACAGGGTA	TCACGAAAGA	CTCGAAAGAT	C			

## 1447RP

	GATCCAGGAT	GATGAATTTG	ACGAGGAGGG	GGGTGCAGAA	GAGAATGACG	ACTACTCACG	60
	GTTTAAAAGA	TCCTGCATGT	CCTCCACGT	CCCCGCGTTG	TAGTAGGCAT	AGCGCTCGTG	120
5	GTACGCGCCG	TGCGCCATGG	CCGGCGCCAT	GGGCGCGGGC	CCATGCGCCC	ACCCCGTGCG	180
	GTACATGTCTG	TACATCCGGC	GCCGCGACGC	GTCCGAAAGC	AGCGCGTAGG	CCTCGTTAAC	240
	CAGCTTGAAG	CGCCGCAGGC	GTTCGTGCTC	ACCCAGCCCC	TGTTGGGCAG	CCCCCGCCGT	300
	GTCCGGGTGG	TACAGCTTCG	CGAGCTCGTG	GTACCGCTTC	TTTAGCTGCC	GTGCATCGAC	360
	GCCGGTCTTC	ACCAGTCCCA	GTACCTCGTA	GGGCGTCCGC	TGCTTGCCCT	GGGGCCACGA	420
	TAGCCCCCCC	TGCCACCCGG	CGACGGTGCT	AGCGCACCGC	ACCGTACTCC	GACCTGACGC	480
10	TGTAAGCGAG	ACCGCCAACG	TGCGCCAGTC	CTGAGCAGTG	CAGTCGGACG	CGACAACATA	540
	ACACTTAAGC	TCCTAGTTAA	CGCTTTGGCG	ATGGAGATCT	TGTCGGTGCA	TGCACATATC	600
	CAGGACGCCG	CTCCGCCTCC	GCTCGACTGC	TGGCCGTCCA	GGCTCCAGTT	GCGCGCTTAA	660
	GCCATATCGG	CGAAAAATA	AAGTCCTGCT	CGAGGCGCGA	TGA		

## 1447UP

	GATCCAGCAG	ACGCTCCGGC	TGGCTGTTGG	AGATGCACTG	GCTCTTCGCG	GCCGAGTGGC	60
	GGCAACGCGC	CCGCGCGGCG	AGACGCGCCC	GCCGCGCGCG	CGTGCGGGTA	CATCCGCACC	120
	AGGTTCTGCA	GCTCAAACCT	CAAGGCCAGC	TTGTTTCTGT	CTTCTTTGCG	CTTCGGCTTG	180
20	TACTTGTAGC	CCGGGTACTT	CTTCGCGTGC	TCCTGCTKCT	CCAGTTCCGC	CTTGTCGTGC	240
	CACTCCTTCT	TCTCCTCCGC	CGTCAGTTTT	TTCCACTGGT	AGCTGATGAT	CTTGCTCACC	300
	TCGCAGTTGT	GCGGGATGTC	CTGGCCGGAC	TGCTTCCAGT	AGTCTGTCTG	CAGCTTCTGC	360
	TGGTGCAGAC	GGAACAGGAT	GAACGCGTTG	CGCGGCCGCG	GGATGTGCTG	CTTCTGCTTG	420
	TAACCAAGCG	GCCCCGCCCG	GCCTCGCCGG	CCTCGCCGTC	CTCGTCCGCC	ATCCTGGTGC	480
	GCTGCCACTC	CTCGCCGCCG	GGGGGCTGGT	GCGAGAAAAA	CTTCTGTGCC	AGAGGCGCTG	540
25	CCGCGCTGCC	GCTGGCTCGC	CGGCTCGTCC	GCCGCGGCTG	CGCGTTGCCCT	GCCTTGGTCA	600
	AAGGCAACAA	TTGCCCGGAT	CTCCCGCCGC	TGCTGGCGCT	GGTGTACGAT	CCGTGTGATG	660
	GTCAGCTTCT	GCTCCAATCA	CAGA				

## 1448RP

	GATCCGCTAC	GTATACAACG	ACATATTGCT	ACGTATCGAA	TGTGATGTGA	CAACATGCAA	60
	GATTCTCAAC	AACAAGCGCA	AGTGGTTTAG	TGGTAAATC	CATCGTTGCC	ATCGATGGGC	120
	CCCCGGTTTC	ATTCCGGGCT	TGCGCATATT	TTTCACAACA	TGCACACACT	GTGTGGCTAT	180
	CGAGACGGAG	TCCACTACGA	GCATCGTCAT	TTTTGTCTAT	AATTTACAAG	CATATTGTAA	240
35	CTATPTGTGC	ATTGATCTAA	ATGTCGAGTC	GATAGAATCC	TTTACGCTCCT	TGTAGCTAAT	300
	GATAATGACG	TTCATCTCGT	CCGGTGTAC	CAAGATTATC	TTTTTCAGATA	CGCCGGTGTG	360
	GAGTTTGTTC	AGGCACCGGA	GTACGTGGGT	GAGGTCCATC	ACGGATTTCG	CGTTCTCGTC	420
	CACCTGGTGG	AACACGTAAT	CGTAGAACAG	AATGATGGGG	AACTTGTCCC	CCGCCTCAGA	480
	CCAGTGGATG	ATTCATGCTG	ATTCCATCCT	ACCAAAGATG	AAATTTAGCT	TGCACATGAG	540
	CCTGAAGAGC	CTGCCATTC	CTAACTCCCG	CGACAAGTGC	TGCTCGATGT	TCTCCGAGTA	600
40	GGTCTGCGAC	GAACTGATTA	TGTCTAACAT	CTTGTGGCTG	AACAGGGCGG	TGAATCCCGC	660
	AATCGTCTTC	TTCTCGTCCG	ACAAAAGGTA	CGCCAGCACC	CGCTTGAACA	GCGGGTGC	

## 1448UP

	GATCTCGCCA	GCGCTGGCAT	CCGCAGCGCC	GCAGGCGCCG	CGCGCGCGCG	CGCGCCGCGC	60
45	GCCACTGCGC	CACAATGCTG	TCCCATAGCC	CTCAACATCC	CAACTAGCTA	GTCACCTTGT	120
	GCAATCGGTC	TACCGATGGT	GTGTGCGGCG	GGGACAAAGC	CGTGGTGAAA	CGGACACTTT	180
	TCAAAATGGG	CTGATCTGCA	GCAGTACACG	ACCGATGAGC	TGCGCGCACG	GCGACAGCAG	240
	TCGCGGTTTC	GCGCCTGGCT	GCGCATAGGG	AACTTACGTA	TAGTATAGAA	GGGCCGTCTA	300
	CTTGGCGTAG	GCAGCGAGGA	TGTCGTCTGT	GTAGCGGAGG	TATTTGCCGT	TCGCGCAGTC	360
	CGGGATGCCT	CTCAGCGCCA	GGTTGGCGAA	GATGGTGGCC	GGGATCTGCG	GGTCCAGCAG	420
50	CTCGCTGTTC	TTCTTGAGCT	CCGTGAAGCG	GCGCAGTGCC	TCCGGCGCCA	TGCGATGGCC	480
	GAACTTGTGC	CGGATGTCTG	TCTGCATCTG	CGTGTGACCA	ACGCCCCGGC	CCACGGCGAC	540
	GCGCGCACC	GCAGGCTCTT	CCGCGGCCAG	CGTCATCGCA	AAGTGGTTCA	GCGCGGGCTT	600
	CGACGAGCCG	TACGCGCCCC	ACGCGGACTG	TCTCCGAGTT	AGTAGCTGCC	CCTGCCCTGC	660
	CTGCGTCTGT	ACATACATAT	GCTTCTGTGC	TGCGCCCCGA	GCTCACGAAC	ACCACACTGC	720

## 1449RP

	GATCCAAAGA	CCGCGTGCTC	GCACTTCCAC	ATGTCTCCAA	GCTGGACGCG	AACAACGATA	60
	TCTTACTGGC	GGTGAAAGAA	AGCCCGAATC	ACAAATGCCC	ACGATGCTGG	AAGCACGCAT	120
5	CTCCCGAGGC	CGACGCTCTA	TGTAATCGCT	GCGCCAGAGT	CCTCCAGTAA	GCCAAACCTG	180
	AAATTTTCAA	AAATTGAAAA	CTTCACCATG	GCTCACATGC	TGACTGCTTT	AATATCCTGT	240
	AAATACAACC	GGACTCTGCA	GGTCGATGCT	CCCTCACCTG	GGCCCCAAC	TCTCCCTTGT	300
	ACCGGGTCGC	GGCGTCGCTG	CCTCATTCCG	CCTGCATCTC	GCTTCCAGAG	GCGGCGCTTC	360
	TGGGGTGCGC	GCGCGCCTGC	CGGCATTACAT	CGCGCGCGCC	TACGGCAGCC	CACCGGGCGA	420
	CGCGAGGCAG	ACCCGCGCGT	GGACGTACCT	CGCGCGCTCG	CGGCTCTTCC	AGCGCCTTTA	480
10	CGCGCGCCCT	TCGTTCGCCG	CGTACATCGA	CCGTCTGCTG	GCCAACGGGC	CGGTGCCAAC	540
	ACTCGCCGCC	TTCTTGCTGC	TCCATGAGGC	CACCGCCATC	GCTCCTCTGG	CGCTGCTGTG	600
	GTGGGGGGTC	TACAGCTGCG	ACGTGGTGGC	GCTGTTGCCG	CAGGGCCTGC	TTGACTACCT	660
	GGCCGAAGCA	CGCATCTGCG	CGTCRAGAGG	TTCTGTGG			

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## 1449UP

	GATCGGCTCA	ATGGGTTGCT	GAAGCCGTGT	CTTTCGTAAG	ATGACCTCAA	CTTAAAGGCA	60
	GGCTCTCGAT	ATCTCGTTTT	TTTTTTTAAAC	AGGTGAGCTT	TGGAAAATTT	TTGGTTCTCA	120
	GCTCATCTCA	TCTACATAG	TATGTCTAGC	ACGCCAGCAA	AGCTTGCGTA	ACCGCTCTAT	180
20	TCAATATGAG	TAAGCAGGTA	AATGATACTA	GCAAGAATGG	TCTTGACCTA	AAGACGCTGT	240
	TTGTCCGGAA	TATTCGGTTT	GATGCTACGG	ATGCAGAGCT	GACAGACTTC	TTCTCGCAGT	300
	TTGCTCTTAT	TAAGCATGCT	GTGATCGTAA	AAGATAATGC	GGGCTCGAGC	AGAGGGTTTG	360
	GGTTTGTGTC	GTTTGCTGTG	GAAAGTGATA	CACAGGCTGC	ATTGGACAAG	GGACGGAAAA	420
	CACAGTTCAA	GGGCCGTCTT	CTGAGGGTGG	ATGTTGCCAA	AAGAAGAGAA	CGTTCGAAAA	480
	AAGGCGATGA	GGCCGAGGCA	CAGACCTCCG	CGGAGGACGC	GGAGAAGCCG	ACTACTGCTC	540
	CCGAGGGTGA	CGAGGCGCTC	ATGCGGGGCA	AGCCCAAGCT	GATCATTAGG	AACATGCCGT	600
25	GGTCTTGCCG	CGACCCGACC	AAGCTGAAAA	AGATCTTCGG	TAAGTTCGGA	GTGGTTGCGG	660
	AGGCTCCATC	CCGCGCAAAG	CGGATGAAAA	GCTGTGTGGG	TTGCATTTGT	CACGA	

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## 1450RP

	GATCAATTCT	GTCTTGAAGT	AGGTATTAAAT	CAATGGGTCA	GGCTGGGTGG	AATTGCTTAC	60
	AAAAATACCA	ACCCAATCAT	CTTGTAAGTT	GGTGAGCGAT	ACGTAGACAA	TTTGCCTCAC	120
	ATCAATCTTA	TAATCGACAG	CATAGGTGAG	TTGATTATTA	ACCAGTGTCT	TTCCGATAAT	180
	GTAGAAATGG	GATGGCGTAA	GTATAAAGGT	TTTGGGTAGC	CTTTGGGCCG	ACCTACCAAA	240
	TTTTGAATGT	AGCGCTTGCC	CATTGATAGA	GAATACGACA	TGATCATTA	TTCCAGCTTT	300
35	CCTTTTGACA	AACGCACCCT	TCGATTTCAG	CTCATTACAA	GAAAGGTAGT	CTCCCAGGAA	360
	TGCCCTGTAA	CCTAACAAAG	ACATTGCACG	CCTCTCCTTT	CTGCCACCCA	ACAACTTGTT	420
	ACCGTAATCC	CGGAGTTGTT	CGAATTGGTT	CCCATGTTTC	ATCTCACGGA	TAGCACGCTG	480
	GATACGAATC	GCAGAATCGA	TACGCCGTTG	TAAAAACCGC	CGCCAGGCTC	TCTGAATGCG	540
	AGATGCCATA	TTATGCCAAT	ACTTATCCCT	CATGTTTTTC	AAAGCAAACA	AGGTCTCAGG	600
	TGTTTTAATA	AATACCTTCG	TTACACCCAA	CTGATATTCA	GTACAGGAA	TTGAAGTATC	660
40	TCTCAAAATT	AAATTGACAG	CATCTAAGGT	ATTACCTTGC	CATGT		

## 1450UP

	GATCGCAAGT	TGGAAGAGCG	AGTATCCATA	TGATTACTCG	CGCGAGACGC	CCGGCTCGCG	60
45	CATCAAGCCT	CAGACAGTTA	TCACTCGGCT	CTCCGAAATC	GCAAACGCCA	CCGAAAGGA	120
	GGTCATCGTG	ACGACCGGTG	TAGGTCAGCA	CCAAATGTGG	GCCGCCAGC	ATTGGACGTG	180
	GAAGAAACCA	CGCACATTTA	TCACATCAGG	CGGCCTCGGT	ACCATGGGCT	TTGGTCTACC	240
	GGCGCCATT	GGTGCCCAGG	TAGCCAAACC	CGATGCGATT	GTCAATCGACA	TCGATGGCGA	300
	CGCCTCGCTC	AACATGACCT	TGATGGAGAT	GTCCAGCGCG	GTGCAGGCGG	GCGCCCCAGT	360
	AAAGATATTG	TTGTTGAACA	ACGAAGAGCA	GGGAATGGTC	ACTCAATGGC	AGTCTCTATT	420
50	CTACGAGCAT	CGTTATTCTC	ACACCCATCA	GCTAAATCCG	GACTTCGTCA	AGTTGGCTGA	480
	TGCAATGGGG	TTCAAAGCAA	TGCGCCTAGA	GGCGCAGTCG	GACATGGAGC	CCATGCTGCA	540
	GGAGTTTATT	AATTGCAAGG	AGCCCCGTGT	ACTCGAAGTG	GCCGTCGAGA	AGAAGGTTCC	600
	CGTCTCTCCG	ATGGTCCCTG	CCGGTAAGGC	CTGCATGAGT	TTATCTACTT	CGACCCAGAG	660
	GTACGCGACA	GCAAGCGGAG	CTTCGCAGCA	GGCGTACGG			

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## 1452RP

5	GATCAAATGT	GGCTCTACAA	GGGCGGAAGT	GGCAGAGAAT	ATTAATGAAT	CAGTTCCGCT	60
	GACATATTTG	TATTGTACAG	GTATTCCACA	TTCTTTTGAG	TACGTATGTC	CGTCTAGGAA	120
	TGGCTGGCTT	AGTAAGGCTT	AATATTAACT	GAAAAGCGCA	GCAGTGTAAAT	CCATCTAGTA	180
	ACTAACACAT	ATCCATTAGC	ACATGTTTCG	TTCACTACTA	CGTCATTCCT	ACGCCGTCCC	240
	TACTGTGAAT	TACACATGGT	CCTCGAGAAG	CCTCATAAGA	TTCTTCACTA	GCGATGAGAA	300
	GGCAGCTCCT	CCATCGCTTC	CGAGAGAAGA	GCAGAAAAGAG	TTCGAACGGC	TTTCAGAAGAT	360
	TGCACAGTCA	CAAGCTGCCA	TCGACGAGTA	CAACAGACAG	TTTCGAGAATG	ACCATACGAA	420
10	GGAGTCAGCG	AACTCTCCCA	TCCTCAAGAC	AGAAATAGGC	TCGTTCCTCAC	CGGAATTCAG	480
	CAAGACGTTG	CCAGAGTTTCG	AGGGCGACAA	GAATCCCGAG	ACAGGGGAGA	TTGGCGGGCC	540
	GCGCCAAGAC	CCACTGCGGT	ACGGGGACTA	CTCATACAAC	GGCCGCGTGA	CGGACTTCTG	600
	AGGTATAACT	TGTGTTTATA	TGTTTGCAGG	TTGGTTAAAT	ACATAGCTTG	CGCTCCAAC	660
	CTCTCGCAGC	TGCAGACAGG	TTGTCGGTGC	ACTCCGTGAT	GAATTTTCGAG	TCCAGCTTT	

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## 1452UP

	GATCACCAAC	TCTACAGCAA	GAAATCCTAC	CCCCAGCAAA	AGCTGTCCTC	GATGTTCTTC	60
	TATTCTGTAA	ACAGTTTGTT	ACTTCTGGTC	GCTTGATATCT	GCATGCGCTA	TCATCTTTTC	120
20	ATCTGGAGCG	TTTTTCAGCCC	GAAGTTGTGC	TACCTTCTGG	GCTGGAACAT	CCTCATCCAC	180
	TTTCTCACTG	AGACGGTGCT	TGAACCTTTC	TTGCTCATGG	TGGCGGGCTG	ACTGTCTCTA	240
	GTTCCACTTG	TATAATATTC	CTTCATCAGT	GAGAATCTCA	TAGTATTGTC	ATATATTAGA	300
	TATTATCTAG	GTCATGTTTT	AGAGAATAGG	TCTCTTCCGA	AAAAATTGGC	TACCACTGCC	360
	AATCATTACA	TGTCAGAACC	GACCATCTCC	AAGTGTCGAA	CCGTCCCCAC	TGCAAAATGCT	420
	CTCACTTAGA	TCCAGCTTCA	GACGCTTATT	TTCTGTTTCC	TGCAGGGTTT	ATGACCAGCA	480
	GGCGCAGAAG	GCCGTGTCTT	CCTGCCCCGC	TGGCACACCG	CTGAATCTGC	TTATAAAGAA	540
25	GGGCGGGAAG	GAGCCGTTGG	CTCTCGAAGA	TCCGACTACC	CGAGTGOTTA	TGGAAGGTGC	600
	TTGACCTGAG	GCGCAAGCCG	CAAAGCTGGC	AGAGGACCCA	TTAAAGCGCG	GAAGAAGGCT	660
	CTGCGGCGGA	TGAACAGAGA	ACACATCCAG	CAGCAGAACT	TCCTGGCGAA	GATGTGAA	

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## 1453RP

5 GATCTTAATT TAAAATTTTA ATTAAC TATT TATAATTTAG AAATATATAA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180  
 ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300  
 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
 TTTTATAATA TTTATTTTTA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480  
 10 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540  
 TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTATTAT TATTTAAATT 600  
 ATTATTAATT AGTAAATTAT ATTTATTTAT TTTATTAACA TAATTTTTTG ATAATAATAT 660  
 ATCATAATTA AATGGTAATT TATTAATAAT TATCTTTAAT GAATTTAATG ATAAACCATT 720  
 ATTA

## 1453UP

15 GATCAAAATT TCAACAATTT CCATTTTCAAT TAGTACTACC ATCACCATGG ACCAATTGTT 60  
 ACATCATTTA GTTTATTAGG TTTACTATTA ACTTTAGCTT TTACTATACA TGGTATTATT 120  
 GGTAAATATT ATCCTTTATT ATTATCTTTA TTAGTAGTTT TATTACTAAT AACTTTATGA 180  
 20 TTAGAGATA TTCTAGCTGA ACTTACTTAT TTAGGTGATC ATACTTTAGC TGTAAGAAAA 240  
 GGTATTAACT TAGGTTTCCT ATTATTTGTT GTATCTGAAG TATTAAATTT TGCTTCTTTA 300  
 TTTTGAGCTT ACTTCCATTC AGCTATAAGT CCTGATATTC TATTAGGTAA TGTTTGACCA 360  
 CCAGTAGGTA TTGAAGCAGT TCAACCAACA GAATTACCAT TATTAAATAC TATTATTTTA 420  
 TTAGCATCAG GTCTAAGTAT TACATATAGT CATCATGGTT TAATTGAAGG TAATAGAAAA 480  
 CATGCTTTAT CAGGTTTACT TATTACTTTC TGATTAATTG TTACATTTGT ATTATGTCAA 540  
 25 TATATTGAAT ATAGTAATAC ATCATTTACA ATTACAGATG GTATTTATGG TTCAGTATTT 600  
 TTTGCTGGTA CTGGTTTACA TTTCTTACAT ATGGTTATGT TACTAATTAT GTTAGGTATT 660  
 AATTATTGAA GAATAAGAAA TTATCATTTA ACATCAACAC TCATGTAGGA TATGAGACTA 720  
 CTACTATTTA TT

## 1454RP

30 GATCATGCCT CACCGGCGTG GAACATGCAG GTGAGGCGTA TGTACCCCAT GTTGCCTTAT 60  
 TTTTTCACCT GAAGCGGATT GGCTCTTGTT TATACAGACT TTTCTGCATC CCTTGGGGCC 120  
 CAGAGCTAGG GCCTAGAATC CGTGTCGTAA CGGTTGGGCA CTGATTCAAC ACGAGCAAA 180  
 TTCCAGTGCT GCTCGTAGAA ACGAGGCCCC TGAAGTATAT GGTGATATCC ACATTGCCGG 240  
 35 AGTATAGTTC TCTGTGGGGG CGACTTCATG CCATGTGCAT CTCCGGCTTA CTCCACAGCC 300  
 GCACACGCTG CATTTGTTTTG GGAACATCAT GTGAAATACT GGTATAGAGC GCATTTTATA 360  
 GGGGTGCCAG CAGCTGTAAT AGGGCGGCAT ACCCGCTCT ATTTTATGTG TTCATGTGCT 420  
 AGTTTAGAGG TATTTTTGAG GTGCATGGGT TATGGCTTAC TTTGCATATG GAGATCTCAT 480  
 TCGCTCGTAA CGTATATAAC TGAGGTAGCC GTAAACTTGC ACTGGTTCCC ATTGCCAGAG 540  
 CGAAGCTACA ATAGCACCAT CTGGCTGCAA GTTGTGAACA ATGCATTGGA ATCGCATACT 600  
 40 CTTTGGGGG CTGTGCGCTT TGCTGCAACA ATTAACAAAT GCCTTTGATG AAGGAGTGCT 660  
 AAGGAAATGT TATGAATCTG GTGTATGCCA CCGGAACAGG CATTACGGAG AGAA

## 1454UP

45 GATCAAGCGC TGTATGGTTC CCGGAGCGCC AGTAACAGCG GTCCTGTACG ATTTCAACGA 60  
 TTCCAACATG GACGATGATG GCTCCAAAGT TATGTTCCCG ACCACGCTTG AACTCAAAAA 120  
 GGTTTTTTTC GCTATTCGTT TTGAGGCCAT CAAACGGGGG CTGCAAGTGT TTCCCATTAG 180  
 GAATATTGCT CCTATCTTCC GACAGGTCGG ATTCAAGAAC GTAAAAATATA CCGTTCTGAC 240  
 ATTCAGCGC GGCATTTTCG TGAATGAAAT GGGGTTTCGTG AACGAGCTAC TTGCAACGTT 300  
 TCACTACGAT TTTCTAGTGC GAACCTTTTT AACTGATCGT AGTAAGTATC CAGTTGGAAC 360  
 50 TGACCCACAG ACACCTGCCA GGAGGTACAT TGATGAGCAC ATGGGCCAAA TAGATGACAA 420  
 TGCAGGATGC TTGCGTCTTA TTGCAATCAC GCGCGAAAAA CCAGAGTAGG TTTCCACCGT 480  
 TGCTATTGCT ACCCGGGGCA ATTCTCCCGG TCATTATATA TGTTAGCAGG TGTCAATACC 540  
 TCCTTACAAC CTAATATTTT AAAACCTAAT ATCTTCTGCT CCTTAGAAAG AGCCACTTCC 600  
 TTTATATCTTA ATATGTAACC CTAGTTCTAT CTAATAATTT TATAATTTTG ATAAATCTTG 660

55 ACGTACATCT TATCACTAAG GAAGATCTCA TCACAACTC CGCAAAGTGT TTCATATATA 720

## 1455RP

5	GATCTCTTCG	ACATAGTGTC	TTAATAGGCC	TGCTGAGGAC	TTCAC TGAGA	AAGCTTCAAT	60
	AGCGGGCAAT	GGCCCATCTC	ATCAACACTT	AAAATTTTTT	GTGGCAAAAG	AAACAACACT	120
	GGAATCACGT	GACCACACAA	AACTCACGAT	T TACTGTTGA	AGGGGAGCAG	GCTACGACGA	180
	CTCTTCTTCG	CATGGTAACT	CGCTGCTGTC	CACTTGCCGC	TTGCGAGCCT	TCTTTGCTGA	240
	CGCTCGCTCT	T TCTCTCTT	CTAACAGCCT	CTCCCGTTA	GCTGTGATGT	AGTGGATGAA	300
	GAAGTCGCCA	TCCTTGCTGC	GTTTCGCATC	ACGCAGGAGC	GTCTCGACAT	CGTCGTATAT	360
	ATCAATGCGT	CGCTTTCGCA	GTTGGTTTAG	CAGCTTGTTA	TCACGCCCTG	CACATTGCAA	420
10	CTTCGCGATG	GCTTTGGTCG	ACTTGAACGA	CACCTCGCCC	GGTTTCATAT	ATCCAGATTT	480
	GCGCAGGTTG	TGCCAGGGCG	TGCTCACAAT	GCTACATTGT	GCCTGCTTGT	TCCCTTGATC	540
	AGACTCTGAC	TTGCACAAC	GCAGGCAGGC	ATGCAGCACA	TCCCGCGGCA	CGTCGCTGGA	600
	GCTCTGCTGC	TTTGATGTA	ACTTGAGATA	GACATGTGCG	CTGGCATACT	TGCTACGTT	660
	GGAACCAGAA	G TAGTTTAAT	CCCGGTACCC	GTGCTTGAAC	AAAAGGTCGT	TC	

## 1455UP

	GATCCCATCA	CATGAAATGT	CTAGAACTCC	CTGCATGACG	CGAATGAGGC	CAAGAATGTC	60
	TGGTGGGCTT	GGCTAACCGA	TGTTTCGCAAC	TGCAACAAGG	GGTACCTGGT	GTTTATAGCC	120
20	GTATGTCGTC	ATCCGGGATT	CGTGCAACAG	GAGAGAAGAA	CGGGACCACA	AGGAAACGCG	180
	GTAAGCATC	TAGAATCAGC	AACCTAGAG	AACGTTTGT	CGTCGTTGGC	GCAAGAGCAC	240
	GGAGCGTAGG	GGCTGGGAGT	TGCGGTGGCT	ATTTCATGCGT	GGGCACGCCG	GGTATATAAG	300
	TAGGGTATGC	TCCGTTGAA	CAGAATGGAT	CCGTCTCAGA	ACAATACCAA	AATCGCATTT	360
	GGAAAAACAA	CCACTAATAT	GAAGTACACC	TCCGCTATT	TACTCGCTCA	AGTCGCTTTT	420
	GTTGCAGCAC	AGTCATCCTC	GGGGTCTGTT	ACCGGCAGCG	CTGCCCCCGC	TCCGGGTGCG	480
	GGGTCCGGCG	CAAGCATTT	TAGCACCACG	ACAGTCACCG	CCTCAGGTT	TGGACCAGGC	540
25	GCGACGTCCG	GTGCTAGCTC	CGGTGCAGCA	GGCGGGGCG	CTGGCGGGG	CGCAGGTGGC	600
	GCCGCATGTG	GCGCCGAGG	TGGCGCCGCC	GGTTCTAACT	CCGGCAACTC	TGGCTCCAAT	660
	GGATCTGGCT	CCCGGCCAGA	ACACTCTGGA	ACAGAACACT	CCGGCCAGCA	ACACTCTGGA	720

## 1456RP

	GATCCACGCC	GCGCTGCTGA	CCAACGTCGT	CATCATCGGC	GGGACCTCCC	TGCTCCAGGG	60
	CCTGGAGCAG	CGCTCGTGA	ACGACCTCAG	CCTGCAGTTC	CCGCAGTACA	AGCTCTCTAC	120
35	CTACGCCACG	CCCGCCACG	TCGACCGCCA	GCTGCAGAGC	TGGCAGGGCG	GCGTCAACAT	180
	GTGCCACCTC	CCGACTGGA	AGCTCGGCTC	CTGGGTCAAC	AAGCAGGAGT	ACCTGGAGTC	240
	CCTCGACAAG	TAGCTGTGTA	GTATGTAACC	GTATGCCGCG	ACCCTGCGGT	TTCTTTCCCG	300
	CTCCCCCACC	CCCATGACGC	CCCCCGCCCG	CTTCGCGCGC	TCCCACGCGC	TGGCGCCCGC	360
	CGCGCCCGCC	CGCGACACCG	TCGAGCTCTA	CCTGGACTAC	TGCTGCCCTT	TCTCGCGCCG	420
	CCTCTTCTCT	GCCTGGCAGC	ACGCCCTTTT	CCCCCGCGCG	CGCGCCGACT	CGCGCTTCCA	480
	GATCGTCTTC	AACCACGTGA	TCCAGCCCTG	GCACCCCGCC	TCCCAGTACA	TGCACGAGGC	540
40	CGCCCTCGCC	GTGCGCCGCC	TCGACCCCGC	CGCCTTCTCT	CCCTTCTCTG	GCGAGCTCTT	600
	CCTCCACACG	GACCGCTGGT	TCGACACGCG	CACCGCCGAC	AAGTCGCGCC	ACGCCGTGTA	660
	CCGCAAGCTC	CGGACTTCGC	GCGCGACGCC	GCCGGC			

## 1456UP

45	GATCTGGAAT	ATTACCGGCA	CAAACCTGGC	GCTGTGCTTC	CACACCAGCC	TCCGGTACCG	60
	CTTCACGGCC	ACCAGCTCCT	GCAGCAAGCG	AATGCACACG	TATGCCAGCT	CCATGCGCTC	120
	CAGATTAGTC	AGAACC CGCA	GGTAGTTGGG	GTTTCGACACC	AGCGCCTCCA	CCAGCTCCTC	180
	GCTCTGACGC	CCCTCCTGGA	TCAGCAGCGA	GACAACTGTT	AAGCACGACA	GCAGCACGAA	240
	CTGGTCGTCC	CCCGCGCTGT	CGCTCAGTGT	GCACTCGTAC	AGCTTGCGCA	CAAGCTCCGG	300
50	GCCCTCTCTG	AAGTACCGCA	GCACCTCGTG	CACGTACTTG	TCGCTCGTGA	ACAGCTCCGA	360
	CAGCAGGTTT	AGCACCGCCC	GCTTCGCATC	CAGGTTGTTT	GACGTTCGCCA	GCAGGTGCAC	420
	CAGCGCTGCG	ACGCTCTGTT	CCAGCGGCAG	ATCCAGCGCG	CCGCGCGCGG	CGTGTTCCTA	480
	CAACGTCGAC	TCGAGCTTCT	TGGCAATCCC	CGCGTCAAAC	TCGCTCAGCT	CGGGCGAACG	540
	CACCAGCGCG	TCCCACGCCA	CATGCCTCGA	GCTGATCGTA	TTGCGGATAT	CGTTGAAGTG	600
	CGTGCTATCA	AGCAGAACTT	TTTGAACCCC	CTGAGCCACG	GGCATCGTCA	CAGCTAAGAT	660
55	CTACGCTTTC	ACGCGACCGT	ACTGCCCACT	TTGAAACCCG	TGGGACTAGT	CAATATCTGG	720

EP 0 866 129 A2

CGTGGTCTGG CGGACTCCC

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## 1457RP

	GATCAATATC	GGGACGAAAT	CTGTTGTATC	TACTACCGGC	ACGGCGACTG	CGCCCAGCGC	60
	ACCAGGATCT	CAGGCTTCGT	CAGCGAGTCC	GGATTTCGTCA	GCTAAACAAA	AGAAAGATTTC	120
5	ATCTCCACTA	CCTCTTGACT	TACCTCCACC	GAAGGATTTT	AGCAAAGAAA	TCGAGGAGAT	180
	TATAGAACAC	GATTTGACTA	AATTGGCCTT	TCAGAATCCT	CTTTTTAAAG	ATGAACTTCC	240
	ATATTGGTTA	CAGGCCAAGA	GGCCATTGAT	CCAACCGTAC	AGCACTATGT	CTGAAAGAAT	300
	GTTGAAACAG	CTGGAATCCT	CATTACTTAA	CTGCCCAGAT	TCGCTTGACG	CTGACACACC	360
	ACATCTCTAT	CAACACCCGC	TCCTTTTACC	GCATCCCACC	TCCATTTTCT	TCCCTAGTGA	420
	ACCGATCAGG	TTCGTGGCTG	CTGGCTGGAA	TAACGATAAT	ACGTCCACTA	AAGATATCTA	480
10	TGGAAAAACT	TCTATGGTTC	AGATAATGAC	CAAGTTCGAT	TTGGATACCC	TGTTTTTTTAT	540
	CTTTTATCAT	TATCAGGGAA	CGTACGACCA	ATTCTTAGCT	GCCAGGGGAA	CTAATCATCC	600
	GTGGGTGGAT	ATTTAATAGA	GTCAATCGGT	GCTGGTTTTA	CAAAGAAGTT	GAAAAGCTGC	660
	CCCTTGGAAT	GGATCAAAAA	GAAGAGGT				

## 1457UP

	GATCGAGGAC	TTGAAGCAGT	TCCGGCAGGT	CGGGTCCAAG	ACCCCTGGGC	ACCCCTGAGTA	60
	CGAGCTTCCC	GGCGTGGAGG	TGACCACCGG	CCCTCTAGGC	CAGGGTATCT	CCAACGCCGT	120
	TGGCTTGGCG	ATCGCGCAGG	CGAAGTTGGC	TGCCACTTAC	AACAAGCCGG	GTTACGAGTT	180
20	GTCCGACAA	TATACGTACG	TGTTCTTGGG	CGACGGCTGT	TTACAGGAGG	GTGTGTCTCT	240
	CGAGGCTTCC	TCGCTTGCAG	GCCATGTAAA	GTTGGGCAAT	TTGATTGCGT	TCTATGACGA	300
	CAACAAGATC	ACCATCGATG	GCCACACTGA	GGTGTCTTTC	GACGAGGATG	TCTTGAAGAG	360
	ATACGAAGCA	TACGGGTGGG	AGGTGTTGAA	CGTTGCCAAC	GGTGACGAGA	ACTAGAAGAC	420
	ATTGCCAGTG	CCTTGGAGCA	GGCCAAGAAG	AACAAGGACA	AGCCAACCTT	GATCAAGTTG	480
	ACGACCACTA	TTGGGTTTGG	CTCCTTGAAT	GCGGGCTCCC	ACACTGTGCA	CGGCGCGCCA	540
25	TTGAAGCGGA	TGATGTCAAA	CAGTTGAAGA	CGAAGTTGGG	CTTTAACCBA	GATGAGTCCCT	600
	TCATTGTGCC	TCAGGAGGTT	TATGACCTCT	ACCACAACAG	CACTATCCAG	CCAGGTGCCG	660
	AGTCCGAAAA	GGAGTGGAAC	GCTCTACTCG	AGAAGTATGC	GGGTGAGTAC	C	

## 1458RP

	GATCCGCAGT	AGCTGATTGT	TCGGGTGGCC	AGGCGAATAT	TGCTGGAAGC	GGTTCAGGCG	60
	CGTATATTTG	CTCTGCGGAC	CGCCAAAGTA	CCCGCCGAGG	TTACTCTTGC	TGGTCGTACT	120
	AGAGAAGTTG	CGCACTGCC	TAGCAAGTGC	GGTGTCTAGT	ACGGGATTTA	GCTTCGCCAG	180
	TAAATGGTGT	AAGACGTTGC	GAAATGGCAC	AGACGCCTGT	ACTGGTCGCA	CTTGCAAGTG	240
35	GATAGCGTTG	CTAAGAAAGA	AACACCGCCC	ATACGAGCGC	GTGAACGTAG	ATAAGCTCAT	300
	GGTCAGCAAT	CAACAAGCCT	AATGATGATC	TTCTTTACAA	AATGAGGTTT	TAAAGCGACG	360
	TTAAAAAGGG	ATGCCCAACG	CTATGTTTGA	CACCTATGGA	ATATCCGTAT	GAATGACTGT	420
	GTATCATTTA	CGACGGTACT	TCCTTACAGG	GCAATGGCAG	GATGGTAACG	CCGAGTAATG	480
	TCCAATAATC	ATCATATATA	CTCTAGTTAT	ACGCTATGAG	GGGTCAATTT	ATGTATTGTT	540
	CGTTCGCCTA	TCGGCTATGC	TTCAAATTTC	ATGAGGTTGG	GCAGCTCGCC	ATTCTGTACCT	600
40	GCGGGTGGCA	TGTTCACTTT	CTCTAGTCTC	TTTTGTGGGC	GGTTGTCTTC	GTCTTGGTCC	660
	ATGTCAAGGT	CCAAGAGATC	ACAGAAAA				

## 1458UP

	GATCTGTTGC	ACCTGCTATT	TCAGGCAGAT	TTGTGCTGTC	AGCAGCGCAT	GGCCATACTA	60
45	TCGTCTTTGG	CGCTCGCTGC	GCGCGAGTTG	CGGGGGCTGG	AAGACAAATA	CGTGCTCAAA	120
	CCCGTCTTTG	ATTTCCCCAC	ACGCCGCCTG	CCCAGAAATG	ACGCACCATC	AAGAGCCCTT	180
	GAAAGCCGCG	AATCCGGTAC	AAGCTCCGAG	GGGACCATCT	CTGCACACCA	CACCGTCTGG	240
	CGGTCGCGCA	AACTTGACTC	AGCGCCAGCA	CCAGAACGTC	CGAACGCCTT	TCGGAAGCAT	300
	GCACCTGCGT	TTTTCCTCCC	GCTGGCGCAC	GCGTGGCTGA	ATGGCATCGA	CCTGGGCAC	360
50	TTTGACGCCC	TGTTCAAAAA	GCACTACCTA	AGCACCCCTG	GCCTTATTCT	TGCAGCCGCC	420
	AACCCGCATG	CAGAAATTGA	CCGGATGTCC	GAACCTCATG	GCTACGTTTT	GCAGGACGCT	480
	GAGGCGCAGG	ATATCAGCAT	TGAGTAGCCC	GTCGCGCATG	TGTCAGCGCA	TCTGTGGACA	540
	ACTCCTGCTT	GCAAACTGTA	TCCCGACCAC	TACCATGCAT	TAGTATGAGA	TCTATAGAGC	600
	GCCAAATTGCA	CGCCTAGAGA	GATGTGAACC	TCGCAATGCA	TCTCTTGGGA	GTCTCTGTGG	660
	CCGGCAGTAT	CTGCTAGTAC	ATACTCTTTG	TAACCTCTACA	GAGATGTGAA	GTCTTGTTAC	720
55	CCGG						

## 1459RP

	GATCATGCTG	GGGCATATCT	GAATGCTCTT	GAACAACGGA	CTAGATTAAT	GGAGCCTTGC	60
	ACTCAGAGGC	TTGGGCAGGA	TGCAGCTTAT	GCGGGAGCGG	CTGTTGGAGC	TTTACAATAC	120
5	CAAGCAATAT	GTGGTGCTGC	CCCCAGATGA	GACAGTAAAA	CTGCAGCGAG	AGGTGACGGC	180
	GAGCCTGAAC	TCAGCAGATC	CAGGACTCAA	CGACGTTGAC	CGCATGGCCC	TAATGGAGAT	240
	GAAC TTCAT	TTGTTGGTGT	ACATTGGCGA	AGAAATAGAA	GCAGACGTGC	TCTACCGCAC	300
	ACTTGT TTGA	CGTATAGGTG	AGAACTCGCC	CCGGATGCAC	CTCATGAAGG	CTACGTTACT	360
	GCAGGTTACA	GAAGGTGATC	CCGCTGCCGC	GAAGTACCTG	AAGAACCTGC	TTGAAAAGCA	420
	GCTTGAATAC	GATACAGATT	CCGTGGATTA	CCTGCAGGTG	GGCAAGAAGC	TAATTGCGCT	480
10	GGAACGGCCC	GCGTTGTCCA	CCGAGCTGTG	GATGAAAAAG	CTGCTGTCGC	CTGCTAGAGA	540
	AGTTTCCACT	GGACGCCGAA	CTATGGTGG				

## 1459UP

15	GATCACGTGC	CTGCGACATG	GCGACTTCAT	CCACTGGCGC	CCAGCTACGT	GGTATATGAC	60
	ATTATGGCCG	AGAGGTTAAG	GCGTGAGACT	CGAACTAAAT	TGAGGGATCT	CTTGGGCTCT	120
	GCCCGCGCAG	GTTTCGAATCC	TGCTGATGTC	GTTATTTTTT	GCTTGCGCGG	CCTACGGGGG	180
	GCTGTATTTT	GCTTGT TGCT	ATTTAGATAA	ACGAGATAGC	TAAACTATGG	GTAGAACTCG	240
	CGGTACTTCC	CGTAGTAGTA	GGCTGTGCCG	AAGCCGCCGA	GGGCGGTGAG	CACCAGCGGG	300
	ACGGGTTTGG	CGAAACGCGA	TGGCACGCCT	CTGATGAGGC	CGGTCAACAG	CATCACGGAG	360
20	CTCGCGCCAA	GGGCGAGCTC	GAGGCCGCCC	TCTGCGTTCT	TCCGGAGCAA	GTACCCTGCT	420
	ACAGCGTAGG	TGCTACCAAA	AACGAGACCT	GCAGCCAGCG	AGGGCACAGA	CCCTTTACGC	480
	CAGTAGCCCA	TCGAGCCACC	GATGACGGTG	AGCGCGGCCA	GAGTGAAAGA	GGGATGTTCC	540
	CTTGCGGTGG	TGGTGGGTGG	TGCTGTGGGG	AA			

## 1460RP

	GATCCGGGTG	GAGACACGAA	AGTAGACAGA	CACGGACGGC	TGTTGGGTGG	AAGGAACTAC	60
	CTCGTG GATA	CATTCCAGCT	GCCCCAAAAG	ACACATAATT	TCTATGTGCT	TGTCGACGAG	120
	CTGATAGAGA	TTTTGCATTT	CGAGGGGAGC	GGCTCTGACT	TTTTGCACCT	GCATAATCAG	180
30	CTGTACCCGC	TGGAGCTCAA	AGACAACGAG	CGGGCCTTGC	TTGCAGACGC	TGGGTTGATC	240
	AAAGGCGAGC	TGCGCTCCCC	ATACTACGTT	ACTGCACCTC	CTTCATACAT	CATTTTGGGT	300
	GCTGCTATTG	TGGCGAGCGG	CTGTAGGATA	ATAGATGACT	ACTGGGAGCA	GCCCTTAAAG	360
	GAGCAGGGAT	TCACCATGCA	CCACCGTGTA	TTCTCTCTGA	ACGGCACGCA	ACTTTTCATTG	420
	CTACGCCTGC	TGAAACCCCC	GCGTCCAGAA	TCGCATCAGC	AGGGTGAGAA	GCTGGATACC	480
	AACTGGCTAC	AGAAGTG GGA	GGATCCATAC	CCAACGATCC	AGGAACAACC	AAATGCTGAA	540
35	GCACGGCGGG	AATACGCTAG	AGAACACGCC	AGAGGTGAGC	ACATAACGAT	GATTGTTCCA	600
	GGTCAAAGTA	TTAGCGGCAG	TATAGAACTG	AGCCTAAATT	ATAAACTTCC	TAAGTACCAC	660
	TACAAAAACT	CATTTGCTAA	TGGGT TGA				

## 1460UP

40	GATCCAACAA	TTCCCGCAGC	GCCGCTCCAG	CCGTGCTCTC	CGTCGCATCA	AATGAGTCCA	60
	CGCTGTCTC	AATCCCGCAC	AGCTGCCGTC	CATGCGCCAC	CTCGAACTGC	ATCCGCGACG	120
	CAAACAGCTG	GATAAACAGC	CCGTTCTGCT	CGCACCCCCG	CCGCAGCTGT	CCAAAGAGCG	180
	CCTCCGCACC	AGCTGCTATA	TCATCGCCCC	AGAAACTCTC	TACGAATGCC	CCCATCGCCG	240
	TGTACCTCGT	CGTAGTTGTG	CATGTCGCTG	CCTCTTCCGG	CTGAATTTTG	ACAGTCTGGC	300
45	CCCCCACC	AGCTCCG GAA	CGCTACGTAA	TACAACACAC	AACCAAATGC	CCTACCCGAA	360
	GGTCGCAATC	GTCTTCTGCA	CCGGCTGCCG	CTGGGGCTTG	CGCGCAAGCT	GGTATGCTCA	420
	AGAGTTGCTA	CAGACTTTTCG	GCGACTCCCT	AGCCGAGATT	GCCCTCGTAC	CGGGTCCGTC	480
	CGGTCAATTC	CAAGTCTCTCT	GTTACGCAAG	CCAAGAACAA	GAGGCCACGG	GACAGCGGCA	540
	ACACCATCTG	GGATCGGCGC	CGCGACAATG	GTTTTCCTGA	TAGTAAATAT	CTGAAGCAGG	600
50	CTGTCAAGCC	ACTCTTTTTCG	CAGACAGCGG	AACCGCCTGG	GCGCCACAT		

## 1461RP

	GATCAAACCA	CCACGGCACA	TCATCATAGT	TGATTAAATC	AATTAGGTAA	GGCAACCATA	60
	GTTGCAGACT	TTGTTTCTGT	ACCATTTTCT	TGGGATTAAA	GAAGTAGGGA	GTCACGAGGA	120
5	AATGCACCGC	ACATGCTTTG	AGATTGGTGT	TTTGGGATTT	TAGAAGGCCA	GTAACGAAGA	180
	CGGTGAACGA	GCTGTCCAGC	CATAGATTAT	TTTAACTGG	ATGAACCTTG	TAGCACTCGA	240
	TGTATAGGAC	AATCGCCAAC	CAGAGCAATG	TCCTCGTGCA	CGGGTTCCTG	ATGACAAGCG	300
	CACGCGGGGT	GCTCGTGAAT	GGTAGGAGTT	GGTTGCTTCC	TATCCCACGG	TTGCTAAATG	360
	CCATGTACTC	TTGGTCCCTG	GGGTTCCGGC	CGACGCTGAC	CTTTAAAAATG	TATTTGAGGT	420
	CCAACCTGGT	ACCATAGCGG	TCCACTAGTG	ATAGCATGAG	TGCCCTCTAAC	GGCAGAAGAA	480
10	GCCCTTGCGG	AAGCGAAACC	ACCTCCCAGC	ATTTGAGCAC	CGCAGACATT	AACTCCAAAA	540
	GCGTGTGGC	CCAGGAGATC	TCCTGCTCGG	AGTCATCTGC	TTCTCATTTCA	TCCCCGAGGA	600
	AGTGTATCAA	AAGCCCCGGC	AAACCCACGG	GCACAGCCCC	CCGCACATCC	GCGTCCCCAT	660
	TACAGTAGTC	TATCCCACAG	TTGTTCAA				

## 1461UP

	GATCGCGCAG	TTTAAACTTA	AAGTTGATAG	AGTTCCCGTC	GTGCTCTCTG	GATACAATAG	60
	AGGCCACCGA	GTCGACGTGG	CCCTGCACGT	AGTGCCCGCC	GTAGCGCCTG	TCGTCCGAGA	120
	TGGCCCTTTC	TAGGTTGATC	TTGGAGCCAG	CTTTCCAGCT	GCTGACTTCC	GTCCGATAAA	180
20	CTGTTTCTGG	TGCGATCCCG	ACCTTGAAGC	TATCGGCCGT	GAACCTCCGT	ACCGTCAGGC	240
	AGATAACATT	GCATGCAATT	GAGTCACCGA	TGTGGCAATC	CGCCAGTATC	GGAGCCGCAAT	300
	CCTTGATAAG	GACTGACACA	CCGTTGCCGC	CTGCCTCGCT	GGCATCGTTC	TCCAAGTACT	360
	CAGCAACAGT	GCCAATGTGT	TCCACTATAC	CGGTAAACAT	CCTATCAACT	TCTATGGGCG	420
	ATATAGGCTT	CGGTATGCCA	TCTATGCATC	TTCTTTTCTG	CTACCGCGAG	CTTTTTAAAC	480
	TCGTAAGACA	AATTACTTAT	AATGGCGGTT	CGCCATGTAG	CTGACTAATA	AAACTAGAAG	540
25	ATACGACTAA	CTATCTGATT	ATACTTTAGG	ACTATCTCTC	CTTGCGCTGG	TCACAGAAAC	600
	ATCGTTGAGC	AAGTCGCGTC	TATCGGGAAA	ATCACTTGGT	TCCTTTGTCT	TAGAGCTAAC	660
	TGCCTGAGAA	GCTGGAAGC	GCTCTTTTAA	AGTCTACTTC	GAATGGTGGT	GTACGTCTGG	720
	GTGCTGGC						

## 1462RP

	GATCTTAATT	TAAAATTTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATAAA	240
35	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCCTTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAACATT	TTTTATTATT	ATTTAAATTA	600
40	TTATTAATTA	GTAAATTATA	TTTATTTATT	TTATTAACAT	AATTTTTTGG	ATAATAATAT	660
	ATCATTATTA	AATGGTAATT	TATTAATAAT	TATCTTAATG	A		

## 1462UP

45	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTAAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCAATTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
50	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACATAAT	AAAAATAATT	420
	AATTAAATAA	ATAAATAATT	AATTAAATTT	AAAAATGTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCTTT	ATTATTATCT	TTATTAGTAG	TTTTTACTAT	660
55	AATAACTTTA	TGATTTAGAG	ATATGGTAGC	TGAACCTTACT	TATTTAGGTG	ATCATACTTT	720

AGCTGTAA

## 1463RP

	GATCCCTGAG	TCTGCTACCA	AGGAGGTCGA	GGAGGAGGAC	ATCGATATCG	AGCAATTGAA	60
	GCAGGAGATG	AAAGGCAACA	AGGAGGCCTC	TGCTTTGTAA	GCTTGCTGTT	TGCCGCTTGT	120
5	GCTAGCCAAT	CGTTGCTGAG	ACTATCTAAC	TTGTATACAT	GCCGCTATCG	CGGCACGCGA	180
	AGCGAACACT	ATAATGTATA	TGTCAAGTTA	AATACATCAT	ATATTATCTT	GTGCCTCAAG	240
	GGTCTTAAAG	ATGTCATAGG	ACAGTCGCGT	GCTCAGACAC	ACGAATATAA	TCATAATAAT	300
	AAATATATGG	CGGTCAGCTT	CATGACCACG	TCAAGCCTTG	ATACCAGAAG	ACACTTCTAG	360
	GAATTTCTCA	ACGGGAGAGA	AAACACTAGG	GTGTAGGTCG	TCATTTCGTC	AGGACATCTG	420
	CTCCTCGGTC	CACAAGTTGG	CCTCTGGTAC	ATAGTCTGGT	TCACCGACAC	CCAATAAGCC	480
10	ACCGTGCGCA	GCCCAATCGC	TGACACGTGG	AAGCTGTAGT	GTCTTCCAGA	CGTCATCCAT	540
	GGCGTCCAAT	AGGACATCCG	ACAGGTCGTT	CGTGTGGCCT	GGAGTAGGAA	TGATACGGAG	600
	TCTCTCGGTC	CCGCGTGGAA	CGGTAGGAGT	TGAAGGGCCT	GTACGTAGAT	GCGATGCTCT	660
	CCATCAAAT	GTCCGAAGCA	CGCTTGGC				

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## 1463UP

	GATCAAACAG	TAGAAGTATT	AGAGCTGCTT	GCAAAGGGCG	TCATAAACAA	GAGAGCTGTA	60
	ATGTCGACAA	ATTAAACAGA	AAAATATCAT	TATTAGTGGA	TAAATAACCA	ACTTGCACTG	120
	AGAGTATAGT	TCTACATGTT	TATTCCGTAA	CAGAATTTCT	ATCCAAATAG	TTTAATTCCG	180
20	TTTTACTTAT	TACCGGAGTA	GCAGTGCAAG	AACCTTGAT	CCCAAAATGC	TAGAGGGACA	240
	TGCAGATGTA	CTAGTAAAGCA	ACGTCTGTTT	CTTTGGATTT	AGCAGCGTCA	GGCGAACAAA	300
	AAAAATAGAA	AGTCAACAGG	GATTGGGAAG	TTATGAGAGT	TGATATGTTT	GTCCATTAGT	360
	AAGTCATTCA	GTTGATATGA	GGTGCTTAAA	TGTTTGTAA	AAGCAAGAAC	GAAGAGAGAT	420
	ACAAAATGTG	CAGTTGTGAA	TCGTGAAATT	GACACCAGAG	GACGTCACCT	CCCGTTGCCA	480
	CTGTTTGCCA	ATTGCTTCTC	GAGCTGCTCA	ACCTTGCGCT	GTAAATCTCT	ATTGACTTTC	540
25	TTTAGTAGTT	CCAATTCAAT	ATGCGTTTCC	TTTCGATCTT	CATAGCTGAG	CAGTTTCGCC	600
	ATCTCCTGGT	TCTCTTTTGT	CAACATTTCC	AGTCGGACAA	TCATCTTGTG	AGCGAGGGCT	660
	TCTTCGTCAT	AACGGCCGAA	TCGGGTAACG	GAATTAGAGG	GATT		

## 1464RP

	GATCGAAATA	ACTTCCGCTG	AAAACGCAGC	AGAGGCAGCC	AATGGTCAAA	TGGAGCGAGA	60
	ATATCCACGA	TATTTCTAGG	GTACTGTTGC	TTGCCAGTTG	GTGCTCGGAA	ACATAACCCT	120
	CAATGGCGCC	CAGTGTGTTG	TACATACCCC	ACACCGGAAA	CAGACCCATG	AATGACCCGA	180
	AAACCACCAG	CCACGCGCGT	AAGCCGCCAT	CCGGGTATTC	GTTGGAGTTA	TCGAGATATG	240
	CGCGTTCTTC	TTCTCTTACC	TTTTCGTCCG	TGAGAGGGAC	AGTCTGCTGA	GCGCACGTGG	300
35	TCGTGGGGCC	ATCGCCAAAA	AGCTCTTTGT	CGCCACAGC	TGTGGCTCTG	CCGCTGTGAG	360
	GACGCTAGG	GCTACGGGCT	CATCGCCATG	CCGTACTTGA	ACGCTGTCTT	420	
	TGTCGATGAC	CACCATCGTT	CCTAGCACGT	ATGGGAGATG	CTCCGAACCG	CGTCAGCGCC	480
	ACCACAGACC	ATCTATCTAC	TTAAATACCT	AATTATCTGG	TGTCCAGCTA	AAAATCCGAG	540
	TATCAGTCAT	CCTGTGGCGG	CCTTATCACC	CATTAGGGTC	CGCTTTGCGG	TAGTGCATTA	600
40	CCGTCGGCGG	GATTCATCCT	CCAAAATGTC	TCAAGCGATG	CCTTGATTCC	GAGTGTACAA	660
	GGGCCAGATT	CCAACGGGCC	AGGAGGCAAC	TAATAGAGG			

## 1464UP

	GATCTTGCGC	TTTTTCTTCA	GACCGCGGTG	GGTGTAGTAT	TGTTCTCCT	TAATGTTGGA	60
	GTTGAGGCGG	GACGAAGAGG	GCGCAGAGGG	GTCTGGCGAG	GCACCGGTGG	AAAGGGGCCT	120
	GTCGGCGCGT	TGCAGGGGCA	GCGCGCGGTG	GTCGTGGTCG	TAGTCGTGAT	GTTGGGGCGC	180
	GGGCGGCGCC	GACTGTGCGT	CCAGCGGGTG	GCCGTGCGAC	GCGAGCGCCG	AGAACTCGGC	240
	GTCGCGGAAC	TCGTACTCCT	TCTGCGGGTC	CTCGCGGCGG	CGCTTGCGCC	GCGGGTCCAC	300
	GGCACGGCGC	GGGACCTTGA	GCCCGTTGGA	GATAATGAAC	TTGTGTTTCA	CCGAGCCCTT	360
	CGGATGCTTC	TTTCCGCCAT	TGCGTTTGGG	CGCCGGCGTC	TGCGCGTCCG	GCACGGGCGC	420
50	GGCCGGGCGG	GCATGCAATT	CGTCTCGTTC	TGGCGAGACT	GGGGGGGGAT	AAACTCGCCC	480
	AGGATCGCGT	CCACGTTAGT	GAGGTCGCGG	TTGCCGTCTT	CTGCGGCTGC	GTGGTGGTGG	540
	TTGGCGCGGT	GAGCCGCGTG	CACCGCGTCC	TCCTCGTGGG	GCTTGGGCTC	CTGCTCGGGC	600
	ATGCCCCGTT	CGGCTGCATG	CCTCCAATCG	ACTTCGACGT	CGTACGATCC	CATCCAACGA	660
	ACCCCGTAAC	TTATCTCGAA	GTATGCCCTG	ATACCTATAC	TGGTCGTTCA		

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## 1465RP

	GATCCACTTC	TTTGGCGACA	AGACATTGCA	GGCGGCAAC	GA CTGGGAAA	TCTACAACGA	60
	CCCGCGCACC	ATCGGCCACA	GCGTCCGCTC	CCCCGAGGAC	ACCGTGAGGA	TCCTCAGAGA	120
5	GCTGTTTCGAC	CTGTAGGCGC	CGCCGCTAGC	TAGTTCTTTG	TAATTGCTCG	ACATTTACAA	180
	TGCATATTCC	TATATACACC	GCGCGCAGCG	CTCAGCTGAG	CAGCCGTACG	TACGCCAGCA	240
	CGAGCGCAAA	CGTACCCGTG	CACACGCCGA	TCAGCCACTG	CATGACCTGC	GTCTTGACCG	300
	AGTCGATTTG	CATCTTCATA	TTACTGACCT	CCTGGTCAAT	TCGCGTGTCA	ATCTCCTTGA	360
	TCTGCAGATT	GTGGTTGCTG	GA CTCTCCC	GGATGCGTCC	CTTTTCCAAC	GAGAGATCCA	420
	GCTTGAACCC	TGCGTTGCGC	TTCTGTGATC	CCTCTCGGAG	CCGGTTCCGC	AGCTGCTCTA	480
10	GGTCGTTTCG	AATCCGCTCC	TGTTGCTTCT	GGATGGAGTG	GATCTCGCTG	CGGTCCGCCG	540
	TCAGCAGTTG	GTCCCGCAGT	TTTGCAAAAT	CCACCCGCTG	CTGGTACGTC	AGCTTCGTAA	600
	GCTTCTCGCG	GGACGCTAGG	TCCTGCGAGA	CATGCGTCAC	GCCCCCGCGC	AGTGCGTCCG	660
	ACATGATATC	CACGATCGCA	TTGCGCTGCT	GGCTTGCTGA	AGT		

## 1465UP

	GATCCCGCAA	TAGCTTGATT	CGATCGTCTG	GTGCGGTACC	TGCTCGACTT	CTCTTGCTCT	60
	TCTCTATGTT	CGTTGCTCAC	GGCCGGAAAA	CCACTACAGC	ACAAAAAATT	CACAAGGTCC	120
	GCCCGCACCAG	CCTTTTAAAT	TAGCGCAATG	GCAGCGAGTC	CTGGTATATA	AGGCAAAAGA	180
20	CGGGAGGCGG	ACAGCTACTA	CAGGCTCATC	GAGGCATGGT	ATGTTGCGCG	ACAGTGCGCG	240
	CAGGGGGCAG	GACTAACCTT	GATGTTGCGT	AGAATGCGTT	GTACAACCAC	GCGGTGAAAC	300
	AGAAAAAGTT	GCTGGAGCAG	GAGCTGAATC	GATTTGAGCT	CGGGGTGGCG	GCGCCGGTGG	360
	GGCTGCAGGG	TTCCATATCG	ACGGCACTGG	TGGGACTGGA	GCGCACAATT	GAGCAGTATC	420
	AGGCGCAGGT	GGCGCAAACG	GGCAGCGGCG	CGGAAGCCGG	CAAGCATGCG	CAGCGCGTGG	480
	GCGAACTGAC	GGAGTGCGCA	ACGAACGCGC	GGCGGCGGTT	CGAGGGGCTG	CGGGCCGCGA	540
25	GCATGCAGCC	GGTGGCGTTC	CAGAGCGGGG	CGGCAGCGCC	GGAGGGCGCC	GTGAACCAGC	600
	CGGCGGCGGG	GGCGCGCAC					

## 1466RP

	GATCTCTTAC	TTTTCTTACT	CACCAATGTC	TTTAACAGAC	ACCCAGAGTC	ACGGCCGGCA	60
	GCCTATCTGC	CGTGCTGGCG	CCATGCCCCG	CCCCTGGTAC	TGGCCCGCTC	GTGCTCGCGG	120
	TAGTCTCACA	GCAACGGAGC	TTGCTCCAAT	TGGGCTGCAT	TCTCCCGACC	ACAGTCTGTT	180
	TGTCACGTGA	CTCTCAGCCG	TCCCGAATGT	ACATTTCTAT	TTATCTACTT	CTTGCCGCCCT	240
	TGCCGCCACC	ACATCCGGTG	CCGGGCAGCA	CACCGACCGC	GCATCGCGGC	CCTCGCGTTC	300
	GTAGAATCG	GCACAGCAGC	TGTACAGTGC	CTCCACTGCC	GCCGCGCAAC	GGCCCTCCTC	360
35	GTACCCCTTG	CGTTTTAGAG	ATGCCTGGAT	CGCACATGCC	TGGGCTTTGC	ATGGGGGCTG	420
	TCCCTCTGCG	CTGCGCCGCC	TATTGTCCAT	GTTTTGTGTT	CTATCTGTTG	GCCGGTACCA	480
	CGTTGTTGTA	CCAGAGTACA	TTGTGCGGGT	GACCCCGTGT	AATGTCACCC	CGTGGGCCAC	540
	AGATGACCCT	GCCACATGCC	TCATTTCTTT	GACCGCACCG	TGCCGCGAGA	CCGCCCACAT	600
	GGGCGGTGCG	CACCTCCGAC	ACACCCACGG	GGCGGCAC TG	CAAGGGTCGC	AGGTGCGGAT	660
40	GAGTCAAAAC	AAACCAGGTG	TGGCGCTGGG	CGGGTGAAAA	TCGACTCATA	GAGAC	

## 1466UP

	GATCTTATTA	ATTTTGTATG	TGCTATATTC	TAAATTCAAG	TAATGATAGC	GCGTGATGCG	60
	GTACGTACCT	ATACATATAA	CGCACAGTTC	ACCATCGTCT	ATGCGTGTAT	GAAAATCACT	120
	CCAGCCGTGC	GACACGCCAC	GTGTAATCTA	GTGAGTTTCA	AGTTCTTCCT	CCTCATCGGC	180
	AGAAAGTTTC	CCCGCGGCGG	TGAGGTTCTT	GAGCCGCTCC	TTGAGCTGCG	CGATAAGGCT	240
	ATTCTCCCTT	TGAGCATGCA	TGCGGATACC	CTCTAGAGAC	ATATGAGCCG	AATCTGCACC	300
	ATCTAAACCA	TGTTGCGTGT	TGCTGCCAGT	GGCAGCTGCC	AGTTTGGGAC	TGGACAGACC	360
	TGTCTGTCCA	TCTTTGTAAG	AATCCTCGGT	CGTTGCCGAG	TTGGAATTCA	TGGTTC CCAT	420
	AGTGTGCAAG	ATTTTCTCCT	CTTCTGTTAG	TTCCAGATGG	GTACCTGTCA	GATTGATCAA	480
50	GGACCTGCCG	CTTTTACGGC	GCGAGAGCTT	GGGCAGAAGA	GAGTGCCCGG	TTGGCGTCCG	540
	TTCACCAAGG	TTTGTAATGG	AGGTGTGAGA	TCTCGGAGTC	CTTGGTAGTC	TCAGACACGA	600
	AGCACCGGCA	TCATGTATCC	ACTTCGCAAC	AAGCGAAGTC	CAGCCACACT	GGTGTGATGC	660
	GCCCAAGCCC	CTACCAGTGT	CACCATCGAA	GTAT			

## 1467RP

	GATCGCAGAC	TCCGCCGGAG	AGACTTTCGC	ACCTCGGGCA	CAGGTCTTGA	AAGAGAGCTC	60
	CGGCCGTTCC	GTGCCAGACT	CTTGTATTATC	ATGTCCGTAA	GAGCAGCGTT	CGTGCCAGGT	120
5	ACGCCCTTCT	TGTTCTGTGT	TCCACCAATT	GATGGAATTT	GAGACGTGAA	CCTCTGCGGA	180
	TTCTRRKCTAT	TGAGCACACC	ATTGGCACCA	CTTGAGCCCC	TTCTGCTCTGC	CATCCCTAAT	240
	CGTCCTATCC	TACGGCCGGC	TAATAAGTTA	CTACCAGACT	CTGGCCCTCA	TCTGGGACTG	300
	ATGTTATCGT	CTGCAGCCAG	ATCCTGTTTG	TGACCCGATC	GAAATCATCG	AGTACGAATA	360
	ACCACGTGAC	CATTATTTCAC	GTGATGAATT	TGGCGGTCCC	TGTTGCCGAC	TCTTACTCCA	420
	GGTTAACCAT	GACTAGATGG	GCATACCTCA	GATACGTTAT	TCATGGGATC	CGGAGTTGCC	480
10	GCGTCGGCCG	AACCGCCCGG	TGAATCTGTG	CTGACGACCT	AAAAAATAGT	GTGCGCAAGC	540
	TTCTTTAATC	TGTGAGATGC	ACACTGACAA	ACTTGAAGGC	TGAACCATCA	AAGCGATACG	600
	CCTCATGCAC	GTGCTCAATA	AGGTCCAGGA	AGTCTCGCAA	TGGGGCAAGC	AGACGGTAGA	660
	TTGCAAGACA	CAGACGATTG	GGTTGTGCCA				

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## 1467UP

	GATCGTCCGA	GTGCAAATCC	ATACCAAAAA	TGTGGACCCA	GGTACGGGAT	TCGAACCTCT	60
	CGAAGAAAAA	TAGCCTCAGT	GAAGTGCCCA	ATTGCCCTTAT	AGTCGTTTTG	CAGAGCATAT	120
	AGAAATGTGG	GACAAGCGCG	TGGGGGGGCT	TGTCGGACGC	GACGGAAGAA	GGGATCTGGG	180
20	CGGGAATTAC	GCGGGTGAGA	GCGAGGGGTG	CGGAAGAGAA	AAAGGTGAAG	CGAGTTGTGT	240
	CCATGAGCGA	GATGCAGCAG	CCAATACCTA	TCCCAATGGT	AAACGAGGCG	GTCCAGATGG	300
	CCCAATGGCG	GAGGGCAACA	GGGCCCCGCT	CCTTTTTTCG	CGGTCTGCGG	TGCTGTTTTCT	360
	TGGACTTGAC	GGTCAGCTCG	GTTTCATAGC	CGGACTCGGA	CTCGTTGCAA	AGGTTGTGCA	420
	GGTGCTTTAG	CAGGCGGTGC	TTCTCGTGGT	GGTTGGACAT	GATTATAGGG	CTGCAGTATA	480
	CTCGGATGCA	TTTGCGTGCG	GTGTAGCGCT	TCAGGAGAGC	CGCCAGCGTG	CTCTTCTGGC	540
25	CCTTCTGGGA	CACGGGAATC	ACGGTGGGGC	AGGGCGCCTT	CTCGCACAGG	CCGTCCAAGA	600
	GCTCTGGCGC	CTGCGCTATG	TCGTGGAAGA	CCACCATAAC	CGCGAGGTAC	CGCTGGCCCA	660
	CGTCCCAGCG	CGTGACCATG	CCGAGGTTCT	TCACGTCAAA			

## 1468RP

	GATCTCGTCG	CTCATTGTCTG	ACCTGCAAAA	AGTGTTTCAGA	AGGAAGGCAA	CATGTGTTTT	60
	TAACTCTACG	GCCGTGGCCT	CAGAGATTGT	TCACTCAATG	TCGTTTCATCA	TTATGAATGG	120
	GTCGCCGGCG	CCTGCCGGCC	TCGAACCCGC	GCCACACGGC	CTCCGCCGCG	CGCTGCCCCG	180
	CTGGGCCACG	CAGGTTCCAA	AACCCACCCA	AACTCACCGC	GCCCACCCGG	CTACACCGCC	240
35	GCCAGCACGT	CACGTGCGGT	TACCCGCCCT	GCCGGCACTG	AAAATTTTTT	GCCGCCAACA	300
	CTATCGCGCC	CGAAAAAGCA	ATTTGCCGGC	CAACCACACA	ACGATCTGTT	ACCGAACAGG	360
	ACAGGACTCA	TGCCCCGTTT	CCTTCTTTAT	TTATTTACTA	GCTCCACATA	GATATTTTTG	420
	ATATTTATAT	GGTGTGTTTT	CCTCCGCACG	CCGCAACCCA	GCACTTAGCA	GACCACGGGG	480
	GCAGGGACTG	ACACCCAGCC	AGAACAGAAC	AACAACAGGC	GACCTTACAA	TGAGCATGGA	540
	AACGCCCCCT	GTAGATATCG	ACAACATCAT	CGACCGCTTG	CTGGAGGTGC	GGGGCTCGAA	600
40	GCCGGGGCAG	CAGGTGGACC	TCGAAGAGCA	CGAGATCCGC	TACCTGTGCT	CCAAGGGCCG	660
	CAGCATCTTT	ATCAAGCAGC	CCATTCTTC				

## 1468UP

	GATCTCAGAA	TTATCGGCTA	GCAATTGATA	TTAGCATACT	TAATTCGTGC	TAAATACTTT	60
45	GGCATCGCAT	CTAGACATAG	GAAGTAACCT	CAAAAAAGCT	ACGCAGATAG	TAAACCTGGA	120
	AGAGAGATTG	CGCAACAACA	ACGGCCAGTT	GGAAAAAGTA	CCACCACTTG	ACCCTGTCAT	180
	TTGTAGACTC	AGCAGTGTTT	CTGTGTGTGC	GTTCGCGAAT	CTCGATGTAC	TGTTGCTCGT	240
	TCATTACTTC	CATTGTGAGC	ATGGAGAGCT	TGCGCACCGC	ACCCTCTAGC	GTCTCCGAGC	300
	TGGAATCAGC	GGCATCGGGG	GAGAGAACAC	CGTAGGTATT	AAACGTGACA	TCCTTAGTCA	360
50	GGTAGCCCGA	ATTGTCTGTT	GCAAAGCAGT	ACTGGTATTT	GCCATCTGTA	GGCGCCTTCA	420
	AGGTCAACTC	ACCGTGCAGC	GACGCACGCT	GCGCATCCAG	CACGTGACCGT	CCGTCAATCC	480
	CGTACACCAG	CAGGTCTCCA	GACAGCTGTT	GATGTGATTG	TGGGTCTCTG	TCGCCGAATT	540
	GATAAGTGAT	TGTCAGCAGC	TCCCCGCCCT	TCAACTGCTC	AAAGAAACAG	CGCCGCCCGT	600
	AGGGGGGAAG	AAGTACATTG					

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## 1469RP

	GATCAACTAC	ATCTGCGAGC	AGCAGCCGAA	TTGTAAGGTG	GCCATCATAG	CATATGACAA	60
	GTGGCTGCGT	TTCTTCAACC	TGCGCCCGGA	GTCGAGCCAG	GCACAGGAGC	TGATTGTGTC	120
5	CGAGCTCAGA	GAAGTCTTCC	TGCCGCTGTA	CAGCGGCCTC	TTCGTGAGGC	CTGCCGAGGC	180
	AATGCATGTC	ATACAGGACA	CGTTGGTCAA	GCTCGAGTCG	TTTATCCAGG	ACGACAAGCT	240
	CTCGCACGGC	GCCGAGGCGT	GCTTCGGGTC	GGCGCTCGAG	GCCGCGCTGC	TGGCGCTGGA	300
	CACTGCCACC	AATGGTAATG	GCGGCAAGAT	CATTGCGACT	CTGAACACGC	TGCCACCCTG	360
	GGGCAACGGC	AATCTGACGC	TGCGGCGCGA	CGACGGCCTC	AAGAAGAGCC	TGAAGTGCGA	420
	CAACAGCTTC	TACACCGCGC	TGGCGGACAG	GATGCTGAAG	GCGTACGTCG	GCCTGGACCT	480
10	CTTCTGCACA	GGCAGCGCCT	TCATGGACTT	TGCCACGCTC	GGCCACCCCG	TGCTGGCCAC	540
	CTCCGGGACG	TTCCGCCACT	ACTCGAACTT	CCAGCTCGAC	GCGACGAGTT	CCCGCTGGGT	600
	CAACGACATG	CTGCACGCCG	TCAGCAGCAC	CGTCGGCTAC	CAGGCGCAGC	TCAAGGTGCG	660
	CTGCTCCTCG	GGGCTGTCGT	CAGTCG				

## 1469UP

	GATCGGGCGA	GCAGGACTAG	AGATGAGCAG	CAATGACAGT	GATTATCTCC	TGGTTACCTT	60
	CAAACCTCTT	ACTCTCCTCA	AGAACTTGTT	ACCTGATGAC	TCCTTCTTAT	TGTCTGTGTC	120
	ACGCGCGCCC	GTGTAGGCGT	CTTCGTCGTC	CTCCTTCTCG	TCCTCAAGAT	AGCCAGAGTG	180
20	GGTCTTAGTG	AGCTTCAGGT	TGCCGTTCTT	GGGGTCGGGG	CCAATCGCCG	ACGCGGACGG	240
	AGGGCTTTTC	CCAGCCTGTG	GGCTCAGAGA	CTTCTTCTTG	CCCACCGTGC	TCTGCTTCAT	300
	CGCCTCTATA	GCGACAGGGG	CCGCCGGCGC	GCCGTCGAGG	AACGTCGTGG	AGCCAAGCCC	360
	CTGTGTCACG	GGCCCATGCA	CAAGGTCCGC	GGTACCTTGG	GCGTCGAACT	GCGTCACCTC	420
	CGAATGGTTC	TTGATAGCGT	TCACCGTCGA	CGACGAGCGC	TCGCCGACGT	CGCGGCGCGA	480
	ATACAGGTAC	GAGTCGTCGT	CCTCGTCGAT	GCCGAAGACC	TCGTTTCATCG	CAGACTTGTG	540
25	TGCGGTGGCC	CCGACAACGT	CGAGTTCGGC	CG			

## 1470RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACRAC	GGGGAATTAA	GCCCCTTTTT	60
	CAATATTTTG	AGCGTCGTTT	CATAGCTCGG	AAGACGCAGC	AGAAGCCCCC	CCAGTAGTGT	120
	CTGTTCATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTGTCAGGA	TTACAGTAA	240
	ATAATGGTAG	AACCGCGGAC	TCACAGAATC	GACGACCGCT	CGAAATGAAG	TCGGCCCGTA	300
	GAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTTACGGG	360
	GGACACCGTG	CCCATAACGT	GCTTCTGCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
35	CCGCGCGAGC	TCAGTCTCAA	GCTCGTCGAT	CCGTGCGAGC	AGCTCCACAT	TGGGCGTTTC	480
	AGCTGAACAG	CTCCCGTGAG	TTACGTCGCT	GCGTAAATCT	AGACAGGTAC	ACACACTCGG	540
	GCAGGCCCTT	CCCAATACAT	TTAGAGCACT	TCGGCCGCGC	CTTGTTGCAC	TTGACGCGCC	600
	GCTTGCGGCA	GAACACGCAC	GACTTGCTGA	CCTTCCGCCT	GGTTTTTACA	ATCTTGCCAT	660
	CGGACTCTGC	CATCCCGCCA	GCTTCAGCAA	AATGAGTAG			

## 1470UP

	GATCGCGGAC	GTGGAACACT	GGCCGGAGAT	GCGCGCGGCC	ATCCTGGTGG	TTTCTGCGGA	60
	CCGCAAGGAC	ACGCCATCGA	CGAGCGGTAT	GCAGCAGACG	GTGCACACGT	CGGACCTCTT	120
45	CAAGGAGCGC	GTGCGGACGG	TGGTGCCGCG	GCGGTACGGA	GAGATGGCGG	CGGCGATCCG	180
	CGCGCGCGAC	TTGCGGACGT	TTGCGCGCCT	GACGATGCAG	GACTCGAACT	CGTTTCACGC	240
	CACCTGCCGT	GACTCATTTT	CGCCGATCTT	CTACATGAAC	GACACTTCGC	GCCGGATTGT	300
	CAAGCTGTGT	CATCTGATCA	ACGAGTTCTA	CAACGAGACC	ATCGTGGCGT	ACACGTTTGA	360
	CGCGGGTCCG	AACGCGGTGC	TCTATTACTT	GGCGGAGAAC	GAGGCGCGGC	TCTGCGGCTT	420
	CCTCTCTGCC	GTCTTTGGCG	CCAACGACGG	CTGGGAGACC	ACGTTCTCGA	CGGAGCAGCG	480
50	CGCCACTTCG	CCGCGCAGTT	CGACGAGTGC	GTGCGCGGCA	AGCTTGCGAC	GGACCTGGAC	540
	GACGAGTTGC	ACAGAGGAGT	TGCCCGCCTC	ATCTTACAGA	AGGTCGGGCA	GGGCCCCAAG	600
	ACACTAAATC	CTCGCTCATC	GACCCCGAGA	CGGGCCTGCC	CCGCTGACGC	TATT	

## 1471RP

	GATCAATTAA	CTATCTAGAT	GAGTCTAATT	AATTAATATA	CTTAAAAGTC	CCGTTAATAT	60
	CATTAGCTAC	CCTATCGGAA	CAGACCGTCT	GCTACTAGGC	CGAAAGGGTA	AAGCAGTTGT	120
5	CAGTCAGTAC	TTGCTGTGTC	TTATGGAATG	CCTGTCTAT	GCCGGCAGCT	TGTTTGTCTAC	180
	TGGAGTACGG	CGCGTGCCGC	CTTGACAGAG	GTACCCATGA	TTCTGAACGC	CAAGGTACCA	240
	CACCTTCCTG	CCACATCTCC	TCGACCTCTT	CCAAAAGTCAA	ACCCTTTGTC	TCGGGGACAA	300
	AGAAGAAGAT	GTAGAAGAAC	GCAAAGATCA	AACAACCCAT	GAACACGTAG	CCGTAGTAAA	360
	ACCTGATCGC	ATTGGTAATG	TATGGTGTA	AGAAGGCGAT	CAAAAAGCCC	CATATCCAAT	420
	TCGCGGCTGT	GGCGATAGCC	ATGCCCTTGG	CTTTGACTCT	TAATGGGAAA	GTCTCCGAAA	480
10	CAATGACATA	CGCAATTGGG	GCCCAGGTAG	TTGCAAAGAA	GAAAAATGTA	GAGGCAGGTA	540
	AAAACAATCA	TAGCATTGCC	TGCCGGTCTG	GAAGAAGGCT	GATCGGGTCC	ATTGGGCCAT	600
	AGTCTTGTC	CACCAACGGA	GGCAAAAATA	ACCATACAAA	CGGCCATTGC	CGCGGCACCG	660
	TAGAAGCAAA	CATTTCTCTC	TGCCAAATCT	ATCGACAGTG	TTACATTG		

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## 1471UP

	GATCTTCGCC	TTCTTCTACA	TGTTCTTCTT	TGTCCCAGAG	ACAAAGGGTT	TGACTTTGGA	60
	AGAGGTCGAG	GAGATGTGGC	AGGAGGGTGT	CGTCCCATGG	AAGTCCGAGT	CCTGGACTCC	120
	TTCTTACAAG	AGAAATGCTT	ACGAGACTGA	GGAGGTGAAG	CCAGAGAAGA	CCTGGGCTTA	180
20	AAAACTTTAA	ACTACAAACT	TTTTTGTTCT	GCTAATCATC	GGGTAAAAAC	CTAAACCTTA	240
	TCATGTCTCA	TTAATATTGT	TATGACGTTT	ACGAGATAGC	ATATGTAAAT	TACTATTAAA	300
	AATATGCGAT	TAATCTGTAT	TTATTAGTTG	TAATTGCAAT	GCCATATGAT	ACTGCAAAGC	360
	AATACATGCC	GAGATAACCA	ACGCCACTGA	GGCGGGACTG	GGCCCCTTCT	CCGGCCCCGGC	420
	GAACATGCCT	GTCGTTGGTG	GGCCGCGTGC	CCGTGCGCCG	CCAGCCGCAT	GCCCCGTCGT	480
	GGTCATCGCC	CCACTTTCAA	ACTTTGTAAT	CGAGCAGGAA	ATTAAGATT	GTTATAAATG	540
25	ATATCAAATT	TTTCGTCGTT	TCTTTTCAGT	GAGTAATATT	GTCCCGGCAC	CGCACGCCGA	600
	TGATGCCGCT	ACATCGCACA	GGGCCAAAGC	ACAGGTGCTA	AACATTGCT	TAGTTGGCGT	660
	CGTTGAGCTC	GTTTATGCTT	AGTGGAATAT	CTGCAGCATA	TTCAATATCA	AGTCTGAA	

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## 1472RP

	GATCTATCTC	CCAGCTTAGA	GAGACCGTCC	GGATGTAAGT	GATACCCAGA	CAGCCAATGA	60
	TACTGGTCAA	GTTTTGTAGT	TTTATAAGAA	AACATATATT	AAACGGCTAA	AGACAGAAGG	120
	CGAAAAGCCC	GACTTTTATG	GGCGTAGAAG	TCGTGAAAAA	GGCGAAAAAC	TATATTTCCA	180
	CTTAGGGCTC	CTCCTTCCTC	ACGTAAACGC	GCATCATCAT	ACGCCTTCTG	TGAGTCAAGA	240
35	GCACTACGAC	ACGCCGTGCA	TTCCCTCATA	CAACCTTGCC	AACACATGAT	CATGTCCAAG	300
	GATATTGCTA	CGACCCCA	ACTGTCCGAA	CCAGACAAGT	ACTTCGTTGA	GCAGCGCGAT	360
	TTGCTGCTAC	AAGAAATCAC	CTCCACGTTA	GACTCCATCC	TGAACAACCT	AAATGGCCCTG	420
	AATATTTCCC	TGGAGAACTC	CATCGCAGTA	GGCAAAGAGT	TTGAGAGCGT	GTCCGAGCTT	480
	TGGAAGGTCT	TTTACGACGG	ACTCGCGAAC	GGAGCGGCTC	CTGGAGTTGC	CGCAGCCAA	540
	CCGTGCTCTC	AGGACCTGCC	CACCTGAGCCC	GTCGCCGCGC	ACCAGAATGC	TGCAGCGGGC	600
40	AATAGTGACG	CACCAGCGCC	ATCGCAGTAG	CGTTTGCAT	CTGCCCTGGC	TTTACACCCG	660
	TGCACCCACA	TTGCGCTCTA	CTTTTATGTG	TCATC			

## 1472UP

45	GATCTCGATT	GAATGCCAAT	GAAGGTTTAT	GGCCGTCACG	GGAGGTATAA	CAGACTTGTA	60
	ACGACTTTTG	GTAAGACCCA	CGGTGAGGAA	GATAGCTGGT	TTAGCAGCGA	CGATGAGAAC	120
	CACGGCAGAC	CAGTTAGCGA	CGACACAACC	AAACTCAGCC	TGAGCCAAGA	TCGATGCAGC	180
	GAATTACCGG	AGGAGACGAT	AGGTGCGAAT	AGAAAACGTC	CGGCGGAGCG	AACGCAGACG	240
	GATCCGGTGT	GGGAGTTTCT	GGAACGGCCG	GCATCGGGGC	AGAAAGCGGAG	AAGACGAGCA	300
	ACATGCGATT	CTACAGAATA	TAGAGAGAGT	GCCAGTCAAG	AGTTTCTAAA	CGCTGTGAAC	360
50	GTTGTGCAAG	GCATAGTGTC	TTCTCTCAAG	CCTGCAAAAG	AGGTAGTTGA	GCACTGGGCG	420
	GAGCTTGAGG	ATGTGCCAGA	GGATCGGGGC	AATAACGGGC	AGGCGGTCTA	TGGCAAAACA	480
	AGAACATGCT	TGCAAAAGCG	GAAGAGGATT	CTGACACCGA	AGCTGCTGCA	CATGAGTCTG	540
	ACGAACCGCT	GCACAGGGCG	ACGAAGCACT	ATCGCGGCAC	TTTAATGAGC	TGCGTACGAT	600
	GGGCGAGACT	CTTAAGTACA	GCGAAGATCT	GGACTTTATA	TTGTCCGACA	ACTCCATGAC	660
	GACACCGGAA	CATAGACGCA	CCACATGCTG	CGCTTGTTGT	TGGATATGAT	GAACAACGA	

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## 1473RP

	GATCGCATCA	TCCTGTACAC	CAAGCGCGAC	GTCTGCGCCG	CGCCACCC	CGCCGCGCTC	60
	CACCGCTGGC	ACGCCGAGAC	CGGCGACGAC	TACATGCTCC	TCGACGCCCC	CAGCGCCGCG	120
5	GACGCGCGCG	CGCTGCTCGC	CGCCGTGCGC	GCACGCTACG	ACGCCGCGC	TGCCGCGCCC	180
	GGCGCGCTCC	CCCTCGGCTA	CCGCCGTGCTC	GTTGCGGGCA	TGCCCAACGT	CGGCAAGTCC	240
	ACGCTGGTCA	ACCGCCTCCG	CGCCTCCGGC	ACCGCGCGCC	GCGCCAAGGT	CGCCGCCACC	300
	GGCGCCACC	CCGGCGTCAC	GCGCGCTACC	AGTGAGTGCG	TGCGCATCGC	CGATCACCGC	360
	GCCGCGCTCT	TCATGCACGA	CACCCCGGCG	GTCGCCCTGC	CCGCCGCGC	CTCCTCCGTG	420
10	CGCCGGATGC	TCGCCCTTGC	TCTCGCCGGC	TGCGTCGGCC	CCGCCGTCTG	CGACCCCGTC	480
	ATCCAGGCCG	ACTACTGCTC	TACCTCCTCA	ACCTTCAGGG	CCTGGCCCCC	TCCTACGCCG	540
	CCTACAGCCC	CCCCACCAAC	GACATCGCCG	CCCTGCTCGC	CGCCGTGTGC	ACCCGCCACC	600
	GCCTACGCTC	CGAGACCGCA	GCCGCCCTGC	ACTGGCTTGC	CATCCGGGCC	CCGGGCTCT	660
	GCCTGGAACC	GGAAG					

## 1473UP

	GATCTAGACG	GAGTTATTAT	GCCGCGGCAC	CTCCAGCGAC	TGATACTCAA	GAATGTGCGC	60
	TCCGTGCGGT	GGTGGAGGTT	CCGAGAGATC	CACGAAATTA	CGCTAGATCC	TAATACGTTT	120
	ACCAAGAAAC	AGGGCTTTGT	GGGAACATA	CACGGGCCAG	ATCAGGATCG	GGTGGAAGTG	180
20	CGGCAGATAA	ACAGGGCTGT	CATGAGTCAG	GACACATACT	TCCACTTTGA	TAGTCTTTTG	240
	AGGGCCAGGT	TCCAGAACCT	CAACTACATC	AGTCTGCACA	ACGTTTCCGA	GGAAATTACT	300
	GGCATCATAG	TGCCTCACCG	ACTGTATTGC	AATGGCCGCA	TCAGCAITGC	AGGCTGCGTC	360
	GTGAAGGGGG	TTGTAATGAT	CTAAACTTGC	CCGGATATCC	CTATTGAGAA	ATAAACACAT	420
	GGGTGAAGTT	ATACATAGGC	GCGGAAGAAG	CCGCTTGAAT	ATTGATAGAC	CGAATAGTGC	480
	GATCAATGTA	ATTAAATAGA	TAGGTTACAG	CCCTACCGGG	CTGGCATTTG	GTCCGAGATT	540
25	GGTCTGCCTC	TACCAAGTCA	GCCAGTTACC	GGAGGGTGAA	GTAGTAGGAC	ATCATAACTC	600
	ATAAAAAACG	TTACATTCTG	TGTGCTTGTC	GGGAAATCAG	TAATCATGCA	GGTGCCTCGT	660
	GAAACCGAAG	GAAACGTAAT	GGCGTGGAAT	AAGTAAAAGA	TGC		

## 1474RP

	GATCGTTTCA	TTTAATCAC	TGGGACGCAC	TGCCTTGCGG	TTCCAGCACT	GCCTGAAACT	60
	TGGCCAGGCG	TTGCATCACG	GCATTAAGCT	CCTGTACATC	GCGCTCGTGC	TGGGCCTCCA	120
	GCTGCAAGCG	CAGTTCAGCG	CTGATATGCT	TCCCGCCCGG	TGTAGACATC	TGCGGCAAGC	180
	TAGGGTAGCT	GCCCGACCGC	CGCAGCGGCG	AGCTGCGCGC	GCCCTTGTC	GCCGCTTCT	240
35	GTGCCCCCAT	TAGTGGCCGT	ATCATCGTCT	CGATCCCGCC	GTTTGCCATC	ATCGGTATGG	300
	GTGTGTTGTA	ATCGTCAATT	ACCGCACTCC	AGTCCCTCGT	CAGGTCCGTA	AAATACTTGT	360
	CTTTTTTGCC	GCCAGCGTGG	TTAGACCCGC	CCGTGGTGT	GCTCCGAAGC	GGGCTCAAGT	420
	GCACGCCGCG	GTGGCTGCTG	CTGTGGCTCG	ACAGGGACGC	TGCATAGTCT	GCGACCTCCT	480
	GATGGCGCTA	ATATTCCCAT	CGCTATCTGC	AGGCTCCAGC	GATGGCGACG	CCAGCTGATT	540
	CGACTTCGCC	GATGACGGCG	TCTTCCACGA	CTTGATCAGC	GAGCCCAACA	GCGACGAAGA	600
40	TGATGAATTT	GACTTTTGGT	ACATTTCTTT	GGACCCATT	CCATTATGGG	GAACCGTCTT	660
	GATAGCCATC	ACAATGTATA	GCTCGCTACT	CTGAACCGCG	TGGCAACCAC	TGCAAC	

## 1474UP

	GATCGAATTC	TCACAGGCCA	GTACCTGCGT	ATTACAGGTT	TGCCATAGTA	TGATTAGAAC	60
	CGTAAAGCCC	AAGAATGCCA	GGGCCAAGAG	AGCTCTGGAG	AAAAAAGAGC	CGAAATTGAC	120
	GGAGAACGTG	AAGCAAGCGC	TTTTAATTCC	TGGCCAAACT	TCGAATAAGC	TCTTGCACGA	180
	TGTTATGGTG	GACCTTGGTG	GACTCAAGAA	GCCTGATGTG	AAGCGCTTCA	CGCGGAAGAA	240
	CGAGCTTCGT	CCGTTTGAGG	ATGCGTCGGG	TGTCGAATTT	CTCAGCGAGA	AGAATGACAG	300
	CTCGTTGGTG	GTGGTCTGCT	CCAACCTGAA	GAAGCGGCGC	AACAACCTGA	CATTCTAAG	360
50	GACGTTTGGG	TACAAGGTTT	ACGACATGAT	GGAGCTGCAG	ATTGCAGAGA	ACTACAAATT	420
	GCTAGCGGAC	TTCCGGAAGC	AGACGTTTGC	AGTGGGGTTG	AAACCGATGT	TTTCTTCCA	480
	AGGTGCGGCA	TTGCACTCTC	ACCCAGTATA	CAAGCACGTC	AAGTCTTTGT	TCCTCGACTT	540
	CTTCCGCGGT	GAGGTGACCA	AGCTGCAAGA	CGTTGCAGGG	CTTCAGCATG	TGATAGCAAT	600
	GACGATCCAG	GGCGACTTTG	AGGATGGCGA	GCCATTGCC	AACGTCCTTT	TCCGCGTCTA	660
	CAGGCTTAAG	ACGTACAGAA	GCAGCCAAGG	TGGTAAGAA			

## 1475RP

	GATCCGACCA	ACGAGCGCAT	CTGCAGCCAC	ATCGTTGATA	ACGTCACCAT	GATCGACGAA	60
	ACCGAGGAGG	ACCAGGGCGC	AAAGAAGGGC	GCCTTTGCTG	TTTGAAGCCG	GATCCTGCGG	120
5	CGTTCAACCG	TAAATAGTCT	TATAGCCAGC	ACGCCAGGCG	CCGGCCGGTT	CCTATGTAGT	180
	CCTGCAATCG	CTCGCTTGCT	AGCCGCACGA	TCACAGAATA	CAGCTACTTT	ATCCTAAATC	240
	CACTCCTATC	AAAATATCCA	GCCGCGACAT	TTGTTCTCTG	TCTCGTGGGA	TGTGGCGGTC	300
	GCCATTGTGG	AGTAGGGCCG	CAACTCGGAC	AGCGACCACA	GGTCGCCATC	ACAGCTGCCG	360
	GTCCCGTGTC	CGTCCCTGGA	ATCCTGCTCC	AAGCCCTTCT	GGTCAAAGCC	AGCCAAGCTC	420
	CCCTGTCTGA	TGGCGTCCTC	GACCGCTGCG	TCCAGCAAGT	CCTGGTATGG	ATCTGCGCCG	480
10	ACGCTTCTGG	GGGCCGCGAG	CGTTGTGTGA	AGCCAGTCGC	ACAGAGAGGG	TGTCGCTGTT	540
	AGCGCAACAG	ACGAGGCGCC	TGTGCCGGCC	GCATGGGCGG	CCGTGCCGAA	TGCGTGCGGG	600
	TTCATGTAAT	TGCTGCCCTG	GTCCGATGTG	TATTGTGTCT	GCGAACGGGA	AATCGGGGAC	660
	GCAGGAACGT	TCGCCTCGCC	GCCATCGTTC	TCGCAGCTCT	TCGGTTGCGG	CACCAAAGCC	720
	TCCTTCTGCA	GCATCCGCCC	TGAGCCGTT				

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## 1475UP

	GATCTTCCGT	CCCGAGTACG	GTCGTCTCTT	CGAGATATNA	GCACGCAGCG	CAACTGTATC	60
	AAGCTAACCA	ACACAGTKCG	CACGCTTTTC	GAGCCGAGCT	CAGGCGCGAG	GTGAACCAGC	120
20	TCTGAGACAG	ACAGACGCCC	CTTGTTTCTG	AGTAGCTCAA	TAACACGTCC	GGCTCGCTCG	180
	CCGAGGTGCG	ACCGCGCTAC	CTCTGTGTAC	AGGAAGGTTT	CAGGACTCAA	TGTCCTCATC	240
	TCCAGTGTGC	ATACCGGCAC	CTCCGCAGCA	CGCTCGTTTT	CGACTTGTCC	ACCTGCAGCA	300
	CCCATAGATC	CGTTTATTAT	GCACTACGAC	CTCGCCCTCA	CTCAAGCCCA	GGGCCGTCTG	360
	GAACGCAATA	CTCGCTAGTG	CTAGTTCCCA	CCTAATATCT	ATCTCATCGC	CCATCGAGCA	420
	GCGGGCCAGC	TAAAAAATCA	CCACTGCGCG	CTCACCACGC	ACGGTTCACT	AAATACGAAA	480
25	CAGTTGTTTC	TCACGTGTTG	CTCACGTGAT	TTTACCCGGC	CCGTATAATA	TCGGGTTCTC	540
	AGCGCGCCGA	GCCAAGGACA	CTTCCTGTAT	CATAACAAAC	CAGCACAGGC	GGTAGGAGCT	600
	ATCGGCAGAG	TCCCAATACC	CTTGCTACTG	TTGACATTAG	GTGGTTCAAA	TGAGTGTCTG	660
	TTTAGTGGTT	ACCAAGAGTG	TGGCGACAGC	CACATTGGGG	ATCTACACCG	GGATGGTGGT	720
	AACGCGGCAG	TTGGTCTCTC					

30

## 1476RP

	GATCGTATCG	CTAACTGTAA	TATCGAAAGA	AGCACAGACA	TCCCGGAAAA	ATGACATCTC	60
	AGTGACACTC	TTCAACAAAT	CATAAGAAGA	AAAGTATGTG	ACTAATGCTT	GCAGAAAAAT	120
35	AAATTGCTCG	CTACCAGTAA	GCGATGTTAG	TAGCGTGCCA	TGGCATTCAA	TAAATCGTAA	180
	GAGATACGTG	GGTGGTATCT	CGATGCTTTT	GAGGTACGCA	AAAATTGGGC	CATATAAATC	240
	GATCTTGAAT	GGTAGCCTTT	TGCATATCGA	TTCTTCAAGA	AGTCTGTMTA	TAAAGTTCTTT	300
	ATCAGAAATG	TGCATAGACT	GATGCAGGAG	AGCACTTAGC	ACATGCCCTT	TATTCTTAGG	360
	ATAGAGCAAA	TATTCCTTGA	ACGAAGCTGG	GTCTTTCCGG	AAGTCAGGCT	TCATACCATA	420
	AAGGTACATG	TATACATTCC	TTGCGACATC	CATATCCTCA	ATACTGCTTT	CAAGCATCGC	480
	AAGGTAAAT	TCGTAGGAAA	ATTCGGGTAC	CCAGGAATGC	TGTTGAAATT	GCGTCCAGAG	540
40	TTTGTATGCT	GTCTTGGGGT	GGTTCTTTGC	GACGGCCAAC	AGGAAGTTGG	GACAGAACCA	600
	GCGTCTGACA	GGGAATCAAG	ACCATCTGTT	GAGCGAATTT	GCGTGAGAAG	GCGATCAAGC	660
	AGCTTCACAG	CAACTTCCAG	GGAATCTAAG	CTGACAAGCC	CAGCTAC		

## 1476UP

	GATCTGAAAC	TAACAACAGC	AGTGCGTGAA	CCAAGAGGCA	TTGGAGGCGT	ATGACGGCGT	60
	GTCGCAAGGC	AAGTACACTA	TCGGCTTGGG	CCAGACCAAC	ATGAGCTTTG	TGAACGACCG	120
	CGAGGACATC	TACTCGATGT	GTTTGACCGC	GTGCTCGAAC	TTGATGAAGA	ACTACGATAT	180
	CAAGCCGGAA	AGCATCGGCC	GCCTCGAGGT	GGGTACGGAG	ACGTTGCTTG	ACAAGTCCGA	240
50	GTCGGTGAAG	TCTATTTTGA	TGCAGTTGTT	CGGCGAGAAC	ACCGACTTGG	AGGGTGTCTGA	300
	TACCGTGAAC	GCCTGCTATG	GCGGTACTAA	CGCGTTGTTT	AACTCCTTGA	ACTGGATTGA	360
	GTCCAGTTTC	TGGGACGGTC	GTGACGCAAT	CGTTGTTTGT	GGTGACATCG	CAATCTACGA	420
	CAAGGGTGCC	GCCCCGCCCA	CTGGCGGTGC	GGGAACTGTC	GCTCTCCTGA	TCGGTCCAGA	480
	CGCCCCAAT	TCTTTTGACT	CTGTGCGTGG	CTCGTACATG	GAGCACGTCT	ACGACTTCTA	540
	CAAGCCTGAC	TTCCGCAGTG	AGTATCCATA	CGTGGACGGC	CACCTTCTAC	TAACATGCTA	600
55	CGTCAAGGGC	CGTCGACCAG	GCTTACCGCG	CCTTA			

## 1477RP

	GATCTTTGCG	AGGGACCACT	CTGCAATCCA	AGAAGACTAG	AGGAGTTGTC	TAGGACAACA	60
	AAGTTTATAA	GGAGACTTCT	GGTGTTTTAC	CGTCCTTTTC	GATACCGATT	CTCGACAGTA	120
5	TATTCAAAGG	CCAATAACGC	CAAACAATAC	GTTAAAGTTG	GCTGCCAGTT	TTTCAACACA	180
	CTACTACAAC	ATTATGAGGG	CATAAAGGTG	CTTCTAGATG	ATAGCAAAAT	CATTCTCAG	240
	CTCGCCAGTA	CTCTCTATAA	GGCTATGGAA	GGGCATATTT	TACCCAGTAA	GCTCTTCTCC	300
	TCTTGGGCTC	TCCAGAATAC	GTTATGTGGC	TCCTACTTCA	AATTCTCCGG	ATTGCTAATG	360
	AAATCTAAGG	AAGGAATCAA	TATATTAGAA	AAATGGAACA	TGTTCACTGT	CATCTATAAA	420
	ATGTTTCAGC	CATCACCCCT	AGCGGAAGAA	TATTTGTATC	TCATGCTTCC	AGAGTTGGAC	480
10	CTCTCTCACA	GCATACATTG	TAGGATTATT	TTTAGCAAAG	CGCTAGTCGA	CAGTAGAGAA	540
	GTCATAAGGA	TCAATGCTAC	CAGGGTTTTA	GGCGAAATGA	TCAGCAGCGT	CAAATTATCT	600
	GATCCCACTC	TGGAAGAGTT	CATGTTAAAC	CTGTTGGTCG	CTCAGTTGTA	CGATTTATCG	660
	AGTGAAGTGG	TAGCAGTGCC	CGACCAGATA	CTGTACCATT	ACTGTTTAA	TCAAAGTAT	

## 1477UP

	GATCCGAATG	TCCTTAGTCT	GTGGGAAGGA	ACCGATGGTG	GTGGTTGGGA	ATAGCGGGAG	60
	CTTGAAAATT	GGCTGCTGCT	CCTTGAGACG	CTCCCCGAAT	GGTGCGGCTC	TCGTGGATAG	120
	CTTCTCGTTC	AAACCAGCAA	CACGTCCTGG	ACAGCAGGAT	CGTTGGTGAT	CGCAGAGGCG	180
20	GCACGCGCAG	CAATCGAGTC	TGCATTGGCC	TTCAACTCAG	AGGAAAAGTC	TTCGCCAGAA	240
	CGGTTCTTAG	CGAGGACAAC	AACCTCATGC	AGCTTCTGGG	TTGCAAAAGA	GAACCACTCC	300
	TTGATCTCTG	GCTCCAAGGC	AGACTCGTTT	TCCAAGTCAA	CTGGAGTGTG	CAACAAGGAA	360
	GAGGACGTGG	CAACAATAAC	GCGGTCCCCT	CCTAGTTTCT	CAATTGCCTT	AGAAATAGTG	420
	GCAGCCGACT	TCGCGAAGTC	ATTCTTCCAG	ATGTTTCTAC	CGTCAACAAC	ACCTACAGAC	480
	AACGACTGGT	TTTCGCCAAC	GATCGCTAGA	ACGTCGTCCA	ACTGCTCTGG	GTTTCTCACC	540
25	AAGTCGAAAT	GTAGGCCAGC	CACCTGGAAG	TCCACAAGCG	CCTTCAAGTT	CGGAACGACT	600
	GTCCCGAAGT	AGGTGGTCAA	CACAATGTCT	AGAGACTTTT	CCGCACCTAT	ATGTTTCATA	660
	GCGGTCTTAA	ACGCAGACTG	TACGTCTCT	GCAAGATCTA	AGACCAACAC	AGGCTCATCC	720
	AGCTGA						

## 1478RP

	GATCATTATG	CATTTTATGA	TATACACTGC	TATCAAAGAC	GACCAGTCGG	TAGTGAATAC	60
	ACACCGGCTG	GCAGACACAA	CCAATGCCGA	GGATGAGGCT	AGTGAGGACG	AGTTAGAGGA	120
	GCTCGTTAGT	AGCATATGCAC	ACAGCGGCGA	TGCTACTAGC	GAGTGAAGAG	GTATTTTACC	180
35	TGACGTTTGG	AATATATAGG	TAGGTGATGA	GCTTTACAAT	ACGTATTCCG	TAACAATGAA	240
	ATGCAGGAAC	TCTCAAGCT	TTTAAGTTT	TGTAAAACG	GTATCAAAAA	CCGTTTTTCC	300
	AGCGCTGTCT	GCGTAAATGA	CCTGGATTAT	CGCATTGCAA	TAGTTGCTGC	TCCTCAAGGT	360
	CAGATCTATG	ACGCCTTTTG	CGCCGAGGCT	GGTACGCAGT	TCGCTGCGTG	GCATGCGGAG	420
	GATCTTGTCA	AATAGGCCTA	TCTGTTTGT	TAGGCTAGCG	ATGTTTCGCCT	CACGAGCATG	480
	GAGCGTATCG	GGCTCGCTTC	GTTGTGGAAG	CAGCTCGATG	GACGAACCAG	GAACAATGTT	540
40	CAAGACGCAC	TCCGTAACAA	CTCTTTTAAC	CACCTGTAAG	TAGTTTCTAT	GCCTTATTCT	600
	ACCCAAAACA	GGTCTTAATA	GGAGAAGGTC	ACCATCAGCT	CTATATTTAT	GCTTGAAGT	660
	TGCTGGCTTG	AGGCC					

## 1478UP

	GATCTGAGTA	TCAAGATACC	ATGAGCGATT	CTTGCTCACT	CTTGACGGG	ACTGCCCCGC	60
	TTATCCAAGT	GCAGACAAGA	TGCAACATGC	ATACTGGCAG	ACCAGGCCCT	CTCGATCATC	120
	GAGTTGCTTT	AAGCAACATA	GTAGGAGGCT	TCGAAGGAGG	AGTTCTTCGG	CTACCTATGT	180
	AAGAGATGCA	GCGGATGGTT	ACTGCTGGTC	ACGTGCTAGA	ATCATATACC	ACGGAAGAGT	240
	GGATATGTTG	CTTGCCCTTT	AGATATGGCA	GTTTGGCCAC	CCTACTTGAC	ACAGCTGTAA	300
50	CAACGTTGAC	TAAGGATAAA	CAAGAGCTAC	TGTCAACGGG	CTATCCATAC	AATGACATCT	360
	GATCTAATGG	AGGTGGAATC	GGCCCATACA	CCGGATGTTT	ATAGCGCAAG	CAAGGACAAC	420
	GTTGACAAGT	TTGTGATCT	GCTTCGCCAG	GTCTCCAAGA	CTACTATAAC	ATTGGACTCC	480
	CGCTATGTGT	GGAAGTCTCT	TCCGCGAGCTA	ATGTCTTTGC	GCAAGGAGCT	GCAGCAGCAG	540
	ACCTCACCA	TCCTTATCAC	GCTCCTATAT	CCGGACGACT	CGGCATTCAA	GGTGCCATTG	600
	CTTCGTGTGG	TGAACAGAA	CTCAAAAGCA	GCGTCGAGGA	TGCGGAGGCA	TTCCAGGGCA	660
55	AGTACCCCGC	AGACTTTATC	AGCTGACTGC	TGACGGCAAG	ATTGAC		

## 1479RP

	GATCCGCTTA	CAGTAGCATT	GTCTCCGCAG	GTTCCTGCCC	TCAATTTTAT	CCCGGCCCTC	60
	GAAGAACTCC	AACTCGAAGA	GGAAGTTCGT	GCGGCACTGG	CATAAATTGT	CTATGCCAG	120
5	CCCTTGTTGG	CAGAACGCAT	GCTTGCACTC	TGCAAACTGC	TGCACCTCGA	ATTCCGCGAT	180
	CAAGAGCTGT	AGCTCCACGA	GCGCATCCTT	GGTAAGCCTG	CTGCCTCCGG	AGCGGTCCGG	240
	GCACCGTTTG	TCGATGCATT	CGTTGATCTC	CTCTGTTAGG	TTGCCGTCTG	TCGTCCGCCA	300
	ATTCTCGAAA	AGCGTCGGGC	GCACTATCTC	CCTGCCTGAA	GGCACCTTGT	TCTCCTTGTT	360
	CCGCTCGTCG	TTTTCGTAGG	GCGAGGTGAC	TGATGATGAA	TCATTTCATA	AGCTGTTTTT	420
	ATTCCGGAGG	CTGCGCTTGC	GCTGCACGTT	CACGTCAAAT	TGTTTCAACG	CCCTCTTATA	480
10	AGGTCTTTTC	TCCATTATTA	TAGCACTATG	CCAAGATCCA	GATGTGGCAA	TCTGGGATTA	540
	CTAGACCTGT	TGCGCCAGCA	TCGAGTTCTC	TTATATACAC	TGGCAGTTTG	TGTCTGACAC	600
	AAAGACGTAA	AATTGGGACT	ACGAAAAGGG	AGTCGCCAAA	CAAGTGGCAA	ACGTTGTAAA	660
	AGGATAGTGT	ATATTTATAC	TATTAGTAAT	TATGT			

## 1479UP

	GATCCGGGCA	TTACGGTGCC	CATCTACGAG	GAGGACATTG	TCGGGGACCA	GGGCGGGACG	60
	GACGTAGACG	GGCAGCCGCA	GAAGCTGGGT	TCGTACCGGG	CGCGGGCCGG	GCGCTTCTCG	120
	AACACGCTGT	CCAACCTGCT	TCCCAGTATC	AGCGCGAAGC	TGCACCACAA	CCGGAAGGGC	180
20	GGGACGGGGA	AAGTCGCGCC	GTCTGCTGCG	GACGCGGACG	CGGGAGCCGG	GTCTACCGTG	240
	GTTGCGGGAG	AGATGGCGGG	CAGCATCAGC	CCTCCGCAGG	ACCTACATAA	CGTGGTCAGC	300
	TTCCCGGAGC	CATACGGGCT	TGCACAGCCA	CGCACTTCGA	GCGAATCGTA	TACGTATGGT	360
	TCTGGATACA	GTGGCCACCT	GCAGCCACCA	GTCTCCAACC	CTGCTACCGG	GACTCGGAAT	420
	AATACTGTAT	CTTCGCAGAT	TACTTCGCTT	TCAAGCATGG	GCCAGCTGGG	AACCCCCAGC	480
	ACGAGCAACA	TCTGGACCAA	CAATGGCTCA	AGCCCGGCAG	ATCCAATCAG	CAACATGCTC	540
25	ACGACGCAGT	TCAACCCGAT	CCCCCTCCCC	GACTTTGGCC	AGTCGAACCTA	CTACGACGTA	600
	ATCACGCAGC	AGCAGCCTCC	GCAGTCGACG	AACTCACTGA	ATGTGCCCTC	CGGGGGTAAT	660
	ATTTCTGGGA	AAAACGTACT	CGTTCTCAAT	CTAATGCTTC	TAGCATATAC	GCAGAT	

## 1480RP

	GATCCTCTGA	GGCGAGCCCT	ATCCCAAGTT	TATTCCAACCT	TCTTGCCGAA	AGGTAACAAA	60
	CCGTTTATTT	ACATGAGTTT	ACACATAACA	CCGGAGAATG	TTGATGTTAA	TGTGCATCCT	120
	ACAAAGCGTG	AAGTACGATT	TTTGTATGAA	GAAGAGCTAA	TAGAGCGCAT	TGGTAATTTG	180
	CTCCATGAGC	GGTTATCTCA	GCTGGATACT	TCGCGAACTT	TTAAACCGGG	CTCTTTGACA	240
	CCTGGGAAAC	ATAGTTCAAC	TGTGTCTCTC	GCATTCCGGC	AATCAGCGAC	CCCCGCAAGT	300
35	ACACAACCAA	AGGCCAAAAC	TGCAGAAAAC	ATGCTTGTCA	GGAACTGATG	TAGCCAAGCT	360
	AAAATTACTA	ATTATGTCTAG	AGCAAGTCAA	AGCTCTACCA	GCTCATCCTT	TTCCACTTCT	420
	TTAAGAAAGA	AATCACATGC	GGCAGCAAAGT	GATGAACTTG	GCAGCATTTG	CGAGGACTCC	480
	CAAGATACAG	CAACATCGAT	GACAACCTCT	ACACAAGAGC	CTAATCATAC	CAAGTCTAGA	540
	GCCATTTTAA	CCTTATTGAA	TAATGAGTAT	GAAGTCGTAC	AGCGGGAAAG	AACGGAAGTA	600
	AATCTCACCA	GCATCAAAAC	TCTAAAGCAG	GAAGTAGACG	AAGATATGCA	TAAGGGAATT	660
40	AACAAGTGTC	TTTGCAGATA	TGACCTATGT	TGGTGTCTGT	GATGCAACAA	GGCGACTTGC	720
	ATCTATACAG	CATGGTTTAA	AGTTATTTT				

## 1480UP

	GATCGCGTCA	TGGGATACAT	AAACCACGGA	ATCAATGAAA	AGCTCGCTTA	CGAACAGTTT	60
	GGATCTGTAC	CGGAGAAGGG	CTACTATATT	CCTCCCACAA	TATTTCTGGA	CGTTCCTCAG	120
	AGCTCGAGAC	TCTGCCGTGA	AGAGATATTC	GGCCCTGTGG	CCGTAGTTGC	GAAATTCAG	180
	GACTACGATG	AAGCTATTCT	TTACGCTAAT	GACACTAACT	ATGGGCTGGC	ATCCTGCGTT	240
	TTCATGAAA	ACATACGCGT	TGCGCACCGC	TTTGTCCGTG	ATGTCCAATC	TGGCACTGTG	300
	TGGGTAAATT	CCTCTAATGA	TGAGGAGGTG	GGAGTGCCCT	TTGGCGGGTT	CAAGATGAGC	360
50	GGTATCGGAA	GGGAGCTGGG	GAAGGCAGGC	CTGCAAACTT	ACCTCCAGAC	TAAAGCAGTA	420
	CACCTGAACT	TTGCTTAGAT	AGAGCAACTC	ATATATTAGA	ATCACTTCAT	ACATCAACTA	480
	TATATCATTA	TGTATATGAC	TATGCCAGAG	GTGTAGTGGA	ACCACTATTT	ATCACGTGAT	540
	AGGCGTTGCG	CGGTCAATCC	GCCAGTACCT	GCGTTGCAGA	ACGCGGGCGA	CACATTGAGC	600
	AGGTGCTATA	TACAGTTGTC	GAGGACAGTA	TGGCACGCAG	TACCATTATA	GCAAGTAAGC	660
55	CGTGTGCTGT	TTGCATAAAG	CGTAAGGTCA	AGTGCGACCG	GCTGGTTCCC	TGCACGAACT	720

GTGTCAA

## 1482RP

	GATCCATTCTG	TTAATATGGA	TTGTCTACAG	TGAGAGCAAA	GAGGGCGGGG	GATTTAAAGC	60
	ATGGTGGGGC	GACGCCTATT	TTAAATGGGG	GTGTGTTGCA	ACGGTMTTGG	CCGGGCTTCT	120
5	TGTCCTGCAT	AGTGAAAAGT	TCATTCGCCA	AAGAACGTAC	GAATTCCTTC	TGATACTGCA	180
	CAAGCTCTTC	AACATTGTCT	TTATTTGTATG	CATGTATATG	CACATCAAAA	CGCTGGGATG	240
	GCACGGCTGG	GTCTGGTCTGA	TGGTTGCCAT	CTACTGCTTC	GAGCGTGTGG	CCCGGATAGC	300
	TCGCATTGTA	CTTGCTGGAG	GCATCAAGAA	GGCCACATTA	ACAGATGTTG	GGGATCGCGT	360
	GCTCAAGATG	ACAGTGGAGA	AGCCAAAGCA	TTTCAAATAT	TACCCGGGGG	CTTATGTTTT	420
	CGTTTATTTT	ATTAGTGGGA	AGGATGCTTG	GTTCTATCCA	TTCCAGTCGC	ACCCGTTTAC	480
10	CGTCCTTAAT	ACACCCAAGA	TCGATGGCGA	CAACCTGGTG	ATTTATTTCA	AAGTGCACAA	540
	GGGCGTGACG	CAGCAGCTGC	TAAACAGGAT	CTTCTATCC	GGGAAAGAGT	CCATCGAATA	600
	CAAGGTGCTT	CTAGAAGGGC	CCTATGGAAA	CACCATTCGG	CGGCTTGCTG	CTCCTGACCG	660
	GCGCTACGTG	GGCGCCAGCG	CAGGTCCTGG	CGTA			

## 15 1482UP

	GATCGCGCGG	TTCGGCGCGG	TGGCGCCAAA	GCTGAACCGG	TCCGCGCCGA	AGGATGCGAT	60
	GTGGCGGCTG	CGGAATTACT	CGATGAAGTG	CAATGAGGCC	AACGATGTGT	ATCTGCTGCT	120
	GAACGGGTCC	AGCCACGTAG	CCTGCGACGT	GAGCGACACA	CTTCTCGATT	GGTTGGCCAG	180
20	CACCGAGGAT	GAGCCGGTGA	TGGAGCTGGT	GCTGCGAGAG	TGGCTCGACG	TGAACCCGGC	240
	GCTGGAGTTC	CGCGTGTTTG	TACGAGGTGG	GGAGGTCTTG	GGCGCGTGCC	AGCGGGACCT	300
	GAACTACTAT	GACTACCTGA	AGCCGCTGGA	GGAGAAGCTG	AGGACGGCCA	TTGAAGACTT	360
	CGTGCACGAC	GTGATGCTGC	AGCGGCTCCC	GGACGACACC	TTTGTTCGGG	ACGTGTACAT	420
	CCCGCGGCCG	TTCAAAAGG	TCTGGCTGAT	CGACGTGAAC	CCGTTCGCGC	GGGAGACGGA	480
	CCCGCTGCTG	TTTTTCATGA	ACGAGCTGTG	CACCTGAAGC	CCAACGCCGA	AGGGCACC GG	540
	AGCTGCGCCT	GGTTGCGGAA	AACTACATCG	GTGCTTCGCG	GGAAAACAAC	ATCGGTGCGT	600
25	TCGCAGCGAA	AGGAGCACTC	GGAACACCAG	GTACCTCTGG	ACGTGGTCTGA	GGCAGGGCTC	660
	AATCCGCAAA	GCATGCAGAA	GCTGGTTGAG	A			

## 1483RP

	GATCCAAAAA	ACCTCTWAAG	GTACAGTCTC	TAATTGCTTC	CATSTCTTTT	TGAACATACA	60
5	TGGACCATGC	ATCCTCGTTC	TTGTTACGGA	CAGAATCCTG	YAATGCAGCA	ATGGCACTTG	120
	GCTCGTTGAC	GTGCTTATAA	CCACCATCCC	TCCAATGGTA	TTCCGCGGCT	TCAGGCAAGT	180
	TGACAGATCT	CTTAATCKTA	AACCTCGATG	GATAMCCCG	CTCGTGCAAT	GAAAAGGCGT	240
	CTTGSAGCAAT	GTATTCAAAG	GTAACACCCT	TAATTCTAGA	AGCGGTTCCT	GCAAAACACA	300
	AATCAATCAC	TGAGTTATCA	ATACCTAAAG	CTTCAAATAT	CTGCGCTCCC	TTGTAAGATG	360
	CCAGAGTAGA	GATACCCATC	TTCGACATGA	CTTTTAGTAT	ACCGCCGTCA	ATTGCTTCCT	420
10	TGTAATTATG	CAACAGTTGC	TCATCTGTAA	TATCAGAGTA	GTCATCGTTA	ACATTCCGAA	480
	CTAAACCTTC	GTTATTCAAT	CTGACCAGGG	TTTCCATCGC	TAAGTAAGGG	AAAATACCGT	540
	CACACCCATA	GCCAAGAAGA	ACACAGAACT	GGTGAAC TTC	G		

## 1483UP

15	GATCATCAGC	CCCGCTGCTC	CGCCGCAGTA	ACGGCTCCAC	GTCGTAGTCT	GGCGTCCCTG	60
	CTAGTCCGTG	GCTCATCGAG	AGGTCTCTTT	CCTCAGGCTC	GGAGTTGGCC	ACGGAGGCAC	120
	TTGAAAGACT	CTGTCTTCGA	TTCAATCCCC	CCGCCCCGTA	TTCCCTCGCCC	TCGTGGCGTG	180
	GCTTGGTGAG	GCCCTCCCGC	TGCAGATCTT	CAACGTCATC	CTTCAGCTCC	TGGAAGTTGG	240
20	CAAGAATTCC	GGTTTCCTGA	GAGACATAGA	ATTTGTCAAT	TCCGCTCAGC	TCCTTATCCA	300
	GCGCCGCAAT	GAATCTTTCG	ATGTAGCTCT	GTGCAAGCGG	CACCCGCTCG	GGGTCTCTGT	360
	CAAACGTCTC	ATGCTGGTAC	AGCTTGTCTT	TCTGCAAGTG	GTACACGAGC	TTCTTCAACT	420
	GCGAGTACGC	GATATACTTC	GACGAACACT	CAGGGACCGC	GTTGAATTGC	AGCGAATGTG	480
	AGAACTTCAT	CTTGGCTTCT	ATCGCCTAAC	GGCCCTGGTC	CGTCGCGATA	CAGGTCTGTC	540
	TCATTGAAAG	TACGCAGCGC	AGGCATAGGT	TTAATTCCAG	GCTCCCAGGA	GATTTTCGTG	600
25	CAAGAGGACG	TTTTAATTCT	CATTATATCA	CGTGCCCTGG	CTATATTTAT	AAAGTTGCCT	660
	CTAACGGG						

## 1484RP

30	GATCCTCTTC	TATAACTCAA	TTAACAATGT	TTCTCTCTGT	GGAGTCGTTT	CTGCATCTTC	60
	CGTAACCCTT	TCATTCTGAG	GTGTAGCCAT	TTTTATCTTC	TGCGCTGGAA	CACTCGGGAA	120
	TTCAAATTGA	GTTATTGGCA	CCTGTGCCTC	CTTCTCCTTG	TCCGGTATAC	TTTCTTCAGG	180
	AGGATAAAGA	GGCTCCGATG	GTGATGATAG	CAGTGTTTTC	TTAATATCCG	GTTCTGAGAC	240
	CTGCGGCTCA	AAGCCAGTTA	CTGATTGCGA	CTGGCGATTG	TCCATCGGCG	AACCTTGTGT	300
	GGTATGTAGG	ATTGCTGGAG	TGAGTTCTGC	AGCGTTGGAA	GAGCTCCTGG	CATAGCTACG	360
35	ATATGTTGGC	TCAGGTTGCG	TCCTCTCGTA	CGGAACAGTG	TTGGCTGGAG	AGGACTCTGG	420
	TTGTCCGTGC	ATTTGATAAG	TGTATGGATC	AGAAGGTAAG	TGTGGCATGG	AATATGTTG	480
	CGAAAGATTA	ATATTCTCTA	ATTGTCTCTC	TAACATGGTG	TCATAAATGC	TCATTATATC	540
	CGAAATTTTG	GCATTCAATG	CTACCAAGGT	ATTATATTTG	TGAAACGTAT	CGTTAAGGGA	600
	ATGGTTTAAAC	CGAGGCCGAG	TTCCAAGGAC	CTTCTGGTAT	AGCATCTGCA	GCTGTGTATC	660
40	CTCTAACACG	GCATTCAATTG	GCTGACCCCT	CCTCTTCTCT	CACTAGG		

## 1484UP

45	GATCTCGGAG	AACGTGCTAC	AACACTCGTG	CCGGGTCAAG	CCGGACCCGA	AGCTGATCGA	60
	CCAGCAGCCG	GAGATGAACC	CCCAGCACAC	GCGGACTGCG	ATCGTGAAC	TTGCGTTCGA	120
	GCTGGCGCAG	AAGACGCGGG	TGACGAACGG	GATCTTTTTT	CACGCGGTGC	GGTTGTACGA	180
	CCGTTACTGC	TCGAAGCGCG	TGGTGCTACG	GGACCAGGCG	AAGCTGGTGA	TTGCGACCTG	240
	CCTGTGGCTG	GCGGCGAAAA	CGTGGGGGGG	GTGCAACCAC	ATCATCAACA	ACGTGACGGT	300
	GCTTACGGGT	GGGCGCTTCT	ACGGGCCCAA	CCCGCGGGCG	CGCATCCCGC	GTCTGTCCGA	360
	GCTGGTGAC	TACTGCGGGG	GGTCGAACGT	GTTTGACGAG	TCGATGTTCA	CGCAGATGGA	420
50	GCGCCACATC	CTGGACACGC	TGAGCTGGGA	CGTGACGAG	CCGATGGTGA	ACGACTACGT	480
	GCTCAACGTG	GACGAGAACT	GTTTGATACA	GTACGAGCTA	TACAAAAGGC	AGCTGGAGCA	540
	CAATCGGCAG	TACGCCAACA	AGCGCAACTC	GCAGGACAGC	AACGCGACCG	AGGAGGACGT	600
	GTCGAGGAG	GACGAGGACC	TGGATAACAA	GATCCAGTTA	ATCAACATCA	AGAAGTTTCT	660
	GATAGACCTG	GCCGTCTGGC	AGTACGACCT	CTTGAAGTAT	GAGGTATTCC	GAGCTA	

## 1485RP

	GATCCCCGCG	TTATTAGCAC	GGTGCCTTAA	CCAACTGGGC	CAAGGAACCA	ATTACACTTA	60
5	AGATGCTATT	TGCAGATATT	TGTAGTCCAC	TCAAGTCAAC	ACGGGCATAT	TTTACTTTCT	120
	AATTCCTAAA	TTCTTAACTC	TAAGCCAAATC	TAAGTAGTTT	ATCCTATCAT	CACTTGATCC	180
	TTGCGTTTGT	TTGGTCTATA	ACCTTTAATT	GGGTAGTGCT	TATGGAAATA	TATATAATGA	240
	GATATTACAT	GGGTCCCATATA	TAACTTCCGT	ATGAGAGTTT	GGCCGAGTGG	TTTAAGGCGT	300
	CAGATTTAGG	TTATTCTCCT	AAAATCTCTG	ATATCTACGG	ATTCGCGGGT	TCGAATCCCG	360
	TAGCTCTCAT	TATTTTTTGT	ATATTGTCTT	TCTCAGGCAT	GTGACATTTT	GCATCATAAT	420
10	CATACCGAAG	ATATGGCTCC	CACCGTGACC	TGATACATTC	TCGCATCTGA	AGGCATGCAA	480
	TTTAATGCAA	CTGTGGCTGC	AGATGCTCTA	GGTAGGAACT	AGCACAACAT	CTAACAACATA	540
	GCCTGCCATA	TACAGCGCAA	TGACAGCGTC	TGAGTCGTTG	TGGCACCAGT	CATAAGCCAA	600
	TTCTGATTGT	CTGAAGACAG	GCTATGAGTC	TCCCACAGTC	CTCCTTGCTG	TCCCATACGC	660
	ATATAAATAC	CCTTAAAACT	CAATTAGCCG	GTATTTTATT	TGAGCTGCAG	AAGGTATCTT	720
	AACTCAGGTA	TAATATACTG	TAATGGGG				

## 1485UP

	GATCGGAGGT	AGTGTTTTTCG	GTGGGCACGG	AGCTGTAGCA	CGCGGGGTCC	AAGAGCGGCA	60
20	TTGTGCTGTG	TATGTTGGTG	ATGACCTCGA	TGAGCTGCTT	GCGGAGGTGC	TCCACGTAAT	120
	CTTCGGTGCG	GAGCCACAT	TCCTTCGGGT	CGCGGAAAT	GGTTGCCAAG	TACTCGAGCT	180
	GCTGCGAGAC	CTTCTTGTAT	TCTAGCTCGC	GGTTCAAGCA	GACGATGGCG	TTGCGCTGAA	240
	GGATCGTGAG	CTCGTCGAGC	ACGTCAACGA	GCTCGTCGAA	TTGTGGCACC	GCGCTCAGCG	300
	CGCCGTCGAT	CGCCTTAACA	AAGGCGCGCC	GGGCCCTTCAG	GGCCTGTCCA	CTAAAGAGAT	360
	CACTGCGCTC	GAAAATGCTG	ATTGCCTCGC	GCATGTACGG	CACAAGCTGG	CGCGACACGA	420
25	ACAGATAGCT	CATGTGCCGG	GAGTTCGACG	TCACGCTAAC	TGCCGAGTGC	TTGGTTGAGT	480
	GGCTGAAGGG	CCTACTGCCG	CGGTAGGGCG	ACCCGAGAAA	TGCGTCATCA	CCTCGTCTTC	540
	ATCTGGCTTG	AGATACAAAT	CCGAAAGCGG	CACGTTGCCT	GTCATCGCAG	AGTTGTTTGA	600
	CAAGAGCAGC	TCGTCTAGTC	GCTGCTGGAG	CTGGCCCACT	TTGCTTTTGA	GTAGTTCCAC	660
	TTCACTGCCC	TTTTTCGGATA	GCATGAGCTG	CAAGTGGCAG	TTCTCGTTTT	GCAACGCCAG	720
	CACCTCATCG	GGCGCGGTAC	CGCTGCTCTT	GCAGA			

## 1486RP

	GATCCTTCTT	GTACATTTCT	GATTTTAAACA	ATGTCTTCAT	AGCGTATATT	TTACCGGTAT	60
35	CTTTCTTCTG	CACCAGACGG	ACCTCACCAG	ATGCACCCTT	TCCTATGACT	TTAACAGTGT	120
	GGAAATCTTC	CAGGGATAGC	CGTGTCTTAC	GCAAGCGCAG	AAACTGCGAC	TCCTTTTAC	180
	CCAGTGAAGA	AAGCTGTCTG	TTCTTTCTCT	CTTCAGACCA	GCCATGAGAT	AATAGCTGGG	240
	ATTCAAGTTC	CACGCGTCTT	TGGTTGCGCT	CAATGGCATG	ATTGACAGAT	GATTGGTAGA	300
	AATTCTCGAC	TTTCAGCTTC	ACTGCAGCCG	CTTTTCTTGT	TGTGGATTG	CTCAGTAGCT	360
	CTGGACGTCT	CTCGAAGTAC	ATATAGTTCC	CCACTCCCGA	GGTTTGCCGT	TGGCCCCAT	420
40	TGGGCGATTG	TGGAAGTGAA	GAGCACTGCA	GGGACTGACG	GGATAGCATA	GCGCCCTGCG	480
	AGCTCTGGTT	TCCCCTAGAC	GTCTGATCGC	CAAGGCTTCC	GTCTAGTAGT	CCAGGTAGAG	540
	CTGCAGGCTG	TAAAGGGGAC	TCCGACCCCC	CAAACGTGTT	ATACGCAGAG	GAAGCAGGCT	600
	GCTGCCCCACT	GTAGTCCGAG	CTGTTGGAGT	AGTGTCTTGG	TGAAGAATGG	CCGGGGGCAA	660
	GAGTAGTGTC	GTTACAGTTC	CGTAAAAGAG	TTGTTGTTCT	GGCTGTAAAT	GCTGGTCGCC	720
	GTAGGCGGG						

## 1486UP

	GATCAAAACA	GCATGTCTAA	GTCTGTTGCG	CGCTGCCCCG	AGTGCCACAC	GGAACTGCGT	60
50	AAGTGCCCTCA	TACAGCAGAA	CTACAGCATC	GTGATTTGCC	CGAACGAGCA	GTGCATGTAT	120
	CCGTTCAATG	AGGCCGAGGT	GATCCAGCAC	CTGGTGACAG	CAAGTGACAA	GGAAATCCTG	180
	GAGGTGCAAC	AGGTGCGGCT	GAAAAACGAT	AATATCACAG	GCAGCGGAGG	CGCGCTCATG	240
	GAATAAGGAA	CCAACCGTGT	GCTATATACG	TGTACTGTCT	ATGTTAAGTA	GGTCTCGTGC	300
	GCCGCGAGCC	CTGCGTGGCT	AAAGCTTTAG	ATTGGAGTTG	TACATGATGT	CGCCATCGAC	360
	GCTGATGCTG	ACACTGAACT	CAAGGTCTTC	GTCGGTGGAT	ATGTCCCACG	TTTTATATAT	420
	CATCATCAAC	GCGAACACAT	TGCAAAATGCT	GCCGATGAAC	AACCCGTCGA	GGTAGTGCTT	480
55	GACGCCCTCG	CAGATCTCGT	ACGAGATGGT	ATACATCAAC	ACCTGCCCCAG	TAGTTATAAA	540
	AATGACACCC	AAAATGGTCG	ACCCTGTCAAT	CCAGAAGTTG	GAGAGCACGA	AGATGGAGAC	600

CACGAGCTGG CACACCGAGT ACATTAGGAA CGCGAGGCCA TTGAGGCCGT ACATTACAAC  
GAAAAGGCCG TCGTGTTTGT TTTCATGTCT GGGTGGTGCT GAATCCAATT TGGTGAAGG

660

## 1487RP

GATCGAGCGC GAGCCCATCA ACAACGAGGA GTTTGCCTAC CAGCAGGAGC TGATACGAAA 60  
GCGGGACGAG GAGATAGCCA ACATCGAGCG TGGTATCGTT GAACTCAACG AGGTCTTCCA 120  
AGACTTGGGG TCCATCGTGC AGCAGCAGAG CGAGCTGGTA GACCACATAG AAAACAACAT 180  
ATACACTGCG GTAACCAGCA CGAACCATGC ATCTAACGAA CTGTGCGCG CACTGAGATA 240  
CCAGCGGCGT TCCAACAGGT GGTGCCTATA TCTGCTTCTC GCTCTGCTGG CATTGCTCTT 300  
CCTGATCGGG GTGACAGTGC TTTAGAACAT CTCAACTAGT CTACTATGTA ACGCTTTAAT 360  
ATACTACTGG CTGACCTACT CCTCCCGCAG TTCCACACAG TTCACGCAGC CGTCATCGCC 420  
GCCGGTCACC AAAAGAACGC GCCCGTCTAA CGCCAGCCAT TTCACCACAT TGATCTCGTA 480  
GACCGTGTGC GCGCAATCTA CGCGGGCTAC CACTTCCCAC CGGCCAGCCT GTACCTCTTT 540  
GTATACCGCC AACACACCAT CCGAGCCAAC GCTCGCGATA AGCCCGTCCG CGCTCCAAC 600  
TACGCTGTAC ACAGCCCGCG TATGCACGGC CGGCAGGACC GTCTCTTGGA TCCACTCTTT 660  
GTCGAAGACG TCGGCGTCTG CAGTGAGGCA CCGCCAGATG CGC

## 1487UP

GATCCCAATA CTGGGACTTT ACTAATACCA GCCATGCGGG CAGCTCTGCA GCAGCTGGTA 60  
ATGACAAGGA GGACAAGAAG AACAAATACT GGAACGCAGA CGCCGAGTAT CTGATCGAAG 120  
AGGTGAAGAA AAACAAAAG AGTGTAGTAA ACTACCTTGA ATCGAAGACG AACGACGAAA 180  
TGACCCGCAA GGGTCTGATC CGGAACCTGC AACGATTTGC AAAGACAATT CTAATGAAGG 240  
AAGGGTTTGA AAACCTGGAG GATATCGTCA CGCTTTCTCA TTTGGAAAAT AGACTGCTGG 300  
TAGCCCTAAA ACTTAAACGAC ACAATGAAT TTACCAAATT ATTGAAAGTC TATTGCATCA 360  
GCCTAGCAGA AATGGGCTTC AAAAATAGAT TGGATGATGT GCTGAGCTGG CTGTATAACG 420  
ATGGAGAATA CAAGGTGGC ACAATAGCTA ACGAGAAGCG GGAGGAACTG CTGAAGCAGA 480  
TATTGGTTGC ATGTGCTGAT ATCCGGCAGG TCCAAAGAGT GACAACCAGT TACGCATCTG 540  
CTCTTGGTCT TCTTGATGTA TCTTTATAAT TATTGCTAGT CTATAGACAA AGTTGGGAAT 600  
CTGAATATAA CT

## 1488RP

GATCAACAAA TGATTTTCCT ATTTTCCGCG CACCGATCAA CGAGATATCA TAGGAATCAA 60  
TGTTCGAGGC AAATCCCTCA CCGAGTATGA AGCTCTGGTA TGCTGTTGGC GTTGTTCCTT 120  
TCATTAACTG CCGGTCCCTG GGCAGTTCCC TTAAGTTTGG ATGATCGAGA TATCCACAAT 180  
TTGGCTCATT CATCGTCTCC AATCCAATGA TGCAGTTTTC TTGGAACAAC TCAGGCGCGT 240  
TGTCCTGAAT GTACTTGTAG AACGTCATTA CGGCTTTCAA GAAGTGCCCC TGGAGGTAGT 300  
CTTGAATATT TCTACCATTA ATTACACATT TAGGGGCAAA TAACTTGCCG CTAATAAAGA 360  
GAGTGAACAT AGTCTGGCAG GCTAGGCGGT AATAGTTTGT GGACCAAATC ATTTCTGGAT 420  
ACTGTGCTTT TTCCGCCTGC GTCTCTGAAT CGATATAGTA GTTGTGCAAT ATGGCAGCCT 480  
CAGTAGCTAG GAACCTCTTC GGCTGAAAGC CTGCGCAATG CAACGTCCAT AATGGCGCTC 540  
CTGATCCCCC AGAAAAGCGA GACCACAGT CCTGGTGGGG GTCTAGGTAT ACGTACATGC 600  
CGCCCGCCTC CTTGATCTTT TTAAGCACCA TCACCGTGTA CTTCATGTAT TCCTCATCGT 660  
ATATCCCTGG GCCGCCATGC TCCAAGGCCT CCCAGGTGAA CAAATAACGG ATACA

## 1488UP

GATCTCGTTT AAGCTGCTGG TGAAGTTTGC GAAGGGGTAT GAGCTTTCAC GACGCGAAAC 60  
AAACCAGCTG AAGCGGTCTA TGGGCGATGT CTTCGGGTG GTGCCCTTT CTGCCTTCCT 120  
GATTATTCCG TTTGCAGAGT TGTGCTGCG CTTCGCGCTT AAGCTTTTCC CCAACATGCT 180  
GCCATCCACA TATGTTTCTG GGACGGAGAG ACAACAGAAG AGAGTTAAGC TAGAGGAGGT 240  
GCGGCGCAAG ACGTCCAAC TTTTGCAGGA GACACTAGAG GAGTCCTCAT TGATCAATTA 300  
TAACTCGGTA GAAGGTTTCA AGAAGCGCAA AAAGTTTCTG AGCTTCTTCC AGAAGGTGAA 360  
CTCCCTAAG GATGGCAAGA CCAGTGTITT TACCCATGAA GAGATTTTGT CCATCTCCAA 420  
AATGTTCAAG AACGACATG TGCTAGACAA TCTCTCCAGG CCGCAATTGG TTGCCATGGC 480  
GAAGTATATG TCCTTGCGGC CTTTTGGCAC TGACAACATG CTTAGGTACC AAATCCGTTA 540  
TAAATTGAAG AGCATCGTGG AAGACGATAA GAAGATAGAC TACGAAGGTG TTGAGTCACT 600  
GAGTACAGAG GAGCTCTATA GTGCCGCCG TTCGCGCGGG ATCAAAGCCT TCGGTGTTTC 660  
TAGGGAAGAT TTGGTGGAAA AAAT



## 1489RP

	GATCACGCCG	GAGCACGTGC	AATCATTGAA	CGAAAGCCCG	GGGTTGCTTG	CTTTGGCGAT	60
	GGAGAGTCAC	AGGGACCCAA	TTACCGGTGA	GAGTACATTG	GTTGGTTTTC	CCTACGTTGT	120
5	TCCGGGCGGT	CGTTTTAATG	AACTTTACGG	CTGGGACTCA	TACCTAATGG	CTTTGGGTCT	180
	TCTAGACTGT	AACAAAGTGG	ACATAGCACG	TGGGATGGTT	GAGCATTTCA	TCTTTGAGAT	240
	AGAGCATTAC	GGTAAATAT	TGAACGCCAA	TAGGAGCTAC	TACCTCTGTC	GGTCACAACC	300
	CCCGTTCCTA	ACCGACATGG	CTTTGAAGGT	CTTCGAAAAG	TTCGGTGGTG	ACCAAAATCC	360
	TACCGCTGTG	GATTTCTTGA	AAAGAGCATT	CATCGCAGCC	ATTAAGGAAT	ACAAGAGTGT	420
	ATGGATGGCA	GAACCGCGGT	ACGACAAAAC	CACGGGTCTT	TCAATTTATC	ATCCAGATGG	480
10	TATCGGTTTC	CCACCAGAAA	CCGAGCCTGA	CCACTTTGAC	GCAATTTGCC	GGAAATTTGC	540
	GGAAAAGCAC	AATGTAACGA	TTCCGGAGTT	CAGGTGCATG	TACGATGCCG	GCGAAGTACA	600
	CGAGCCCGAA	CTAGATGAGT	TCTTTTGTGA	TGATCGTGCT	GTACGTGAGA	GTGGACATGA	660
	CACCTCTTAC	CGTCTAGAGA	ACGTCTGTGC	TTACTTAGCG	ACGATTGATT	TGAATCGTTA	720
	CTATACAA						

15

## 1489UP

	GATCGTAACA	TTGCCCAATA	GCTTGTTTTAG	CTCGTCATCG	TTTCTGATGG	CTAGCTGTAG	60
	ATGTCCTGGG	ATGATCTTGG	TCTTCTTGTT	GTCTCTGGCG	GCGTTACCGG	CCAACCTCTAG	120
20	GATTTCCGGC	GCCAAGTATT	CTAGCACAGC	GGTTAGGTAC	ACAGGCGCGC	CCGACCCGAT	180
	TCTCTGTGCG	TAGTTGCCCT	TTCTGAGCAA	TCTGTGGACT	CTACCGACAG	GGAAAGTCAA	240
	ACCGGCCTTA	GCCGATCTCG	ACTGCGAAGC	CTTGGCGGCA	GAACCAGCTT	TACCTCCTTT	300
	ACCAGACATT	ATTTGTGTTG	TGTGTGTGTG	TGTGTGTTTA	GTGTGAAC TG	CGTGTGCTAT	360
	GAGAAAACAC	TACGCTGAAA	CTGCTAAATA	ATCCAGACAG	GTCCCCCAC	CGCAAAGGAT	420
	CCACGCTATA	CTTCTCTCTA	CATATTTATA	CTTGTCCTTT	TGCCCTTCTAA	TECTCGATCG	480
25	TACGCGTCTG	ACGCTTCAAC	AGACCTTCAC	TAGACGCTCG	ACCTGTGCGG	GCTGGTTTTT	540
	TCCGATGACA	TGTCCGTGCT	GGTTTTTTTC	CGCTGAAAAG	GAAAGCGCGT	GGCTCCCAGC	600
	ACCAGAGCCG	TACTAGCTCT	TTCCGCGTTG	TGTCCTATGT	GCACGCGAAA	TTTCATAC TG	660
	TAGAGTGTGC	CATCAGCTTC	ACAGAGTACA	ACGGTAGG			

## 1490RP

	GATGACCTTC	CGATACATATG	CGAGCGCTTC	ACGACATCCA	AACTGAAGTC	GTTTCGAGGAC	60
	CTGAGCCGCA	TCCAAACGTA	CGGGTTCCGC	GGAGAGGCAC	TTGCCAGCAT	TTCTCACATT	120
	GCGCGACTAC	ATGTGGTGAC	GAAAACGAAA	GAGAATCAGT	GTGCATGGAA	GGCTGTCTAC	180
35	GAGAAATGGG	TAATGGTGGG	GGAGCCGAAG	CCGACGGCAG	GCAAGGATGG	GACGACAATC	240
	CTCGTACAGG	ACCTCTTCTA	CAATGTGCCG	TCCAGGCTGC	GGGCGCTGCG	ATCTCCAAGC	300
	GAAGAGTTTG	CGAAAATAGT	GGATGTGGTC	GGCAAGTACG	CAATCCATTG	GGATGGTGTG	360
	GGATTTTTCGT	GTAAGAAGTT	TGGCGAAACA	CAGTACGCGT	TAAATGTACG	TGGGACTTCT	420
	TCAAAATCAG	ACAAGATACG	GGCTGTATTT	GGTGCTCCAG	TCGTTGCCAA	TTTAGTTGAG	480
	GTAGATATTT	CTGCAGACCC	TGAGCAGCGT	CTTACATCCA	GTTCCGGGCCA	GATTACAAC T	540
40	CCAGACTTTA	ACAACAAGAA	GTCTATACCT	GCTGTGTTTT	TCATTAATAA	CCGCCTTGTT	600
	TCCTGTGATC	CTCTGAGGCG	AGCCCTATCC	CAAGTTTATC	CAACTTCTTG	CCGAAAGGTA	660
	ACAAACCGTT	TATTTACATG	AGTTTACACA	TAACACCGGA	GAATGTTGAT	GTTAATGTGC	720
	ATCTAC						

## 1490UP

	GATCTCAAAG	ACCCAGTACG	ATCGCGTCAT	GGGATACATA	AACCACGGAA	TCAATGAAAA	60
	GCTCGCTTAC	GAACAGTTTG	GATCTGTACC	GGAGAAGGGC	TACTATATTG	CTCCCACAAT	120
	ATTTCTGGAC	GTTCTCTAGA	GCTCGAGACT	CTGCCGTGAA	GAGATATTCT	GCCCTGTGGC	180
	CGTAGTTGCG	AAATTCAAGG	ACTACGATGA	AGCTATTCTG	TACGCTAATG	ACACTAACTA	240
50	TGGGCTGGCA	TCCTGCGTTT	TCATCGAAAA	CATACGCGTT	GCGCACCGCT	TTGTCCGTGA	300
	TGTTCAATCT	GGGACTGTGT	GGGTTAATTC	CTCTAATGAT	GAGGAGGTGG	GAGTGCCTTT	360
	TGGCGGGTTC	AAGATGAGCG	GTATCGGAAG	GGAGCTGGGG	AAGGCAGGCC	TGCAAACTTA	420
	CCTCCAGACT	AAAGCAGTAC	ACCTGAACTT	TGCTTAGATA	GAGCAACTCA	TATATTAGAA	480
	TCATCTCATA	CATCAACTAT	ATATCATTAT	GTATATGACT	ATGCCAGAGG	TGTAGTGGAA	540
	CCACTATTTA	TCACGTGATA	GGCGTTGCGC	GGTCATCCCG	CCAGTACCTG	CGTTGCAGAA	600
55	CGCGGGCGAC	ACATTTCAGCA	GGTGCTATAT	ACAGTTGTCT	AGGACAGTAT	GGCACGCAGT	660

ACCATTATAG CAAGTAAGCC GTGTGCTGTT TGCATAAAGC GTAAGGTCAA GTGCGACCGG  
CTGGTTCC

720

## 1491RP

GATCATCTCC GAATAGGTCT CGGGCACGAC GGACACAAAG CGCGCGTCCG AGTCACTGCC 60  
GTCCTGCTGG GCGGGTGCGA AGAAGGAGAA GATGAACGAC CCCGACTTCG ACTTGTGCTC 120  
CGACGCCAGC TCCTGGACGA CCGTGTCCAC CTTGACCTGC ACCAGCGTGC CAGGACACGA 180  
CAGAAAGTCG TCCTTATTCT CAGACAGCTT GTTCACAGCT GTAGGCTGGT AGTCCACCAG 240  
CGCGTCCGCC GCCGGCGTGG CCCCCTCTGG TCCACCACGG ATGTGCTCTG TGTACACGAC 300  
CGTCGCGTCC ATGTGCAGGA TCGAGCCGAC CGGCACTGGC GCGCGGAAGG TGGTGGAGTC 360  
CAGCGATACG AACCGCGGCA GAGAGTGCGA GATCGATGAC GCCGCGCAGT ACGCCAGCTC 420  
AAATGTCTGC CGCATCAGGT AACCGCCGAA GATCATGTAC GAGTGTCCGT TCCGGTATTG 480  
CGGCTGCATG AACATCGTCG ACTTCAGGTT CGTGTCTCTG ATCGACACCA CGCCGCGCGG 540  
ACGCGCTCG CCGCGCGTCG CCGCGGACGC GCGCCACAAC CCGTGGATCA TCCGCGACTC 600  
CTCCGCGGTA GCGGGGTTCC TCTCTAGACT CTCGCTCTGC GCCTGTAGCT TCTTCGCGCT 660  
GTTGTGGCTC TCCGCGCGCC GGAACCTCAC CCACTCCTGC TGGTTCTGCG GTAGCA

## 1491UP

GATCTTGAAC AAAAAGTAGT TTGTTATTCT CCAGCTGCGC AGTCTCTTCC AGGGTTTTAC 60  
TTCCGATGCT TATTAATACT GGTTCCTTAG ATGGTTCCTG ACTTTGGCTA TAGGCCATG 120  
GTTCCGCGGA CTTGTGAAGG TATGCATTGA GAGTCCTCTG GGTAGAACGT GTGGTCTCC 180  
CTGTAGTTTT AGCAGCGGGC TTGGCCGGGA CTGGTACATC AGGCTGAGGT AAAATCTCGG 240  
CTGGCGTTGC AGGTTCTATT TCTGTGGGTG GCTCTACACT AGGATCCAAT ACTTGGGCGC 300  
TACTAGTATC GCATTCTGTA ATATCATCTA TGGCCACGAT GACAGAAGTT TCTTCTTCCA 360  
TAGGCTGGGA GCATGCACTA ATCTCGGAAC ATGTGGTAGT ATTATGTAGG TGATCGTCTT 420  
CGAATGTCCC AATCAGCTCC TGGCTGGGAA CGAGTTTGCG CCTTTTGACC TTCAACTCGG 480  
AGTCTTGATG TGGGACTGGC AGTGACGGTA AAGATTTAGG CAGCATGAGC TCCTGTTCTG 540  
TAAAATGCCC GTCCAGTTTC TCTGCTAAAC TTTGGAGGAC ATACTCTTCA TTGTGAAGCA 600  
ATACAGTCCCT CTTATCCGGA GTCACATTCA CGTCTACAAA CTGCGGGGAG AGCTCAAAAT 660  
TTAGAATAAT GACGGGATAC TGGACGTTGT TGAAGCTTCG ATATATGTCA TTGCAACACT 720  
TCAGGACTT

## 1492RP

GATCTACTTC TCCAACAACG ACCTCCTGTG GTCCAATGGC TACCCCGTGA ACCGCTTTGG 60  
CCAGGGCGCG TTCCGCATGC TTATCGAGCG CCTGTACGGC GAGCTCAACG CCGGCTACAG 120  
CCTGGCCCAT ACCACCTAGC GCAAGCCCAA CCGCATTGCC TACGACTATG CTGCCCGCGT 180  
CCTGGGCGCC TGGTCCGGCC TCCAGACCGC ACAGCCGCCC GCCACGGTAT ACATGGTTGG 240  
CGACAACCCC CACAGCGACA TAATAGGCGC ATACAACCTAC GGCTGGCGCA GCTGCTTGGT 300  
GCGTAGCGGC GTCTATCGCG ATGGAGACAC GTTACCATGC CAACCGACCC TCGTCGTGGA 360  
CTCCGTCTTG GACGCCGTAA CCGCCGCTCT CCAGCACTCT TCACATTAACT TTCTATACTT 420  
TTACGTCTTC TATATACCG GCTCGTCCGT CCGCAGATGC CTAGATCTGA ATCTTCGCCA 480  
CCACAGTTTG CTCCTGAGCC AACTTGTCTG CGTTGCGCCG GCGCATATGC TCCTTGACAG 540  
TGCGGAGCCC GCGGCACGTA TGGTTTTCCA TCAGCCGGTG GCGCGAACAG AACTGGCCGT 600  
CACAGAACTG

## 1492UP

GATCATGTTG GTGGCCTCCT GCGTCGGCTG CCGCGTGAAG TTGGGGTTTG ATTCCGCGAC 60  
GAGCGCCTGC GTGAGCCGGT TGATCTGCCG CACGTTCCGC TCGAGCGCCG AGGCCTTGTA 120  
CTCGTCGGCC GACACGTCGT CGTCTAGGGA GAGCTGCTTC GAATTGGAGT TATACTGGAG 180  
CATTTGGTGAT CTGCCTGTCC GCAAGAGTGG TGGAAAGACGT GTTCTTTGGC CTGTTCCGCTG 240  
AACAAAGCAC TCCGTGTTTT TCATGACGCG CCGTGGTCCCA GGAGCGCAGA CCGGAGAAGC 300  
GAGCGTCAGG GCCGCGCGGC AGGGACGCTAG GCGGCTGCTC CCCACTATGT AATGCTGGAT 360  
ATGAAGAACA GAAATACTAG ATAATATATT TGTATTAGAC AGTCGTGCGG ACCGGCAGAG 420  
GGCGGCGTTC ACAAGTCCGC ATCGTCTCTA TCCGGCAACG GCAATGCCGT AGCGCGCTCC 480  
AGTCTCTGCT GGTACTGCTG CATCAACTGC TCGTCCCCCT GCACCTCTGG AGGCGCCTAG 540  
GCAGGCGAGC CAC

## 1493RP

	GATCGAATAA	AGTAGGTTTG	GCGCTGACCG	GCATCACCCG	CGGACGTAGC	GGGAACAAGT	60
	TCCCCGTGTA	AATGTTTTCG	TAGTCGATGA	AGGTATTAGT	ATTTCATCTC	TCCAGCAAAG	120
5	ACAATTCATA	CTGTTGGGCG	GGCCGCGAAG	AGTTACCACT	GTATTCTGCC	AACGCTGCCA	180
	CGCTTCGGCA	ACTAGATTTC	AGTGCCCTTC	GGAGCTCTGA	AACATTATCT	AGGATGTTGA	240
	ACGGATCGAA	AGCGGTGTTC	CGGGGCATAG	CGGACATGGC	AGTTCTCAGA	TTCTGCATAG	300
	AACCGGCATA	TAGAGCCAGT	GCCTCCTGAT	GCTTGCCCTC	CTCTTGGTAA	AGGGGAGCGA	360
	GCCCGCGGCC	TACAAGCTGC	GCACGGTAAA	ACACCTTGAC	AAGCTTCAGA	TATGCAGTGA	420
	GCTCATCGTC	TGAGTAGACA	CCGGGTAGAC	CCATAGCCTC	CTCTGCATGG	GTGATTATGT	480
10	TGTTGATGAC	GTGGTTCAGC	TGCTTGTAAT	TGCTGAAGCG	AGCGGTCTTC	CGGCCTTCCT	540
	GCCATTTCGAC	CCACAGAGGT	TGCAACAGCG	CAACATCGCG	GCCCATCGTC	GCGCACAAGT	600
	AGTTGAATTG	GAGGTATGTG	AGCAATATCT	GGTCGTCTTC	TCCCTCATAG	TGCACACCTT	660
	CCTCTGTCTT	GCGCTCCATT	GACTGCCTCT	GGGCATCAAT	TGCCGCGTTC	CACTTCAGT	

## 1493UP

	GATCATACTT	ATCCACCGGT	CAAGCCAGGT	CTCAATCTTG	ACGATGAGCC	AGCCGGGCGG	60
	CGTCGCCATC	TGGAGCCAGC	GCTCCCCGAA	GCCAATTAGG	TACCCTAGAC	CAAGCCCGAT	120
	TAGGTGGCCG	ACAAAGCTGG	AGCCGGGCAT	TAGCAGCGTG	ACAAGTACCA	GGAACACCAG	180
20	CGGGATATAT	AGGGTCGGCA	TCCTTCAGACT	TGCGAGCTCG	TAGTGGGGGC	GGAAGCCCGC	240
	CTCCTGCACT	GCGAAGTAGC	CACACAGCGT	AAAGCACCAC	CCGCTCGCCC	CGCCTACGTA	300
	AACGTTTGGG	TACAACAACA	TGCCAACTAA	GCAGTACACG	ACGCCCGTCA	CAATGGCCAG	360
	GAGGTTGAGC	GTGATTCCCG	TAAACACCGT	CCCGTGTGAC	GCTTTCGAACA	TGCACAGCGG	420
	CACAAACAGC	GACATCAGAT	TCAACAGCAA	ATGGAAGATT	GACAGGTGCG	CCAGTGGATA	480
	GAGGGAGAGC	CGCGTCAGCT	GCAGCTTCCT	AAGCGCCCCC	GGATCCAACA	GGATCTTCTC	540
	GTTGATTGGG	AACACCCAAT	TCAGCACATA	CACAAGCGTA	AGGGAACACC	GACAAGCCTG	600
25	CAGTAAGAGC	GCCCGGCTTA	TGGACCCCGG	TCCGTAAACAT	CGACTTCCAA	TCCATCTTGC	660
	TCAATCAAAG	TGGCAGTTTG	CTTGGGCGTG	GCAGTGGACT	ATGCCTCGCC	AGTTGCCCAT	720
	CAAAAC						

## 1494RP

	GATCTTCGTT	CGTGAAAACC	TTGCACGTCT	TCATGAGCTC	AAGAATTGCC	TCTGCATCTA	60
	TTCTGTCCGG	TTGGATTCTG	CCTTCCTTAT	AGTCCTGAAT	CATGCGCGCA	AAAGCGCGCG	120
	GCGTCCAGTC	ATGACGGGAT	CGGCCCTTAT	AGGACTTCCC	TGCAAGCCGC	ATGAGGCTCC	180
	GCCAGCCATT	TTCTTCAATA	ATATTGACAA	GTCTTTCGTT	TTCCAACACG	ACCTTGTTTCG	240
35	CGAGACTGTG	GAACGTGTTT	ACGTCTATCT	GCTCAAGTAT	TTCTACCCTT	TCCTCAGCAG	300
	ACCATCGCAA	GTTGCAATCT	GCCTCTTGGA	ATGTCTCCAT	AAGCTTTTCA	TTGATGTTAT	360
	CCACTGCTTT	ATTTGTCAAG	GAGAGGATTA	GTATTTTATT	AGGAGCTACA	ATCCCTTCGT	420
	AAACCAGGTT	GTAGACTTTA	TGCAGTAGTG	TCACGGTCTT	GCCAGACCCA	GGTCCCGCTA	480
	CCACATTGAC	AGTTGTACAA	GGCTCATATG	GATGTGTTAC	TACTCGTGAT	TGGGACGTCG	540
	TCAGTGCTTT	CATTTCATGA	TGATACATGC	TCGAGCGTCG	GCGAAGGAAA	TAAATTTCGTG	600
40	AATTTCCGTT	TTAAGATACT	CAAAAGAGAT	GAGATAACCG	CCCGCAAGGC	GGAGTAGAAT	660
	TACAGCAGCT	ATTGAATATA	TTTAGTTTAT	TTATCTGGCT	AGCTTAACCA	CTAGTGT	

## 1494UP

	GATCCTTTAG	GCCATCCTCT	CCAAATTACC	CGTGCTTGCC	TTCACTAGCT	CAGTCGGAAG	60
	AGCGTCAGTC	TCATAATCTG	AAGGTCGAGA	GTTTCGAACCT	CCCCTGGAGC	AAGTTTTTTG	120
	CTCCGGGAAA	TAAGTATTTG	GAGCTGGACT	GAAGCGCCAA	CCTATGCAGC	TTTGCTGGTG	180
	CGAAGTGTTT	ATTTCATGCT	GCGGACTATG	TCTATATATC	TTGCGCGTCT	TGTTCTTCTG	240
	CTGGCGAAGA	GGAAATTGGAT	TCTTGGGCGT	GGTCTGCAAG	CTCTGCTAGC	TTCTTGCGCG	300
50	GCAGAAGCTG	TTCAAACGCC	TCTTTCCAGT	CATGGTTGTC	AAAGTATCTG	AGCATAGTCT	360
	GGATAACGTG	GGTGGTGGTC	AGCACCTTCC	TGCCGCATAG	CTTGATGTAC	TCTCCTATTG	420
	GTAGGCGACG	AGTAGGAATG	CCCAGTTCTT	TGGCCTTATT	GTAACAGAGA	GCTTTGTGGC	480
	GCTTCTTGTG	CACAATGCCG	CCCCTATAT	ACGTCGTACC	GGGTTCAGC	GTCTCCAGCG	540
	TCTCATCAGT	ATCTGCAGTA	AGGTAAACTG	CGTTTCGTAGT	TGGAAGGGGG	GATTCTGCTG	600
	TGAAAT						

## 1495RP

	GATCGAATTA	GCGGGTTTTTA	ATGAAACATA	AGGAACGAGG	TCTAAATGCG	CAACATCCTT	60
	GAATGCAGTG	CCAAGATGTA	TGCCGTTCTT	GGTAAAGAAA	ATTGTACCAT	CGACATAGTT	120
5	AATGCCACAT	CCGATCACGT	CGTCTCGACC	ATAGGGCTTC	GAGTACGACT	TGAACAAAGA	180
	GCCGTCATTT	ATGTAACCGT	CCGACCCGTT	GTAAATGTAG	ACATCCTTAC	CAGTGCTACT	240
	CTGTTGCGAA	GTTGGCCTGG	AACCCCTCAA	AGGCCCTCTT	AATATGTTGG	AAGTTTGCCG	300
	GTTCAAGGCA	GAAAATTAC	CCGGGTCCCT	CGAAGGTGGA	TCGCTAGTGT	TTGCTTCGCC	360
	AGCATTTGAC	GCGACTTTTG	ACCAGTCCTT	AAATCCAATA	TTGATATTGC	AGGTTTGCCG	420
	TGACTGCGCG	CTGGTCACCG	ATAGTACCTT	AAATTCATAG	TAAAAGATAG	CCACTTTCTT	480
10	ATGATTAATA	CAAGCATTCG	CCCAGGTGGA	AGCCCACTGC	TGCTTCTGGT	TATTAAGTGA	540
	AGTCCGTAGC	CTATTATTTA	CAATAGGGCT	GTTGTCTATG	CCAGAGTAGA	GCTGCCAGTT	600
	GCGGTTAGGC	CGCAAGTTTG	TGAAACCGTC	TGTTGAGACC	AAAACGAGT	TGTTGCGACTG	660
	TGTGGTCCAG	AGGTGGGGCA	AAAGGATACC	TATCGAGGAG	TATACGTCTG	AGAAA	

## 1495UP

	GATCAGCCAA	CAGCTGAGTT	CTGATTTCAT	GAGAGCTATT	AGTAAACTTT	TTGTGTTTAC	60
	GGTGCTGGTC	CTGGGATCGT	TACAGTACTA	CTGTGGACGC	TACGGCGCGT	GCCCCGCGCA	120
	GATTGCAGTG	ATAAGCCATT	ATACGTGGCC	TTGCACGTAC	GCGCCGGCAG	TACGGGATAA	180
20	ATTAGGGAAG	GCCAGCGAGT	GGTACGGGGC	CAATGCGGCT	CCGCATGTGT	CGGTGGCGAG	240
	CGGGTGGATG	CAAGGGAAGG	TGATGCCGCA	CCTGACGAAA	GTATCCCAGT	GGACGGAGAA	300
	GCATGTACAA	CCGCGGATGC	GGCAGGCTGG	CGCGGACGCG	ATAGTAACAG	CGCGCGTGCC	360
	ATGGAATGTC	GTACAGCAGT	ACCAGCGGCG	GCATGTGGTG	CCTCTGACAG	GGCGACTGCT	420
	GGCGAAGTGT	CCGTGTCTCG	AGAGGTGGGC	CGAACAAGCT	GCGCGCGGCT	GGCAGTGGCT	480
	CTGCAAGCAT	GCTCGGGCGC	TACCACAGCA	GTACAGCAGC	AGTATCCTGC	GTTTGTGGCG	540
25	CATATGGGGG	GCATATGGGA	GCCTTTGCAC	GGCGCCTACA	ACCGGATCTA	TCTGGACTTG	600
	GGCCGCCAG	TGCAGGAGAA	GACGTCCGAG	GACSCAGTGC	GGCGCCCGGG	GGGACTCAKT	660
	ACATCACATC	CACTATCACA	ATGACCATGA	CTCGTCTCAT	GAATC		

## 1496RP

	GATCGTTTTT	TGTCAAACCG	CAGTCGGGTT	CAAGGAGTAC	GTTGAATTTA	GCTCTTGCTAT	60
	TCAACAAGTC	TTTCCCAGTT	TCCACAATGT	TGTCGATAAT	GAAGGGTTTA	AAGTCTAGAA	120
	GCTCTTCTTG	CGTGAAGCCG	TTCTGGTGAA	GAATCTTCAG	TTGTTGCTAGT	ACGGTCGATT	180
	TCCCGCTCTC	GCCAGAACCC	AACAACAAAA	CCTTGAGCGC	GCGATTGCTG	GCACTCGGTT	240
	GCCCCATTGA	CCCTGGTCCA	GCCACTGCCG	TTGTCTGCTG	ACTCGTCCCG	GATACCAAGG	300
35	AGCGTTTCCT	GCCGCCCGCT	GTAGCGCCGG	ACGTGCTATG	ACTGGGTGAC	GTCTCAGGTT	360
	TGACTTCTGC	ACCGTAATCT	ACCCTCTTTG	CTCTGTGTTT	TACCTTCTGA	GAAGCACCAT	420
	GTCGTCTCTG	ACGCCGCTTT	TCCGCGTGTC	TTGCTGATCC	CTTGCTCTTC	GACGCGCACA	480
	ACCCCATTTAT	GTCGGGCTCT	ATATCCACCA	GTACTTGGAG	CACCTAGCG	CCTGGCTTTT	540
	TTTGAAATAT	TACCGTCCGG	GCAAAAGCCA	CTTATAGCGC	CTGATCAATG	GATTCCACTG	600
	CTAGAGGCTA	ATTAGGCTGC	CGCTTGTGTC	TTGCGGGGCC	ATCACATTAT	ATTTCATAGCA	660
40	AAGTAGGTGC	CAACAGAAAA	AATCAGCCCC	CCTCCTTTAT	TGATCACGTG	AAGAAATCCA	720
	CATGAACAA	CACGTGAACA	CACATTTGG				

## 1496UP

	GATCGAAGTC	AATGCCAGAC	TATCTCGTTC	TTCTGCATTG	GCGTCCAAGG	CAACAGGATA	60
	CCCCCTTGCC	TATACTGCCG	CTAAGATTGC	TCTTGGGTAT	ACATTACCAG	AGTTGCCTAA	120
	TCCTGTTACC	AAGTCGACGG	TCCGCAACTT	TGAACCTCA	CTGGACTACA	TTGTGGCCAA	180
	GGTTCCAAGA	TGGGATCTCT	CCAAATTTCA	ACACGTGGAT	AAGACTATTG	GGTCTGCCAT	240
	GAAGTCCGTA	GGTGAAGTGA	TGGCGATCGG	CCGGAATTTT	GAGGAAGCTT	TCCAAAAGGC	300
	TTTCCGTCAG	GTTGATCCAT	CTCTACTAGG	TTTCCAGGGC	TCTGACGAAT	TCCGAGACCT	360
50	AGATGAAGCC	TTGCAATTTT	CTACAGATAG	AAGGTGGTTG	GCTGTGGGAG	AAGCGCTAAT	420
	GAACAGAGGT	TACTCTGTGG	AACGTGTACA	CGAGCTTACG	AAAATTGATA	GATTTTTCTT	480
	GCACAAGTGT	ATGAATATTG	TCCGAATGCA	GAAGCAATTA	GAGACCTTAG	GATCAATAAA	540
	TCCGCTAGAC	GAGGTTCTGT	TGCGGAAGGC	TAAAAAGCTC	GGCTTCTGTG	ACAAGCAGAT	600
	TGCACGGGCT	ATTTACAGTG	ACCTCTCTGA	ATTGGATATT	AGAGCGCTCA	GAAAAAGCTT	660
55	TGGCATTTTG	CCATTTGTTA	AACGTATCGA	CACCATGGCG	GCAGAAATTC	CTGCGGTAAC	720

CAACTACTTG TATGTTACCT ATAATGCGGT CAAA

## 1497RP

	GATCATTTTGG	TCCTCTTCGC	CTCTACAAAC	TGTGAATATC	ATACTAGACC	TGAAGTCAGG	60
	TAGGGAGCAA	CCCAACCCCT	CGGTTCGCAGT	AGAGGCTGGC	AAATCCATTA	AAAAGACCGA	120
5	TTCGAATGGG	AACTCTAAAA	TTGAAACTAA	GCAATTTTCAT	GAACCTCTCGA	CAGTTCCCTGG	180
	TCCTTTCCAGT	ATTGACTATT	ATAACCTTAA	GAGAAGGTAT	CGAACTTACA	AATCTCTGAA	240
	AAGGGCGACT	ATTGAAGATA	TATTACATGT	TGTTGTTCGAC	AGAGATCTGG	CGGAGCGCAT	300
	TGTTACTCAT	ATCCAAAGAG	AATCTGAGCT	GCAACAATAT	GAGGAGGATG	GGAGGAATGA	360
	GGTATGAAAT	GTTCCCCATT	TGGATTAAGG	TATCAGGTGG	TCACGATATC	CACTATATGG	420
	TGCTATTAAC	GGCATGCAAA	GTGTAGAATT	AACCTAAAGA	ATATGTTATA	TATATATATT	480
10	ATAAACTACA	AACTAACGGA	CGCAATGAAA	TCTAAGTGTC	GCAAGGTTAG	CCTTAATACC	540
	GGTACTTGGG	TAAAATCTCC	TTTTTCAAAT	GATACAAGCG	TCCCATTTC	AACGCCATGC	600
	CAGAATCACT	GGCTGGATT	ATCATGATTG	TGATTGCGGT	TGCCTCAGTC	GGAAATAAAT	660
	TAGCAATACT	CATTATACCC	TTTCGCGACCT	CCAGCCGCTT	CTCTTGGGTA	GGTTCAAATG	720
	AGGCAATTTG	CATACTCTTT					

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## 1497UP

	GATCCTGTCA	CAGCGGGCGA	CGCCGCAGGC	CGCGTACGGC	GACCTGCAGG	ACGAGGTGAA	60
	GGTAGGAGGG	TCCGAGGCGG	CCTTTGGCGA	TCGGGCGTTG	TTGCGGGCGA	TGGGCGGGCG	120
20	CGCGCCGGAG	GATGGCGACG	AGGGCCACAC	ACTTGGTGCC	GGGGTGGCGC	CCATGGTGAC	180
	GCCGCACCTT	CCGATGGAAC	CCTCGCAGCC	GCACGCGCTG	CCACAGCAGG	CCCCCACTCC	240
	GCACCAGCCA	CAGCAGCCGG	CCCAGAAGCG	AATGCACATG	CTCCAACAGC	TGCACGAAGA	300
	GCAGAAGAAC	TATTCTTACG	TGGACCGCCA	ACCGTCAATT	ATGCAACAGC	AGCCACACAT	360
	GATGCAGCAA	CTGCCGCAAC	AACGGCCTCG	GATGCAGCAA	CTGCCGTTGC	AGGGCCAGTC	420
	CGAGACGCCG	AAGCCCGCAG	GCAGTTCTCC	AATGGTGGTG	CCCGTCAACC	ATAGGCAGCT	480
25	GTTGCAGAAC	CTCGACCCCA	GCATCCAGAA	AAGAGTATCA	CAGGATCTGA	ACAGCAAGCA	540
	GTATGAACTA	TTTGTGAAGT	CTTTTCATGGA	ACATTGTAAG	CGGTGTAATA	TTCCGTTTAA	600
	CCCAACCCTG	AGATAGGCGG	GACGCGGGTG	AACTTATTCA	TTTTATACAT	GTTGGTACAA	660
	AGAATGGGCG	GGGCAGATAA	TATCAGCAGG	CTGCAGCAAT	GGCGCGGCTT	GGCAGAAAAA	720

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## 1499RP

	GATCAGCTTC	ATCGATTACC	CAGAATTCCG	CTTCAACAGC	AACGAGGCCA	CCGAGATGCC	60
	CTTCCGCTAC	GTACTGGACG	CTGCTGGCAG	GCCCATTTCTG	CCATCAGGCA	TGCTAGAGCT	120
5	CATCAAAAAG	GACTCCGAAC	AGAGTCTGGA	TGACCTACTT	TAGGCTCGTT	GAACAACAGC	180
	TTATAGATGA	TGTATATATG	CGCGTCGTCC	GCCAGAGACT	GGCATCGGAA	GCCACGCAAC	240
	CTAAAGTCGA	TAGAACTCTG	TCAACAGAAT	CAGTTCTTTT	CCTCCTTCAG	CATCTCGCCA	300
	AGCAGCTGCT	CGAAATCGAT	ATCATCAGAA	GTGGTTTTTG	CAGGAGCAGC	TACGGCGGGC	360
	TGCTGCGACG	CACGTCCTCT	AGCCTTTGTAC	AATGACACAC	CCCCGAACAG	CGTGAATAGC	420
10	GTGCCAAGCA	CCAAAACATG	AGGCTGAACC	GGCTTTCCAA	AGATGTTGTA	AGCTTGACCC	480
	ATCGCTAATC	ACCGAATCCG	CTGCAGATAT	GGGGTCTGAT	GGTCTGGTGT	GTAGCGGTGT	540
	GCATTTGTGA	GCTCCTATTG	GCGGAGGAGG	CAAGTCGATC	TAGAGGGCTA	CAATGAGGTG	600
	TTCGGGTGTT	TGTCAGGGTA	CGGAGGAGGT	AGCACGTGAT	CGTTCAAATA	TCTGTACCGC	660
	CCCATGAACA	TCTATTCCGT	GCATTGGGTT	TGGAGCACGG	GCGATCATTG	GAGACTAACA	720
	CTCACGAATT	TTGCCTGGCG	GA				

## 1499UP

	GATCGCAATG	GAGAAGGTAA	CGCTGCTACC	GAAGGTTATC	AGTGTTTTGA	ATAAGGCGAA	60
	CCTTGCGAGC	ACAATTTTGG	ACAATAATTT	GCTACAGAGT	GTGCGGATCT	GGCTTGAGCC	120
20	ACTGCCGGAT	GGATCCCTAC	CATCCTTCGA	GATACAGAAG	TCTCTCTTTG	CCGCGATTGA	180
	GAACCTCCCC	ATAAAAACAG	AGCACCTCAA	GGAGAGCGGA	CTGGGGAAGG	TGGTCAATT	240
	TTACACCAAG	TCTAAGCGTG	TAGAACAACA	GCTGGCCCGG	CTAGCTGACC	GGCTGGTTGC	300
	AGAATGGACG	CGCCCTATTA	TCGGCGCTTC	CGATAACTAC	CGGGACAAGC	GTGTCCTGAA	360
	GATGGACTTC	GACGTGGAGA	AGCACCGTAA	GAAAGCGGCA	CTTGATTCTG	CCAAATCTAA	420
	GAAACGGAGA	AAGGCTGCAG	TGGACGAGGA	GAAACACAAG	TCACTCTACG	AGCTTGCCGC	480
25	TGCGAAGCGG	AACAGAGCCG	CAGCGCTGTC	GCAGACAACC	ACCGATTACA	AATACGCACC	540
	AGTCAGCAAT	ATCTCGAACG	TACAGACCGG	GATCCGCACG	GCAGGCGTGG	GCTCCACGCT	600
	CAACAACAAC	GATCTGTACA	AGAGACTCAA	CTCGAGACTT	GCCAAGTCTA	AACGGTCCAA	660
	GTAACCGCTG	TGTACTTCAG	CTAATAGTAT	TATAATAACG	TTTAATGATA	CTGAAA	

## 1500RP

	GATCAGCTAA	TGGCTGCTTG	TCAAAGACCA	AATCCTTCAC	CCCTAGAACT	TTTCCTAGAG	60
	CATCCATTCC	GATAACCTAG	GTCGCTTTGT	GTCCTTAAAG	AATATTGGTT	TAATTTGCTT	120
	TCGCGGACGG	AGTAAAGCGT	TATGTAGCAT	TTTTCAAAAG	AGGCTTAATG	GACACATCCC	180
35	AGGATAGTAT	GAATGAGAAA	GTCCAATTCC	TGGCACCATT	GTGCTAGTTC	TTATATTTAC	240
	TGTTATACAT	CTACTGCAGA	GTCAAGCATA	TATACCAAA	AATTCACCAA	ATACTAGCTC	300
	TTCTAAGTCT	TCAGCTGATG	GATTTCGCGC	AAGGCGCCGC	AGAGCTGCAG	GTAGGTACCC	360
	ACACCTTCCA	AAATCCTCAT	GTCGCTGAAT	CCTATTTCTT	TAATCATCTC	CAGCCGCAGG	420
	GGTTCTTTAA	TCTCTGTCAA	GTTCTTCATG	ACACGGAAAC	ATGTAGTGAT	TATGTCCACC	480
	GCCGAGTACC	TTTGCCCCAC	AATTCGCGTA	AGTAATTGAG	CGACTCATCA	AGAGTAGCAG	540
40	ATAGCAGCAT	TTTCTTGATG	ACCAGGGGAT	GCGGCGAGTC	CACTATCTTA	AAAACGTTGT	600
	CGCCGTTTAC	TAACGTGAAG	CCCGCCACGG	TGCTCTGCAG	ATTGTTGATG	GCCTGCCGCA	660
	TGTCACCTTC	CGCAGTGAAT	ATCAGCGCCT	CCAGACCATC	ATTGGTGTTC	TGTACGTTT	

## 1500UP

	GATCGCGACC	CCCCGCGTCA	CGGCAAGGCC	CGCCAACCGC	GAGGAGGAGA	TCAATGGCTT	60
	TGACCTCGAG	GCGCCGCCCC	AAAAGAAGAC	CAAAATACTA	TAGTAGTACG	TACATTGTAA	120
	TACATGCGCA	AGACTTGCCG	CCAGTTAGCC	GCCCCGCTCC	CAGGTCTTCA	CCAGCGCCGT	180
	GCCGTCCGCA	GACGTGCTCA	GCAGCTGGCG	GCTACCCTCC	TTGTAGACGG	TGTCAATGAC	240
	TGCGCCCGCA	TGCAGAGACG	CCAGCTCGTC	GGACACCACT	ACCTCGCTGG	TCACGTCCAC	300
50	TACGTAGCCG	TACGCCGCAA	CATAGCGTTT	GTCTCTACG	AAAGCGCACC	GTGCCAGGAG	360
	GCGTCCGGTG	TTCCGCGCAG	GGAGGGCAAA	TCCCCGCTTT	AGACGCTGTC	CGGCCTGCTG	420
	GCCGTAAAAG	CTCACACTGT	CATCGAAGCC	CAGCGCACAC	ACCTCCTCTC	CATGCGCGGA	480
	AGTGACACAG	GAGGTACACG	CACCTCCGTG	GCGGTTCTGC	GTCTTCCACA	CTGCGTCCCT	540
	GCTGCGCCGC	TGCTCGTAGG	CTCGTACCAC	TGGCTCAATC	CCCGACGTGT	ATACCCGCCC	600
55	GGCCGAGACC	GGGCAGACGG	CGGCTGATAG	CAGCGGAAAG	TGGTGGCCA	CAAAAGCCGC	660
	CGGG						

## 1501RP

	GATCTATTTA	AATATAACAT	ATTATTTATT	TCTTTTTTTA	AACATTTTAA	ATTTAATTAA	60
	TTATTTATTT	ATTTAATTAA	TTATTTTAT	TAGTTAAGAT	AATTTTATAA	CTTTAATTAG	120
5	AGAGCTAAGG	TACACACCCC	TAATGCTTTC	AGCATTCCTG	TGGTACCACT	CTAATTAAAG	180
	AGTTATTATA	TTAATGATAT	AATATGTAGA	TATTCAGTTT	TGAACTGAAG	ATATATGTCC	240
	CTAAAACATA	TGTTTTACCA	ATTAAACTAT	ATCCACTAAC	TTTTATTATA	TAATTTAATA	300
	ATTAAGAATA	TTTTAAGATT	GAATTAGAGG	AGTATTAAAT	GAATGAATAA	GAGGTGGTGA	360
	ATTTAATATA	AACCTCAATAG	ATGATGATTT	AGTAGTATTC	ATTAAGAAAA	TATTTATTTGA	420
	TTCAATAAAA	TCAGGTAGTT	TTATATAAAT	AATAGATTTA	TTATTAACCT	TATTAGTTAA	480
10	ACCATTTATT	AATTGATCAT	AAATAATATA	AAGGAATAAC	ATTAATGATA	TAATAGTTAT	540
	TATAGAACCA	AATGAAGATA	CTAAATTTCA	ACCTAGGAAT	AGATCAGGAT	AATCAGGAAT	600
	TCTTCTTGGT	ATACCATTAA	TACCTAAGAA	ATGCATAGGG	AAGAAAAATA	TATTAAGACC	660
	TAAGAAAAAT	AATCAGAAAT	GAATTGTGAT	AATTTT			

## 1501UP

	GATCAAAATA	AAATAGAAAT	TAGCTTAATG	GTAGAGCATT	CGTTTTACAC	ACGAATAAAT	60
	TGAGTTCGAT	TTCTCAAAAT	CTAAATAATA	ATTAACAATA	ATTTAAATTT	GGGTAAAAAT	120
	TAATAAATAT	TAACGTATAT	AATAATTATA	TACTTTTATA	AATTACTCAA	TGTTATTAAAT	180
20	AAATTTATTT	CTTATCATTA	ATAATGATGT	ACCTACTCCA	TATAATATAT	ATTTTCAAGA	240
	TTCACTACTA	CCTCATCAAG	AAGGTATTTT	AGAATTACAT	GATAATATTA	TATTCCTATAT	300
	GTTACTTGTT	TTAGGTTTAG	TTTCTTGAAT	AATAATTATT	ATTATTAAAG	ATTATAAAAA	360
	TAATCCTATT	CTTTATAAAT	ATATTAAACA	TGGTCAAATA	ATTGAAATTA	TTTGAACCTAT	420
	TTTACCAGCT	ATTATTTTAT	TAATAATTGC	ATTTCCATCA	TTTATTTTAT	TATATTTTATG	480
	TGATGAAGTT	ATTTCAACCAG	CTATAACTAT	TAAAGTTATT	GGTTTACAAT	GATATTGAAA	540
25	ATATGAATAC	TCAGATTTTA	TTAATGATAA	TGGTGAAACT	ATTGAATATG	AATCTTATAT	600
	AATTCCTGAA	GAATTATTTAG	AAGAAGGTCA	ATTAAGAATG	TTAGATACTG	ATACTAGTAT	660
	TGTTATTCCTG	GTGATACTC	ATGTAAGATT	TATTGTTACA	GCTCTAGATG	TTATTCATGA	720
	TT						

## 1502RP

	GATCGCTCCC	AACCCCTGCT	TGATCTCCAT	ACTCATCTGG	TTTTTCAGGT	AGCGCGGGTG	60
	GTTGAATACG	GACTTGTCGA	AAACGAACAC	ATAAGAGAAT	GACGCCACGA	TCAGGTACAG	120
	CAGCCAGCCA	AACACTGTCTG	TCACCAAAAA	CAGAGACAAG	CTCTGCCGCA	ACAGGCTGTA	180
35	TCGCGGCAGC	ACCGACCCGA	AAGCATGCGG	GCTAACCTCG	AACATAAACG	GTGCATACCC	240
	ATATACCTCC	AGCGGCCTCT	CAAGCGACCT	CCCGAACACG	CGCGTCGCAT	TTACCATCTG	300
	CTCCTTAATC	ATCGCCTGCT	GCCAAGTCCC	GCCCATCTTC	GGCGACAGCG	ATGCTGGCAG	360
	CAGTGTGGCA	TACACATAGT	CGAAGAAGTA	CGAGTCGCAA	AACTCGAGCA	CTAAATCCAT	420
	GGTCGGAGAA	CGCTATAGAC	TAGGAGAAAC	AATTTTAGCT	CTAGGTTGCC	TGCCTTCTAG	480
	CGTGATAACA	GATCCTTGCTA	CAGCTACTAA	AGCCCATCTG	CCGCTCTCCT	CTGGCTTTTT	540
40	GCACTTTTAT	ATGGTCCATC	CCGGCACTGA	CCTAACGTAC	CGGGCTCTAT	ACGACGCTAA	600
	AAAATCAAGT	TACGAATGCA	CTATACGAAT	GCGTTGAGCA	AGGAACGAAT	CCCTTTTGGA	660
	ACGACGATAT	CACGTGAACG	AAGCCGCAAC	GTTCCGGGTGC	CGGGCGCCTA		

## 1502UP

	GATCAAAAAAT	ATTCGACGCA	TTTGCCGCTC	TTTAGTGTAC	TTCCGGTTCAT	TATGGAGATG	60
	GCCAATTTTAC	ATCGGTATTT	TCGCCTTACT	CATAAGAGTA	TACAGTGCCA	ATTTCCGTGA	120
	ATTGAGGCCT	ATAAACATCT	GGTATGTCTT	ATCTTCAGTT	CTCTCTGGGG	ATTCGCCCAT	180
	CACCTGGGATT	CCATTCAGTT	TCAGGCTGCC	AGGAGTTGGA	ACTAAAACGT	GGTTTTTGGA	240
	TCCCTGTGAGA	TCTCTGTTGC	CATCAAGCCG	AAGATAGGCA	GCGGTGCTTT	TGTATGAATA	300
50	TGCGGTTGAG	GATGTCTCAC	TCCAGGTTGG	AAACCTATAT	TATGGTGCAA	TATATATTAA	360
	TGATAAGAGC	TTTCTCTGAC	TAACAGCAGT	AACTCTTAAT	TGAAGTATTT	GTTATTTCCA	420
	ATCTTCATAC	AGTATGTCAC	CCTGTTGTAT	TATAGATTTT	GTTTACGAAT	TGGATCGTGC	480
	TTTCGTGGCT	GCGAGGTCAG	AAGATCGATA	TAATAATATA	TATATTATTA	AATTATGGTA	540
	GGTAGGGAAT	TGCTATTTGT	GTCTAGTACT	CGATGCCTTA	TCTACAACTT	CTAGTTGCAA	600
	CACATGATAT	GCTGTGGACC	AAAACGCTAC	GGCGTTATTG	ATTTTATTCA	AGGTCAAGAT	660
55	CATATATTAG	CGTAATATCT	GTGGAGGTTT	CT			

## 1503RP

	GATCTTCGTA	TACATGTGCG	AAAGCTCCTC	CAAAATCTTT	TCGTCTCCAT	CATGAGAGGC	60
	TGCTACAGCT	TTTGAGCCGA	TAGAATTGGA	AATACCATTG	GAGATTGCTA	TTAGTAGGAA	120
5	GACAATATAA	GTACCATCTG	TCGATGGGGC	AGAGGCTTTA	TCAAGAAGGT	CCATCAGCTT	180
	GTTCTTTGGAT	ACAGCAGTCT	CATTTAATAA	TAATGCCTGC	TCACCACTGG	GCAAAAATTC	240
	AGAAACATTG	AGCAGTTCAG	AGAGTGAGTT	CGACTCAAAG	TTTTCGGTCA	TTGTCTCTAA	300
	CAAGACAAAA	ACAACGTCCT	TCCTGCTCTC	ATGAACATCA	TAAGCCTTGA	AAACCTCGAG	360
	CAAAATAGTA	TTGTCTCTGGA	TCACGTTCAA	AAATACCTCT	AGAATTAATG	CCTTCCTCCA	420
	CAATAAAGTG	TCAGATTTAG	GAGACAGAGT	GTGGATTAAAT	AATGATAAAA	TAACTTCCAA	480
10	TTCCAATTCC	AGCAATGTCA	AATACTGAAC	CTTTATGAGA	AGTGAATAC	ATCTGGCGCT	540
	ACGAACCACA	ATTGCAAAAT	TTTTGGATGA	GGAAATGTAC	CTCAATAGCA	GCGGCACCGC	600
	CTTTGTTTCG	AACAGAAATA	ACAGATCTCG	GTGTGTCAAA	AATAATAATT	CATAGTTCAA	660
	TAAAACCAGT	TCTAGGAGCT	CTAATCCATA	CTCCTCATTT	ATGCAATTGC	TATCCA	

## 1503UP

	GATCTGCGCG	CTTCGAAGGG	AAAGGCGGGC	CCCAATCCCC	AGTCTATGTT	CAAGAGGGCG	60
	AACAGCAGGC	CGTCATGGCA	TTCAATAAGC	GAATGGGCAC	TCGAGCGTTG	GCACATCATG	120
	TGCTGGATAG	CATCATATAC	TACACAGACA	AGGTGGTGTT	GAAGGGGCTT	GGAAATTTGT	180
20	CCGCGAGCTT	ACCTTCCAAG	ACCTCCTCGG	CGACAAGCGT	CAGGGGTCGT	GTAAGGAAAC	240
	GCATTGGTCT	CGAAGGCGCA	AATGATGTCT	TTGTATACCG	CACAAAAGAC	CTGGTATTCG	300
	ATAGTGATGA	AGATATACCC	AGAACCTAAC	TACTTGTGTC	GATATTTCTC	ACACCGCCTG	360
	GTGCGGAACC	GGGGGCATAC	ATTCTGTTTT	CACAAGAGGG	GTTGATGCAT	AAAACGCGCT	420
	TTCAAAAAGTG	GCAAGCGAGA	GCTGCCGACT	GTCGTTGCTT	TTGGTGCGGC	GACTGTAGGC	480
	AATGTGCCAT	CCCGTGCGCC	TTCTTTTACG	CGAGATCCAG	TCTCGCAAGC	CTGGCTGTAA	540
25	CCAGAACACT	CGGCTGAAGC	CCGCGACAGG	TCCCTCGTGG	ACCAGGCAGG	CAGCCTTGCA	600
	TCTGATAGGC	CGGATACTGG	GTATCTGCCA	AGAGAGG			

## 1504RP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTAAATAATA	AATCTATTAA	TTATATAAAA	60
30	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCAATTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAATAA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATAA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATWAT	300
	ATCATTAAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
35	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACTAAT	AAAAATAATT	420
	AATTAAATAA	ATAAATAATT	AATTAAATTT	AAAAATGTTA	AAAAAAGAAA	TAAATAATAT	480
	GTGATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCCTT	ATTATTATCT	TTATTAGTAG	TTTTATTACK	660
	AATAACTTTA	TGATTTAGAG	ATATTGTAGC	TGAACTTACT	TATTTAGG		

## 1504UP

	GATCTTAATT	TAAAATTTTA	ATTAACATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
45	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATGAAAA	TTAGTAAAT	120
	AAATAGAAAA	CCATAAGTTA	ATTGATTCAT	AAAGAAAAAT	GGAATTATTT	GTGGCATCTT	180
	AATTTTTATT	ATTTAATTGA	TTATTATCTA	TTTAACATAA	AACATTTTAA	AATGTTATAA	240
	AATAAATAAG	AAATTACTTA	TAGAATATTT	ATTAAATAGT	ATTTAATTTA	ATTTTAATAT	300
	TAAATATACC	ATTTTTATTA	ATAAATAGAT	TATTAAGTTT	ATTAATATTA	AGTGATATAT	360
	AATTTAATTT	ATATAAATTA	TTTAATTTAC	TTCAATTGATA	TATATAATTA	TTAAATGTAC	420
50	CTTTTCATAAT	ATTTATTTTT	ATTAGTCTAG	TAATATTTCT	ATTTAATAGT	CTACCCTTTA	480
	ATTGGATATT	ACTACCTACT	AAATATTTAC	CTAATAATAT	ATTATTAAGA	ATACTTAAAT	540
	CTAATAATTT	ATTATCTAAA	GTATATAAAT	TAATTAATATC	TTTTTTATTA	TTATTTAAAT	600
	TATTATTAAT	TAGTAAATTA	TATTTATTTA	TTTTAATTAA	CATAATTTTT	GATAATAATA	660
	TACATTATTA	AATGGTAATT	TATTAATAAT	TATCTTTAAT	GATTTAATGA	T	



## 1505RP

	GATCATCTTT	ATACCATGG	CTCCTGTTCC	GTGTGCACCA	ACGTAATCAA	AAGCGTGTGC	60
	CCCCTCGCTA	CGCAGGAAGC	ACTAGAACTA	GCTGAGTAA	GCAACGGTGA	AAGTCGATCC	120
5	CTGATATATA	TACGAAACCA	GAGATACCTT	CATCACAAGG	ATCTTGTTCC	TCGTGGCCCA	180
	ATGGTCAACGG	CGTCTGGCTA	CGATAGTAGT	TACTTCTGAA	ACCAGAAGAT	TCCAGGTTTCG	240
	AGTCCTGGCG	GGGAAGTCCT	TATTTTTTTT	GTTCCCTCTT	GTTTCAGCTT	TTTGTCTTAA	300
	AAGGAGCAGA	AAGATTATTT	TGCAGCTCTC	TTTTGGCGCC	AGCTGGCAAA	AGCGAACTGT	360
	TGATTGACAA	GCTTTTAACC	TGTTATTAAC	CACCAGCAAC	CTCTCGAATT	TATCATGTCT	420
	CCATCAAATA	AGGATATTGC	TGCCCTAATT	GTTGACTTCC	TAACACGTC	CGCCAAAAC	480
10	GTAGGAGAGG	ATTACGAAGA	TTCCCTCAAA	GTGGCAATTG	ATTGTATCAC	TGAAGCTTTC	540
	GAACTTGGAC	CAGGCGAAGC	TGACACATTA	GTTTCCGAAA	AGTGTGGCGG	AAGAAGCCTC	600
	TTCTAGTTGC	TCACCACTGG	CATGGCTCAC	ACCTCAGATG	CAGGCGAACC	GAAGGTAGCC	660
	GCCGAAGAGT	TGAAGAAGGA	AGCTGAGGCC	TTGAAACTGG	AAGGTAACAG		

## 1505UP

	GATCAAGCTG	GACAAAAACT	TCCGTAACCTA	TCTGAACCTA	CTGGAAATGG	TTTCAAGGGTA	60
	CGTGGAGCTT	AACATGTATG	AAGATGTCTG	GCGAAAGCTC	GTTCAATTAA	ATGGGAAAAA	120
	TGAGCCTGAT	AGAGTTCCAG	GATATTATAT	TACGAGGTCT	ATCTCACTGA	ACCAGCTTTC	180
20	CACCACTATA	TATCCTGAGG	AGTTGGATAA	GTTTAATCTA	TCTCCTGTCA	CCGAGATAGA	240
	AAAGAGGGTC	GTGCAAGCCA	CTGAGTGTMT	CTCGAAACTA	ACATTAACAA	ATAGCCATCA	300
	TGAAGAGCGG	CGCATACTGA	TATCAACCTT	TCAAAAAATTG	ACAACGAAAA	CTTCTCAAGC	360
	TACTTTGGAT	CCATGATTTG	ACGCAGATAC	CTTACTGGGT	TTGATGGTTG	TTGTAGTTTG	420
	TCGCGCACAA	GTTAAAAACT	TGAAGAGTCA	TCTAGATTAT	CTTAGAGAAT	TTGCGCAGAA	480
	TTCCGATGAC	GTAAAGTTTG	GGCTCCTTGG	GTATTTCGCTA	TCGACGCTCG	AAGCGGTGGT	540
25	CGGATATTTT	GATATTGGCG	GCAGCTCAAT	TAAACTTGAA	AGATTGATCA	CACCATGTCC	600
	AAGGAATAAG	ATCTTCTGGA	ACTTGATAGA	GCAAGGAATT	CCAATAAATT	TAAAGGAACA	660
	TGAAGAAGTC	CTCATATCGC	GCCTCCGTC	CTGTGAATCA	TTTGTCTTT	ATGTT	

## 1506RP

	GATCTACCGG	TTCCGGTATCC	CCCTTTGAAA	ATAAATTCCT	TGTCTTTTGC	ATGCAACTAA	60
	AATGGGATGA	AGATGCAAGG	GATGTTATTT	TTAAGTATCT	CCATCTTTTG	GAGCTTTCTT	120
	CACAGGCTGT	AACATTAAACA	AGGTCAAAAA	CTCTACAGGT	TATAGAAAGG	CTTTGTCACA	180
	GAAAATTAGC	GTATACGAAG	TCGGATGAGT	CTATTTTCAG	CAGCATTAGT	GATATTCCGA	240
	TTGATGGACA	TGACTTGTC	ACCGCTGAAA	CATCTTCCGA	AGAGCAGCCG	AAATCTCAAT	300
35	CTTTGTTCGA	GCTATTTGAG	GAGAAAATAT	ACAGCCTAAA	CACCGACGCT	CCTTATATGA	360
	CTCACGATGA	CCACTTTCATC	CAATTTGTGG	CTCCTCAAA	TCAATTGAGC	ACTAAGGAAT	420
	CGCCCGGAAC	GTGTGTGCTT	GTTACTGCCC	CTTCGATGAA	ACTGAAAATT	ATAGACTTTCG	480
	ATTCAAATAC	TTCCGGACAAT	GAGTATWATG	AAAATGTCCT	TATGACGAGG	TACACTGCAG	540
	CATTGATTCA	AGCAAATGTA	TTTATCTTCC	AAGAAAGTGA	CTATAAAGTC	TTTGAGAACT	600
	CATTGTTTAA	TCCCAAAGGC	TACGGTGCTA	AAAGTACAGA	AAATTGGCAA	CCTTGGCTAG	660
40	GACTGGAAC	ATGTTTTTGAA	CCGGAGCCCT	TGCAAACTAA	TACGGTTATT	AAAGAAATTC	720

## 1506UP

	GATCTCCCCA	TAAGCTCAAC	ATTTTCGATA	TAAGATATTT	GCGTCCCCCG	CCAAAACACG	60
	ACGGTCCGGT	CCAAACTCAA	TGCCCCATTT	GCAACAAACG	GCAAAATCATG	ATTCCATCTG	120
	TCCCTCTCGT	CAATCACCAG	ACTTAACAGT	AGTTGACGCT	TTGTCACTTG	GACTAGATAG	180
	TTGTTGGTAA	CGAAGTAGTA	TATCGTGCGG	CCAGCCAAGT	CGCTAAGGAT	GCCATCAACT	240
	TCGTGCGATT	CCATGTCTTC	TTCCGGAAGAA	AAATAAAGTA	CAAACGCCCT	GGTTATGGTC	300
	GCCCCATCAG	AACCAATAAC	CAATAAACCT	TTATAGCGTC	TATCATCGCC	ACAAAGTCTT	360
50	GTATACACTT	CTTCGGCAAC	GGCATCCAGT	CCTATGCTCC	ATATGCTGTT	AAAACGCAGG	420
	AATTCTCGCA	GTTTAAATAT	GTTTAAATAT	TGGGCTACAT	GACCATTAGT	TGATATGTTA	480
	GACAGCACGG	ATGATGAGCA	AGAACATAAC	TCTTCTGTGA	TTGTACCTGA	AATGGCAGGA	540
	GTTTTATCGC	GGAAAGAGAT	CAGCTCTTCC	GCGTATGCAA	AGCTGGTATC	CTTGGTGTGT	600
	CTTCTAAGAA	TATTTGACAT	AGACTCCACA	TAGGCTCTGT	CATCGAGGAT	TGCAATGCCA	660
55	AGAGAGATCT	AGCGTTATCT	CAATACCTT	CCAAAACCTA	TAATCTGTAA	TTT	

## 1507RP

	GATCGGCTGC	GCTCCAAACGA	TGGCAGCATT	GCTCCTAACG	GGGCTGAAAT	ATATGTCGGA	60
	CTCATGGCTG	ACTTTAGCGT	CGGCGGGCCA	GACACGTCCA	ATGCGCCCGA	GGGCTGTGTG	120
5	CTGCGGATCC	ACCTCGAAGG	ATGGCGGTGC	CAGATGGTTC	TAGACGGGAT	CCATATCCCG	180
	AACGCTATCA	ATTGGAGTGC	AGATGGCTCG	CAATTCTATC	TGACTGACTC	GCTAGCATTT	240
	ACCATATGGG	CGTGCCCGGT	AGTGGACGGT	AGCCCACAAC	TCCTCAAGAG	AACCCCATTC	300
	TACTGTACCA	AAAATACTGG	CAATGACTCA	CACACTTCGC	CGGAACCGGA	TGGTGGATTT	360
	GTGGACTGCT	TTACTGGGCA	CACTTTCGTG	GCCGTGTGGT	CCACTGGCAA	AGTCCGAGAA	420
	CTCGACAACG	CAGGCAGACT	ATTCGCTGCA	TATACACTAC	CGACGCCACG	AGTCAGCAGC	480
10	TGTTGTGCGG	GCCCCGCAGG	CGAACTGCTC	CTGTCCACGG	CGCACGCAGG	CGATTTCAAG	540
	ACTGGCGCAC	ACTCTGACGG	CGTCGGAGGC	AGCATTTTCA	GAGTGGTAAT	CCCGGGCCGC	600
	CGCGTTATCC	CAAGCCGCAT	CCCCGCGTCT	TGCGGAAGCA	TCCTTTAAAT	AATATTTACT	660
	TCTACACCCT	CTCGTCCCCT	CTACCGCCCA	GCTCATTGAT	GGGCCGT		

## 1507UP

	GATCGTACCA	GTATAATACT	GGGAATTGAC	GCGCGCAGCC	AAGGCGTCGT	AATCATCGTG	60
	TTGATAATTA	TGTCCATAGC	CATCCATWAT	GGAATTAGCA	TCAGCTATTT	GCTTACGGTG	120
	TTGACGAGCG	ACTGTTAATC	TCCATAGAGA	ATTCTCCTCA	ATAATTTCTG	AGACWGTCTT	180
20	CTTTTTTAAA	ATCGGCTTTG	GCCCCGGACG	TTGAGGGGGG	CCAGTGCTAC	CACCAGACTT	240
	CTTCTTCGAA	ACCCGCTTGG	AATTTTTCGT	ATCGGAACCA	TAGACAAGCT	CTTCCATATC	300
	CGCTACGGCA	TTGCGTGTCA	ATGTCTGAGC	GTGACCGCTA	TCACGTAATA	TAGGCCCATATA	360
	CAGCCATGTG	ACGTCCGAGT	CCTTGGACCA	GTTGACAACC	TCTGGGCTCA	CGGTGCGTAG	420
	ATTATTCCGG	GCTTTGGCCC	ACCTCCTCCA	GGATGCGTTC	TCGAGCCGCG	CCGCGTTCAC	480
	GAGGTCTCTG	TCTCCCTTCT	GTCTCTTCTT	CAGGATGATG	TACTTCCAGG	ACTGAGAGAT	540
25	GTCTCACTCA	GCCCAGTCGT	GCGAAAGGTA				

## 1508RP

	GATCCACAGG	CAAAATTTAT	GCATATAGCT	TGCTTATATT	TATGCGGTGG	ATTCTATATG	60
30	TCGCACGCTA	AATACTAATA	GCCGCCGGTA	AAAAGTAGTC	CTCGGCAAAC	TCGGTAACGG	120
	CAAGGTTCGGA	ATTATAGAAA	CGGACTCAG	AAAAACTAAT	CCAGAGTAAT	TAAGGGACTC	180
	GGAAAGCGGA	GCCGGTTCTT	ACCGAAAACC	TCAACGGAAG	TATATGAAAA	AATTTATCCT	240
	GCAGATTATA	CCCATGCCCTG	TTTTATCCAA	GGTAGCCCAA	ATATATACTA	CAGGAAATGA	300
	GTGACTTTTC	ACTTCGAGAG	CCCAAATAAC	AATAATTTTA	GTAAAAATTTT	AGCATTGCTG	360
	CTACTCCAAC	TTTCCAATGA	ACACTTCTGA	AAGCGTAAAT	ATATAGCTAT	GCGGTTTGCC	420
35	TCCCAGGCTC	TAAC TACAAA	TTCCACCTTA	TGTGTGTTAT	TCAGGAAATG	CAGGGGAATA	480
	GTTGAATCAA	CGAAATAGCG	TTAATTTGCA	ACCGCCTTGT	ACGTGTATAA	AACCCACCCC	540
	CCTCCGAAAA	AGATGACTAT	CGTTATAAAC	TAAAAAACAT	CATCAAAAAA	GAAC TAAGTT	600
	ACTGAAAAGA	AAATGGTTTA	CCGTCTAGCA	GTGAATTTCA	GCAACCAGCC	CACATGGGTA	660
	ACCAATTTCC	GAATCTATCG	TTGCAGAATA	CT			

## 1508UP

	GATCTGGTAA	CGACTAAATA	AGAATCCTTA	CGCAGCAACG	CCGGCCGCGT	CTCGGCAGTG	60
	TAGTGTCTCT	CAAGTGCGCG	TCTGGCACTA	GTTAGGTCTT	GCAGGTGCGC	TTTGAACCAG	120
45	TGCGGCTCGG	TAAGCACC GA	GATGGCGGAA	ACTCCCGCCT	CCGCATATGC	AAGCGCCTGT	180
	TCTGTGCAAA	GCGCCTCGCT	AATATTGCCA	CGCGACGGAG	ACGCACGTTT	TATCTCGGCT	240
	ACCACAGCCA	GCCGCGGGGC	GTCCCGCGCC	AGCCGCTCAT	GGAAAGTCCAC	CACGCCCCGC	300
	AGAACCCCCA	ATCGAAAGCT	CGCCTCCAGG	TCCGCCATAC	CAGTTCCCGG	CATAGCCATC	360
	TGCGCTGCCA	CGTCTCTCTG	TCGTTGAGCG	TATATCTCGC	TCAGCACAGA	GCCCGCGCCT	420
	GCCCGCAGCT	GGAGCTTGTC	GTTCTCAGCC	CACGTACCGC	CTTCCAGCGC	TAGCATGTTG	480
50	CGCACCATTA	GCTGCCCGTG	GTCCGTCAGA	ATCGACTCCG	GGTGGAACTG	CACACCCTCC	540
	ACGGTGTACT	TGCGGTGCCG	CACGCCCCATA	ACCACGCCTG	TCTCCGTGCG	CGCCGTCAAC	600
	TCCAGCTCCG	CCGGGAACGT	TGACGCCAGT	CCAGCCAGCG	AGTGGTACCG	TGTCATGCCC	660
	ACGGCTGGGG	TACCCCTGGA	AGAACC CGCG	CCGTGCTGAC	GCAGCTCCGA	CGTTCT	

## 1509RP

	GATCCAGTTT	CTCTCGCATT	TTCTGAACGA	TGAGATATGA	GTCTAAGTTG	GCTAGATTAC	60
	TATATAGCCA	GTTGTTTCGCT	CGACGGGCCA	AAACCGAGAC	CGGTTCCCTC	CTTTGACAAG	120
5	AAGAATAATC	GCCATCTACT	TTGTTTGAAT	TCTTTAAACC	GTCTAACTCT	TGCAGTACCG	180
	TTTTTGGTAC	TACTATGCGA	TAGCTGTATT	TTGGGGCAAG	CACTCGTAGT	TCTTCAAGGA	240
	TATCCAGATG	TGATAACACA	TAATTAGTAT	CAACGACCAG	TGCAATATTA	TGCAAGTCTT	300
	GCCGCACTTC	AACCTGCGGC	TGAATTACTT	TTGCGAAAGT	CTCTTCGCCC	GGAATATCGA	360
	CTCTCTTGTC	AGGAATAGTC	TTAATGTTGT	TAATTTTCATG	GCTGTGATAT	TCGTCTATAT	420
	CCATCATCGC	TTTCACTTCG	TGTTCCCTTA	TAATTTCTGC	TTCAACCAAT	GCATCCAATT	480
10	CTGCAATGCT	ATATTTCTTA	TTAGAGTGCT	TAGGGTTCCA	AGTATGCGGC	GAGCTTATGG	540
	TATGCGTCTT	ATTCTGATGC	CTACGCTTGC	TCTTCCTCCC	ATGGTCCCTA	GACATCTCCT	600
	GTGTAGCTTG	GTGCATAGAC	TGTATATGAT	TGGACTCCAT	CGGAAC TAGT	GGCACGTTTA	660
	AAAGACATTA	ATTAGGTATC	ACCTCCATTA	ACGTACCTTT	GATATTTATT	ATATGA	

## 1509UP

	GATCTCGAGT	TTTATGACGA	GTGCATGGAA	GATGTGTTTC	TAAATGCAAC	TAAGGTCCGT	60
	AAGGTCAAGT	AGGTGCAGTC	CTTTATCACT	CTAAAATTCC	CCTCTTCCTT	TGATGATGAG	120
	AATCGCACTA	CATCGATGCC	AAC TACAAGT	CACCATCAAG	ACTTAACAAC	TCAAGACGTA	180
20	CTTGGTGGAT	TGGTCGATGC	TATGGATGAT	AGGCGCGACC	AAGAAGACGA	TATCGATTTCG	240
	CAACAACCCC	TGGATGTA CT	TCTTTTGATC	GGCTGCGACA	GTCCAGTTTC	CAACTTGCCG	300
	CGGATTACGG	GGGTTGCTCG	TTCCGAGGAT	GCAGACGAAT	GGGATCTTGG	ACAGAGCAGT	360
	ATTACTCCTA	ACAAACTAGA	AATCCATTCG	GTCCAGACGC	CTACCACACA	CCGTGTGCGT	420
	GTGCTAGAAG	AAGAACAATC	GCCTTTGATC	ATGCTGCAGA	AGCGCAGACT	AGCCAGGAAT	480
	GGGTCAAGAA	CATTAGCCAC	AGCTACAATC	AACCATGACC	AGGAAC TGCA	ACTAGAAGTG	540
25	CCAGATAGAG	AAGCCGCTTC	GCCTGCCATT	GAACACGAGC	AAGCCACCTC		

## 1510RP

	GATCAGAATT	GGAAGGGATG	TTTGCCGGAA	GAAGTTCGTG	ATATCGAGGA	GCCCACTATA	60
30	CCCGTCATTG	GCCGGAAGTT	TTTCAAGTAC	GAATCTCCTA	TAAAGCACTT	GCTACCCCCC	120
	AACGCCACTA	TAAACGACCC	CATTCCCTCAG	CCAAC TGAGG	GAGCGGTCAA	TGCTCCACCA	180
	TTGGTTGGCG	CCGTTTATCT	ACGCCCAAAA	ATTAAAAAGG	ACGACTTAGG	TGAATATTCC	240
	ACCTCCGATG	ATTGTCCCGAG	GTACATTATC	AGGCCTGGTG	ACCCGCCTGA	GGTTGGTAGA	300
	ATCGACCCAG	AAACGGGAAC	CATCATTACC	AATTTCCAGA	CCGCCAGTGT	ACTACCGAAA	360
	ATGAATATGT	CTACACCAAG	TCTGTGCTCT	TTGAACCGCA	ACGGTAGCTA	CTCGAATTGG	420
35	ATAGGCCGTT	CCGGTAGCCC	AATTAACATG	ACCAGGTCCA	CCCAATACTT	CGCACCAGTT	480
	CCTAACGGCG	ATCTGAGAAA	TCTGCCAATC	GTGCAACAAA	TACCGAATAG	CACTATCCCA	540
	TCTGCGCAGT	CGTCTGCAAA	AGGCGGCATA	CAGGGGGACC	ATGGGCGGTT	CAATTAACGG	600
	TACTACCCCT	GCATACCAAC	CCCCTTCCAT	TATTAATAAC	CTAGCCGCCC	AGGCTAAGAC	660
	AAACAATACC	GTTCTTTGAA	ATATCTTTGGT	CGATACGCCC	GGTGCCCTACG	TTCTCCTATA	720
40	TCT						

## 1510UP

	GATCGCCGCT	ACTGTTCTAC	GACCACGCGC	GGGGGCTGAA	CCTGGCGATG	GGGTTCAGC	60
45	TGGAGGACCC	GCACGCGCGG	GGGAACGAGC	GGCGCTACTG	CCTGGTGCTT	ACGGTGGACC	120
	TGCGAGAACC	GGCGCCGGCA	ATGGAGATCG	TGTCGCAGCA	CTGGAAGTTC	ATCTCGGGCG	180
	CGTTTCGAAA	CATGATCGAG	TACATCAAGC	AGCAGCGGCG	CGCGGAGCTG	CTGCGGGTGA	240
	TGCAGCAGGG	GCAGGTGCAG	GGCACATCGA	ACTTTTCGTC	CATGGTCAGC	GGCACCTATC	300
	TGCGCGGGAA	CAACCTGAAG	ATACCGAAGA	ACATCACGGA	GCTGACCAAC	GATAGACTGC	360
	TGTTCCGTAC	GATACACAAG	TGGAATGCAT	TTTACTTGGA	TAGACTGGGA	GGGCGAGTGG	420
	ACTGAACCCT	TGGGGCGGTT	GCTGCGCGGC	AACAGTTGGA	AGATAGAAGA	CAGAAACGCC	480
50	CGGGAAGCCG	AGGCCGGAGG	TGGGAGGCGT	TACATAACTT	ACATTCTTAA	CTAGATAGTG	540
	TTGCGCTGTA	CATCAAGTTC	AGACGTTAAG	GTTGAACGCG	GCATCGGTGA	TGTGTTTCGCT	600
	GAAGGGGGCC	AATGCAGATT	TGACGTCCTT	GTTGATGAAC	TTCTCCACCT	GCTGTGGGGC	660
	CCTGCCCAACA	AACGTGGAGG	GGTCCAGCAG	GGA			

## 1511RP

	GATCGACCAG	CTGGTGATGG	ATAGGCGGCT	GGTGCCGCTG	GGGCGCTTCG	TGCGGGGGCC	60
	CGATTTTGGG	CTGTTGTCGT	GGGTGAGGTG	GACGCTGCAC	AAGGTGGTGG	ACCTGTCTGT	120
5	GAGGAGCCCG	GTGCGGGAGA	ACGGACGGTA	CCTGCGGAAC	TGCGCATACG	TGAACATGGA	180
	CGTGCTGGCG	GCGCGGCACG	GCGCGGTGGA	GGGGGCGCTG	GAAGAAAAGG	TGGTGGCGCG	240
	GGCGACGCGA	TATACGGACC	TTGTGTTCTC	GCGGGAGGAG	TTCTACGGCG	TGGTGCGGGA	300
	GAGCCTACGG	GGACGCGGGG	AGTACGATGT	GGTGCTGGCG	GACCTGGACA	AGCACCAGCA	360
	GGCGATTCTA	GTGGACGGAG	ACGTTGTGAA	GGTGGTGATG	CCGGCGGTGC	GCGCGCTGGT	420
	GCAGCCGTTT	GGGCCTGACC	GCGTGACCGC	AAACGACCGC	CACATCGCAG	AGTTCAAGGG	480
10	CTCGCTGCGA	TTGGTGGAGC	GGCAGGTCCA	AGCGATCCAC	GGGCACGTCT	AAGAGACAAC	540
	CCGGGCGCTG	CGTTGGCGCC	GTCCCGGCGG	GCGCCGCACC	CGATGTGCAG	CGGCGGTACC	600
	TGCGGATGAA	CAACTCGCGC	AGGCCAGCCT	GTCTCGCGCG	CTCAACCAGT	TTACGAACCT	660
	AATGGAGATC	AAGGAC					

## 1511UP

	GATCTTGCCC	CACGGCCCCGT	CGCTCAAGTT	CCCCCGTCC	GCCACAAACG	CCCGGAACAT	60
	GCCGTCAATC	ACGCTGGGCT	CGCTCCACGG	CGTCTCCCCA	GTCAGCAGCA	CAAAACACAAG	120
	CACTCCCGCA	GACCAGATGT	CCGCCGTGTC	CGCGTGGTAC	GCCCCGCTCG	CCACCACCTC	180
	CGGCGCCAGG	TACGGCAGCG	TCCCCCGCCG	GTCGCGCGCC	AGCCGCGCGG	TCCCGTCCGG	240
20	CCGCGGGAAC	CGCGTCGCCA	GCCCCAAGTC	CGCCACCTTC	AGGTTCCTCC	CCCGGTCCAG	300
	CAGCATGTTT	TCCGGCTTGA	TGTCCCGGTG	CGCCACGCGC	CACGCTCTGT	GCAGGTGTGT	360
	CAGCGCCCGC	ACCAGCTGCT	GGTAGTAGAA	CGCGCCACCT	CCGAGTCCAC	CCCCACGTCC	420
	GGCTCGATCT	TGTCGAAGAG	GTGCCCCCGG	TCCGCCAGCT	CCATCGCGAT	CCATAGGTAC	480
	TCACGTGACA	CATTGCAGTC	CAGCACCCTC	ACCACATGTC	GGTGCCCGCG	CACCGCGTCT	540
	GCAGCACACC	TCGCGCGTCA	GATCCTCGTC	CGTCATCCCT	CGCGCTTTGC	AGCGCTCGAA	600
25	GTGCACGAAC	TTCACAGCCA	CTATCGTCTG	CGGGTCTGCG	CGCAACGAAG	CGGTTTTGAA	660
	GAACGCAACG	TGCCCTGCCC	AATCGTCTCC	CGAAGCTCTA	ATTCCCTTAAT	CTCCGGGAAG	720
	CA						

## 1512RP

	GATCTTGACT	GGAAGGATGA	GGAGCAAACC	CCCGACAGCG	GAGAAACTGC	TATTTGCGTG	60
	TCTACACCGG	GCTCTACTCG	CATCCAAGTT	TAGCTATACC	TGCACTATTA	CTAGATATCT	120
	AATGCCTACC	ATATGTTGTG	ATGACACTGA	CATTTCAGCCT	TTAACCACCT	CAGCTTATTA	180
	AAAGATTCCA	GACATACAGA	AAAAATCCGG	TGTTAAAAGT	TATACATATA	CACCATTTTA	240
	CCTATATACG	TGTAGACGAG	TAGAGCTACT	AAGCAGCCCA	AGAAACACTA	CCATATTCTAT	300
35	AATGGCGAGC	CTAAGGACTT	TCGATGCGTT	CCGTATGTGC	CGAGGGTTAT	AGTGACACAA	360
	CGATGCAGTA	CTAACAGTCG	TAGCAAAAAC	CGACCAGCAG	CACGTCCGTC	GGTCATCTCG	420
	CGGGGGCATT	ATGTCCATAA	TGATGTACCT	GTTCCTGCTG	TTTATCGCGT	GGGGGGAATT	480
	TGGCAGCTAC	TTTGGGGGCT	ATTTGGACGA	ACAGTACATC	ATCGACCCCG	AACTGCGGCA	540
	GACAACGCAG	ATTAACATGG	ACGTGATGGT	GCAAATGCCG	TGCAAATACC	TCGACGTCAA	600
	GGCAACTGAT	ATTACCAGGG	ACATTAACGA	CGTGTGGAAG	AGACTGGTGT	TCAAGAAATAT	660
40	CCCTTCTCTC	GTACCGTACG	GCACCACATT	TGACTCTGTT	AATGAGGGTC	CGCACCCCGG	720
	AC						

## 1512UP

	GATCGAATGG	CATCCCATTC	ATCCGATGAG	GACGCTATGT	TAAATAAATA	TTATCTATAT	60
	ACTCTAAATA	CTATATGGTT	TCATCCGTGT	TACCCGGATT	TAGAGATGCG	CGTTCTCGTC	120
	TCCAAGCTTT	AACTCGTGTG	GCTGACGATT	CTACATAACG	TGTATTGACC	AGGCTGAGCA	180
	GTAACGTTAG	CAACTTGGAC	ACCAGTTATG	AGTACCGATT	TCGACAGAAT	TTATTATAAC	240
	CAGTCAAAGG	TGAGCGGTCTG	CTTCCGTTTG	GGCGAAGGTG	GCCTGGGATG	GAAGGCTTCC	300
	GCCACTGGCG	GGTCCGCTGC	CATGCAAAAC	AACGAACCAA	TTCTCTTGAC	TGCGGACGAA	360
50	CTGGCTTCCG	TGCAATGGAG	TAGAGGGTGC	CGTGGCTACG	AACTAAAGAT	TAACACGAAG	420
	AACAAGGGCG	TGGTGCAGTT	GGACGGTTTC	TCGCAGGAAG	ATTTACATTT	GTAAAGAAG	480
	GATCTCCAGC	GCAGATTCAA	CGTGCAAGTT	GAACACAAGG	ACCCTCGCT	TCGGGGATGG	540
	AATTGGGGTA	CTACCGATCT	GACAAGAAAC	GAGCTGATCT	TCTCCCTAAA	CGGGAAACCA	600
	ACTTTTCAAA	TACCATATTC	GCATATCAGT	AACACGAATT	TAACATCAAA	GAACGAAGTT	660

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GCGCTGGAAT TCGACTTGC

## 1513RP

	GATCAACTGT	TGCTCCAGTT	GCTCCTTGGA	CTTGGTTCTC	AATTCAAAAAG	CTTTAACACC	60
	GGCCTGAGAT	GAGATGTTAG	TACTCCGCGC	ACCTATCAAG	CTTGGAATGA	CATTGCTGGC	120
5	AACCTGCGGG	GCCGCATCTA	CCCCTCGGCT	ACCGCTCGCT	GGCTAACCCG	GTATGCGCTG	180
	CTGTGCGCA	CTTCTGTCCC	ACGGATTAA	GCCTCTAACG	GTCACCTCGA	TACCCAACGA	240
	AAAGCTGCAT	GCCATCATCC	CACGCTATAC	ACCGCTGAC	ACATACCATT	ATGATTGATT	300
	TTGCTGTATT	TTGCACTAAG	AGCCACTCCA	AATGAACTGC	CTCTTCTGTT	GAAGATGTTG	360
	GCCTGCTGTG	GAAACCGACT	GTGCTCCGCT	CGGTGTGCGC	GAGCGAGTCT	GTCGGACCGAC	420
	GCAGAATCTT	CAGCTATACA	ACCCACACAC	CTCCGAATGT	ACGGATGCAA	CAGTCAAACA	480
10	CAATTCACAA	TCACGTGACC	TACAGGTGAA	ATTAACGATT	TCGGCAGATC	GCAAAGTGAG	540
	CGCCAAAGGC	GCGACGGAAC	ACCGGAGCGG	GTACACGATG	GGTGCGACTT	CTTACACTAT	600
	ATATCGATGG	TAACAGTGCA	CGCACAAAAA	AAAGTAGTAT	ACTAGGGTCT	ACGAGACTTC	660
	GCTAGTTCAT	TTACAGCCTA	ACCTAAAGAT	TAATTATGCC	AAGACAGTGA	TTGGAAGGAG	720

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## 1513UP

	GATCTTTAAA	ATTTGGCAAG	AACAGCCAAC	ACTCCCGTCA	AAATAAAGAG	CAAAGCGCCT	60
	CCACACCTCT	ACGAATCAGG	TCCGAAAGGC	GATCTTGCAA	TGACGAGCAA	GGTTACAAAG	120
20	AAAGTTAGAG	AGTCGCACAG	TGCATGTGAC	GACCAGCAGC	ATAGTTCTCG	GGCTCGCGGC	180
	ACTGCAGCAG	AGGGAGCGCC	TAGTAACGTG	GTTC AACCGT	CCCTCGGTGA	TTTGAAGAAA	240
	CTCGCAGAA	ACACACTCTC	CACCCCTACG	TCGAACGAGT	GCATTAAATA	ACGGCTGCGG	300
	TCCACGAACG	TGCAGGAGGT	GAAGCTGGGG	GGACTGCACT	TTCTGTTTAA	CAAGACGCTA	360
	CTACTGTGTC	TTTACATGGC	ATATGCGTTC	TACCGATACT	TCCAATACCA	GTACAACAGG	420
	CTGCGTATCA	AAC TACTGAA	TCTGGCCTAC	TCGCCGTCCA	ATACCCCGCA	GCTGATCAGA	480
25	CAGGACGTGC	TAAAGTTGCA	GAAGTCCCT	AAGCGGCTGG	CAGCGATTTT	GGCATACAAG	540
	TCTGAAGGGG	AGGTGCGCGG	TGGCGTCCAC	GGCTTGATAA	ACGACGGAAG	CAACGTANTA	600
	TGCTGGACTG	TGCTGTGCGG	CATCAAGCAC	CTGTGCGTTT	ATGATCATGA	CGGGGTGCTC	660
	AAGGCCAACG	TGCACCAGTT	CCGCCAGGGC	GTGTACGATA	CCTGGCGCGC	TACTACGGCC	720

CAACAA

## 1514RP

	GATCTGCGTG	TATATTTGGA	TGTATATGGA	CTTCACACTT	TCGGAAGCAA	TGGAACTCGA	60
	AAGCTGGTTG	ACCACCTCTG	TGTATTTCTG	TAGTCTTTCT	GAAACGACGG	TAAGAAAATT	120
35	AACCTTGAGC	GGCGATAGGG	AAGATGCAAC	TTTAAATTTC	TCTACTTGGT	TACTCAAATA	180
	CTGATATAAT	AATGCAGCCT	CAAATATGCT	GTGGAAAACA	CCACTTTTCG	CGTTCCGGAAC	240
	ATTGGGTGGG	ATTTTCGATA	CCTGATTGGA	GATCGGGAAC	AAACTCGACG	TAGTAGCCAG	300
	TAACGTGTAG	GAAATATACT	TTAAAACGTC	GGCCTCGGGC	ACCATGTTGC	TGTAGTATGG	360
	GTTAGACAGA	TATGCCAATG	GAGTATCGTG	CTGCTGCGGC	CGCTTGGGGA	CCGGGCGGCC	420
	GTATGCAGAG	GTTACCGCCG	ACCGGCGCTC	TGAAAGCCGC	TCCACATCTT	CGAACGACTC	480
40	TGCATAGACA	CTAACC GCCC	TCCGACGGCGT	CATCAGCGAG	TTGTGCCGTT	GCAGCGTGCC	540
	GTTTCGTAAGA	TATCCAGACG	CGGTGCGCCT	GTGTCCGAAG	GGCGTGCTCT	CCTGCGGCAC	600
	GCTGTTTCAGC	ACCGTCAGGT	ACTTCAGCAC	CTGCTCCTTG	CTACCGAAAC	TCTCCAGCAC	660
	TTTCACGAAC	ATCTCGAACT	TCCCCCACTG	CTGCGTCTGC	TCCGGCGTCC	GCACCATCTC	720

CGCCCGGTAC

ATGCTC

## 1514UP

	GATCTCCACC	GCGTCCAGCA	CCACGATCCG	GTCACCGTCC	CACCGCGTCA	TCGCCACTGT	60
	CCGCGCGACG	CTTTTCGAAA	CCGCCCGTCC	CTCCGCCGTC	GCAGCCCTCT	CCCCGCTGTC	120
50	GTGCGTCCGG	TGCTCGGCCCT	CCCGCGACCG	CAGCGTCGCC	ACCACCCGCT	CTATATTAC	180
	GCCGCGGGC	TTCAGCGTGT	CGCGCTTGAT	GCCAGGCTG	GTGGGTTTCT	CTCCCACCAC	240
	CTCCAGGCTC	TTGATAAACG	TCGTCTTAAT	CACCTTAAAG	CTCGCAGTAT	GGCCCTTGCG	300
	CCCACATAGT	AGCGTCAGCG	TATGGTTTCC	CGAATCGTAC	GCGTATATCT	TGCCCTGTGT	360
	TACACCGTCG	AGGACGTTGG	TCACCCGCAC	CTTGAATCCA	AGGATATGTT	CCAAGTTGAT	420
	GCTCATCTCT	CTCACTTCCA	AGCCCAACA	GCTATCCTGG	CCACCTTAGA	ATGCCACGCC	480
55	TGCTCCCCGT	CCACTGGCTG	ACTCCCAATC	GTTTCAGTTG	CGGTGTGGGT	ATTTTTTTGA	540
	AGTGCGCTC	TAGCGATGAA	GTAAGATTTT	CTATGTATTA	CTATGTGCGA	CAAAGGTTAG	600

EP 0 866 129 A2

TTCCAATAGT GCTTGCAACT ATCAGGTGCT GTGGAGTCC CAAGCAGACG AGTTGCTGAT  
AGTGGAGCCG ATAGAGAATC CGATAAAGAT TATTCCCGAA AATCTAAGGA CAGGTGG

660

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## 1515RP

	GATCCTTCGC	CGCGTGGTCA	AAGCCCGGAT	AGGATATCAC	AGGGCACTGT	GCAAAGGTAT	60
	CGCATATTGT	TTCCATGAGC	GTTTCGCCCT	TCGGTCTCTT	CGCCGGCTTC	CACTTGCACG	120
5	TGGCCGCCAG	GAGCTTACAG	AGCTGCAGAT	AGTTATTACT	GTCAAACGTC	CAGGGTGCCC	180
	CGCGCCGTTT	GTGCGCCGCA	GCAGCATCCG	CGAAGTGGTC	CAGGTGCGCC	CGCGACAGAT	240
	GGAACCCGTC	CATGGGCACC	ACCTCAGCTA	TATTGACCGA	TGACGCTGGA	TCCAGGGCTT	300
	CGCTCGCGAT	GCGCACCGAA	TTGGGGAGCC	CGCCGCGCCC	GAAGATAACT	GCGGTCCCAT	360
	CCCCATCGTA	GAACCTTGTGT	GGCTTGAACC	CCGGGTCTCT	CACGTGCGCG	AAGAACCCCC	420
	GTGCGCGCTC	CTCGACCAGG	GCGCCTGACG	CAACCGGCAC	AGTCTCGTCC	AGGCTTTCCG	480
10	CAGCAATGCC	CGCGGAAATC	CTCAATCCAC	CCCTTCGTGC	CTTCAGGTGA	CTCTGGAATT	540
	CCTGGTTTCAG	GTCCCGCTTA	AGCCTCTGCG	CCATCGTAGA	CTTGCCGGAC	CCAGGATGCC	600
	CCACCACCAC	TACAGCCACC	CGATAGTTGC	TCTCGATATT	CTGAGCAAGG	AGATCCCACA	660
	CTCGCTTCTT	TAAGTCTTCG	TAGTCCATGC	CGCTTGCTGT	GTATGCCTGC	TGGT	

## 1515UP

	GATCTAACGC	CGGCTGTCTC	CTCCAAGCGT	GTTCCCTGCCT	CTCTTATATC	TGTATCTGGT	60
	AGCTTCAGCA	TTAAAAAACC	GTCCAGAGAA	TTGGCTTTTCG	GCCATGCTCG	AAAGCTCACT	120
	AGTCGGAGCG	CAGCATCTAG	GACACCAGTA	GGATGCAGAC	AGTGTTTAGG	CCATTGAGAA	180
20	GTGTGATTCT	GACGCCCGCT	CGAGGCCCTGG	CGCGGTCCAG	CAGGCTGCAG	TCGGGACACA	240
	ACAAGTGGTC	GACGATCAAG	CACGATAAAG	CGAAGAACGA	TGCTGAGCGG	AACAGGCTTT	300
	TCACGCGGAT	GGCCAACCAG	ATATCGGTGG	CAGTCAAGCA	GGGCGGGTCT	GCCGACCCGA	360
	CGTGAACTT	GCGACTGGCG	GCGGCGATAG	AAGCGGCGTC	CAAGGCCAAT	GTGACCAAGA	420
	AAAGTATCGA	AAACGCAATC	CGCAAGGGCG	TCGGCGAGGG	TGGGGCGCGC	GACAACGCGC	480
	AGGCATGCAT	GTACGAGGCG	ATACGGCCCG	GTGGCGTGGC	GTTTGTGCTG	GAGGCCTCAC	540
25	CGACAACAAG	AATCGGACCG	TGACCTGGTA	CGCGCCGCGT	TCAACAAGCA	TGGCGGCAAC	600
	ATGTCGCCCG	CTCAGTACTT	CTTCGAGCGC	CGCGGGTACG	TGGCAATCCA	GCCACCGGCC	660
	TCGTGCGAGA	GTTACAACGC	GGTGTTTGAG	GTTGTGTCCG	AGGTGAGGGG	CGTAGAAGAA	720
	CTGGA						

## 1516RP

	GATCCGACCT	TTGGTGGCTT	GGCTCGAGTC	TTTCTTCAAT	TTAAACCCCT	GTTCAACAGC	60
	AGATGAAATT	GTTAGTCTAT	CGAGTCCACG	TAAAAGACAA	TTTTTCGACG	TTGAGATGAA	120
	GGGTACGGCC	TCTCCCGACA	AGCGGCATCG	CCTGCACCGA	AAAGTATCCG	GTCACTCCTT	180
35	CATCATACGG	TACCTTCACT	ATCTCTTTCC	GCCGGAAACT	AAATACAGAA	ACATACCTTT	240
	AACATCCTTA	TTCTGTATTAT	CCTTTCTTGA	TTTCGACTGG	AATGTAGCGG	CGAAAGGGAT	300
	CTGTTTCAAA	AATTGGAAAC	GCTTACCACC	TCACCAACAC	ACCAGGACTT	TATTTTCGTAG	360
	AAACAGGGCA	TCGGCCTGAA	CAACAGTCAC	TAGAAACGGT	GCACCAAGGC	AGCTTGGCAA	420
	CGAGGAGGCA	CCCTAGGGCT	CAATGCGTTG	ATAGTAAAGC	ATGTACACGA	GCTTTGTCTC	480
	CGAGAGAAGG	AACGACGTCT	TGCACTCCGA	CACGTACGAA	TCTGAGATAC	ACCACCACGG	540
	GTGCGTAGTG	GTGCGACGTA	AAGCCTTCAG	TTTGCGGGGA	CGGCCTGGGG	ACGGGGGAGT	600
40	ACTTCGTGGC	AGCCGAAGAT	ACGCCGATGA	GCTCGCAGAG	CTGGCTCCGG	AGCTGTCTCTG	660
	CTCGGCTGAC	GCGTCCGGCT	TGGAGAC				

## 1516UP

45	GATCATTAAC	GAAATTCTTG	TGGTTGATTA	CGATGTTTCA	TGGGAAGATA	TAGCTGGTCT	60
	TACAATAGCA	AAGAAGTGTT	TGAAGGAAAC	AGTTGTTTAC	CCATTTTTCG	GGCCAGACCT	120
	TTTTTCGGGT	CTCCGGGAAC	CTATCTCCGG	GATGTTGTTA	TTTGGACCTC	CAGGAACAGG	180
	TAAAACGATG	ATTGCCAGGG	CCGTTCGGAC	TGAATCGAAT	TCAACTTTCT	TTTGCATCAG	240
	TGCTTCTCTT	TTGTATTCGA	AATACTTGGG	TGAGTCGGAA	AAACTTGTCA	AGGCCTTATT	300
50	TTACCTAGCC	AAACGGCTTT	AGAAACGAATC	ATCCAGAAGG	ATTAAGACGG	AGCTCTTGGT	360
	AACTAGCCGT	TCAGATAATG	GCGCCACGGC	TAAGGAAACA	AGAGAAGGCG	AAGAGGCCAG	420
	CCAATGGTCC	TCCCTAACGA	CAACCAACTT	ACCGTGGGCG	ATAGATGATG	CTGCTATTAG	480
	ACGCGTTCTT	GTCTTGCCCG	ACATTCCATT	GACGGAATAC	GAAACAAGAC	TGTATCATTT	540
	ACGTTTTTCA	CGGCGTCTAT	AAAAGAATGA	ACTTTCTGAA	TCTGACTTTC	AACTCATTTG	600
	GAAGAAGCTT	ATGGCCCTTC	CGGGATCTGA	CATAACTGCT	CTTGCCAAAA	GAAGCAGCTA	660
55	TCGCATGACT	GAGGGCTACT					720

TGGA

## 1517RP

	GATCAATGAA	AAACATGCAT	ACGATTTTCAT	GAAGCAAAAT	TTGGCTTGGA	ATATTGCCAA	60
5	CTCTATTCAC	AAAACAGAAA	TACTAAAGGA	AGAGAACTTC	ACGTTATTAT	CCAAAGCCCA	120
	AAGAGATGAC	GTGAAAGGAA	GAGAAAGCGA	GTTATTACTT	CCAAGCGAAT	TAAATCAATT	180
	AAAGATGGTC	AATGAGCGTG	AGCTGAACGG	CCATGCAAGA	AAAATAAGAC	TACTATCCAT	240
	GTGGGAAGTC	TTCAAAATGC	TTTAGGTTCT	GCATTATTAT	ATACACATTG	TAGATACAAC	300
	TCGAAACTAA	TGCATTTTCAC	GTGAGCAGTC	TAAAAGTGGT	CATGCAGTAA	CTTCACACCT	360
	TCTTTATTCC	AAGGACAAAG	GTATATTCCC	AGCTGTGTCT	TAGACAGTGT	CCCCAGCTTG	420
10	AAACATGTGT	TACTCAAATG	GTGAGCAGTA	ACCTTACATT	GCCCAGAAATG	GGTGATGCGG	480
	TTAGAAGTGG	TATAATCCAA	CTGCTTCCAA	ACATCAGCGT	TATTAGGTGT	AAAGAAAGCG	540
	GATCTCTGCC	ACAGAATTTT	AGATGGAGCG	CGCAAATTCA	GTGCTCTGGA	AATCTCATCC	600
	ATGACAAGTG	GAACATCTTT	GTATTTGTCC	GACAGGATGC	CTTTTAATGG	TAGGTTAGCT	660
	AAATCTTTCA	TCAAAATTGA	AAGTGGTCCA	CCTTGTTCCT	CATGAGACAA		

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## 1517UP

	GATCCTCAAA	ACTACAGAGC	GAAGTTGAAA	AAGATCATAT	TTTGATAGAG	CGTAAGCAGT	60
	GGGATGAAGC	ATACGCTCTT	CTCAAAGGTG	TTGTGGATAG	ACATCCACAT	CTATATGATG	120
20	CACATTCAGC	ATTCCGGTTGG	TGTCAGCTGC	AGTTGGGCGA	CACTGAAAGC	GCTTTAGAAA	180
	CATTCCAGCT	TATTATTAAT	AATGTGAAGA	GCAGCGACGG	CACGTCGTCT	CAGTTCATTA	240
	GCTCAGTACA	CTGGCGAACC	GCACAAGCAC	TTATTACTAA	GCAGCAGCAT	GAAGATCCTT	300
	CAGGTAATGA	GTTTATAAAG	ATTGCTTTCC	AGCATCTGGT	ACAATCCCCTG	AAGATAACCG	360
	ATCTTTTTGC	TCCAGGTTAT	TCCCTTCTTG	GACACATTTA	CGAAGTGTAT	TTTCAAGACC	420
	TGACTCGCGC	ATTTAGGTGT	TACGTTAAAG	CCTTTGAGCT	AGATGCCCGC	GACCTCGTCG	480
25	CTGCTAAATA	CATGGTGGAA	TACTATAGTG	ACCTGTGCAA	TTGGCAGGCG	GCGGGCAACA	540
	TCTGTGACCG	TGTAATCAAG	AATGATATGC	ATCTCAATTC	CGTCAACTGG	CCGTACAGAG	600
	TTCTGGGTGT	TTATTATTTG	GAGCTTCAAC	AGGAGGCTGA	ATCGATCGAA	TGGTTCCAAT	660
	CC						

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## 1519RP

	GATCAGACTG	AACCCATATA	TCAGCGAGGT	ATGGTACGAT	TTGGGCACTT	TGTATGAGAC	60
5	ATGCAACAAT	CAGCTCAGCG	ATGCCCTGGA	TGCATATAAA	CAAGCTGTTC	GCTTAGATCC	120
	GAATAACGTC	CACATAAGGG	AGAGACTAGA	GGCTTTGACT	GCCCAGCTAG	CCAACCCAGG	180
	GGCCCAGCAG	CCTCAGCAGC	AGCCTCAACA	GCAACAGATG	CAACAGCCTA	GAGGGCCAGC	240
	ACCCATTATG	TTGCAGCCAA	CATTGCAGCA	GCAAGACCAA	ACAAATCCGT	TGAATAACAA	300
	ACCTGCGTTC	TACCGGTCTT	CTCCCCACGG	AGTTGCGGTT	GCCGGAACAG	AGTCCGCAGG	360
	CCACACACCA	ATGTCAGGAC	GGCCTCAGCC	GTTGCAGCAG	TTGAACAATA	ACGGAAGTAT	420
10	CCTGGAACCG	TCATTGTTGC	CGCAAAAGAG	GCCTATGGAG	GGTGGAATGG	ATACATTGGT	480
	AAATGCCATT	TCGCAGCAGG	AGTTGCAGCA	ACATCAGAAG	AAACATATGC	CTTCTCAGAA	540
	CCATCCTAGT	TTGGCCCTGG	CTACAGGACA	GCCGCAGCAG	TTACCACCCG	ATGCCGCTCC	600
	CATAATACCG	CCCGAAAAGA	AAGGTGCGCC	TCTCCCCCAG	TTTCAGAAAA	CTGAACCAGA	660
	GCATGCGGCA	AAAAGACTGA	AGCCCCAGCA	GAATAACGT			

## 1519UP

	GATCAGGTAT	CGGCCAACAT	ATCGCGTCTG	TCGATAGCGT	CGAAGATTAT	CGTGATAGAT	60
	ATAGACTATG	AAGTGACGGA	CGGCAAGGTG	ATCGATGTTA	AGCTGGTGGT	GGCAAGCAAC	120
20	TTTCGACAAGT	TTGACTACTT	CAATGGCGAG	GCCAACATCC	TGCACCGGTC	ACTTACCACG	180
	TATAGCGACC	TGCACGAGTT	CCACCACAAC	CTGAAGTTCT	TAACCCCTACT	CGACGCGTGC	240
	TCAAGCATCG	ATATCGAGTC	CAATGTGTCG	CAATTCGATT	TGTTTCGAGTA	TTACTCGATG	300
	CTGCCGCAGT	ACATGCAGAG	CTACCTGGAC	GACAATGGCG	CGCAGCTCAC	GGTGCAGACG	360
	AACCTGAACG	ACCGTPTTGG	GATCTACTTG	CTCGACCATF	CCGAAAAGAA	GGTCGCCAAG	420
	CTGACATTTG	CCGCTACGCA	GGACCCGAAC	CAGCGGTATT	ACGAATACAA	ATACTCGAGC	480
	GAAACGAAGG	AGTGATCAAA	CCAGTCGGCC	GAGTCCTATA	CGACCCGGCAT	CACGCTGGTG	540
25	TTCGAAC TTC	TCGGTGACCC	TCCGACGTAC	CTGCCTAAGG	ATAGTTTGCC	GCCAGAACAC	600
	CCTGATGAGG	GCTTCACGAG	TGCTTCTGCG	TCCGAGCTGC	AGCGCCGCTT	TGCATTCAAG	660
	TGTCAAAATC	CACGAGTCAC	CCTCGTAAAT	GACTTC			

## 1520RP

	GATCTTCTGG	ACGCTTTCCCT	TGAGTTTCGTT	CATCTTGCCA	AGCACGTGCA	CGTTGGGGTT	60
	GCCCCGAAAA	GAGTTGAGCA	TCGGCCCCAAG	GCGGCCGTGCA	ATGGCGCCAA	ACTTGCTCTAG	120
	CACCTTCGTG	AGCGTAGTTG	GGAGCTGCAA	AAAGCGCAAC	GTATGGCCCCG	TGGGCGCGGT	180
	GTCAAAGATC	ACCGTGTGGA	AGTGCTCGCC	GTCGCCCTGC	TCCTGCTTCT	TGATGTGTTT	240
35	CATCACCTCC	ATGAACGAAA	GCGCCTCGTC	GATGCCCGGA	ATCGACCCCG	TGAGATCTGC	300
	GAGTGCGCCG	CCCTGTAGCA	AGCCCCGAGAG	CCCCGTCA TCA	TCGCCGCGCT	TCGCGATCGC	360
	CATGTCTGTT	ACGTCTCTCA	ACGCCGCCGA	AGGGTCGATT	TCCATACACG	ACAAGTTGTC	420
	CATGCCCGTG	ACCTTGCGCG	CGTCCCTTCCC	AAACTTCTCG	TTGAACGCAT	CGCTAAGGTT	480
	ATGCGCAGGA	TCCGTGCGAG	TCAAAAGAAA	CTGCTTAGTG	GGCTGCGCAA	GCGCCATCTG	540
	GATGGCAATG	GAGCACGAAG	ACGTGGTCTT	GCCCCACCCG	CCCTTCCCGC	CGACGAAAAT	600
40	CCACTTGTGT	GTTGTAGAGT	TGATCAACGA	GCGCAAAGAG	GCCTCTGGTG	TAATATCAGT	660
	CATGGTTGGT	GTACCGCGTG	AATCTGAGAG	TGCAGGCGAT	CTGAGATCTT		

## 1520UP

45	GATCAAACAG	TAATGACTTT	GTAAACGGTT	TTGAAGTACT	GCACGAGCTG	CGACTCTCTCA	60
	CTGCCCTGTG	GCGCCACAAG	CGCCGAAATC	ACAGCAACTT	CGCTTTTCAA	CTGAATGGCC	120
	TCCTGCATGT	TCCGTGGGAA	CCCAAGTAGC	ACGACGCTGT	CCCCAGCCTG	GCACACCTCC	180
	TTCAGATAGC	GGCCCATCAA	CGCAACCAGC	GCACCCCTTG	GCAGGTGCGC	CGAGTAGTCA	240
	TCGCCATGCA	CAGCATGCAA	CTCCTCTAAT	AGCGCGTGTT	ATTTGTCTGT	CTCGTCCGTT	300
	CGGAACCGCT	CCAGCGCCTG	CTGCACGCGT	ACGGCGCGGG	CCCCCGCTGG	CGCCCGGATC	360
50	TTCTCTACGG	GCACATCGGC	AAGCACCGCC	AGCACCTCCA	GCTCATCTGG	CTTGAACACC	420
	GTCACCCGCC	GCCTCAGGCC	GGAGCGGACC	TTCTCGAACT	CCGCTTCGCT	GAACTCTGTC	480
	TGCGGCTTGC	TCCGGTCAAT	CGACTTCGCT	GCCTGCACGA	AGATGAGCGT	GCTGACCACC	540
	GCAACGCCAA	CCGCTTCCA	CGCGCTAGGT	AGATCTTCCG	AACCAGGGGC	CTTGCTGGCG	600
	TATGGCCGCA	AAAGTCCCTG	CTGACGCCGC	AGAAGGAACA	ATCTAGGCTT	ACAAGTCTGC	660
55	GAAACATTTG	TCCTGCGAGT	TAGCC				

## 1521RP

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GATCGAATCT	KGTCTGAGGS	TCTTCCACGA	WTTGCAATGC	AATCTCCGGA	TATCCGGCCT	60
TCTGTAGATA	CGAGATGATG	TTCTGGCCCA	CAAGGTTGGA	CGTACGAATG	AGACGCAAGA	120
CTTCAGGGAA	GTTCTTGTTT	ACCAAAGCTT	TCTTAAAGCG	GTACTCGGTT	GGGTCAATGG	180
TCAATATCTC	AATATCGCCG	TCTCTGTTCA	AAGCATATAT	ATGCTTGCCA	TGAGCTTTGG	240
TAATGTATAG	GGTCTTGCTC	AAAGTTTTTA	TGATCCCGCT	GTCACCATTG	AATAGGCAGT	300
ACTWAATATG	GTTCAAAGTA	GACAAGAGCA	GAACACCAGT	TTCATCCCAC	GCCGCTGACT	360
TGATCCTGAT	CGTCTCATGG	TTAGACGTAG	TAATCTCCAA	CTTCCTAGTA	GCAATGGTCA	420
GCGTGTGTTT	ACTCATTAAA	GCAACGTATT	GCCCATCTGG	GGACCAGACT	GCAATTTTAA	480
CCATCTTCAG	AGCTACCTCC	GCCAATTTTT	TCCCCTGCTG	CACGTGGAAC	AAGACTACCG	540
CCTTTGGTTT	CAAGATGAGT	ACCGCACCAG	GGCCTCCATA	GACAATGTCT	TTAACAGTTC	600
CTTCTATCTT	GATCGATTTG	GTTACCTTGT	TGTCCAACCC	ACGTACTTCA	AGAGATTCCG	660
ACGCAGAGTT	GTAGACAGCG	TTACCTATGC	CGAGCGACAA	AAGTCGCAAA	GCTTCCCTTA	720
TC						

## 1521UP

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GATCCACTTC	CCAGATTACA	TGATAACATC	GAAGCCGAAG	GTCGCAAGGG	AAATGTTGGA	60
GCAGTATGAC	TTTATWCATA	GCGGCTTCAT	CAGCGTAGAC	GGCAAAATCAG	AAAGCCTCAT	120
CTTGGGCATG	CCGAAGAAGA	CCACCGGCAG	TTTGATCAGC	TCATCGAAAG	TTTTCTTATA	180
TGGCAGAGCA	GCGGTCACCA	TGAAGACAAG	CAGAGGCCCA	GCGGTCATCA	CCGCAATTGT	240
ATTCAATGTC	TCTACCCAGG	ACGAGATAGA	CTACGAGTTC	GTGGGGAGCG	AGCTCCATAC	300
TGTCCAGACG	AACTACTACT	ACCAGGGCGA	GCTCAACCAC	TCGAGAAATG	GCCGCCATTG	360
GCTACCCTCC	AACAGCCACG	AGGAGTACCA	CATATACGAG	GTTGACTGGG	ATGCCGAACG	420
CATCCACTGG	ATGGTCGACG	GCGAGATAGT	GCGCACCTTG	TTCAAGCGCG	ACACCTGGGA	480
CCCGGTCCAC	AAAATATACA	AGTATCCACA	AACGCCCATG	ATGCTCCAGA	TTTCCCTCTG	540
GCCCGCGGGC	ACCCCCGATG	CGCCGCAGGG	CACCATC			

## 1522RP

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GATCAAAAGC	GAACAGCGCA	CTTATGTCTT	GCCCAACCGA	CGCGTGCTCC	TGAATACCCA	60
ACGAGCACTC	CCTGGCCTGC	TATCTGCGCG	TATTCTGTCA	GAACGATCGC	CGCTAGAAAG	120
TTACCAAGCG	CGTCACACCT	GTATTCCTCT	GCTTCTCTCT	CGGCCTTCGA	TGTGCTGGCA	180
AGTAGTTCTC	CACGTTCTGC	AGCTGCCACT	GGAAACGTGC	AAACCAAAAC	AAACCTGACA	240
CCACTTCTGT	CTCTCGATCG	CGTCCAGCCT	CCAGAACTCC	CAGCGCACAG	ATTTTGTACTA	300
TAGCAACCCC	CGCGACTAGC	ACTCAAGAAC	TTTCAATTTT	CGCTTGAGCC	CGACCTTGTT	360
TTTCGAAGAT	TCTGACCTAT	CCTCCTATCG	ACGTCAGGGA	CACAAATCAC	ACTATAGTAC	420
CTCGAACAAC	AGTACAGAAA	AGAAAACCAG	CTGCTCCAGC	CAAAATTCAC	AAGTCCCGTT	480
AGCTGCTAAG	GCCAATGGGT	GATACTCAGT	CTTTAATCTT	TACCCAATTG	GGAAACTTCA	540
CCAAGGAGAG	TCTTGCGTCT	TAAGGTTTGG	CAGTTTGGTT	TAAAAATTTT	CTTGCACGAA	600
ATGTCAGAAAT	GTCGCGGTTT	CCCTTGTCGG	TCACGTGGGT	GTCGGTACAG	TGGGTGCTAA	660
TCACGTGACA	CGTGGATGAC	GACTGAGGCG	GAAAATTTGC	AGGTT		

## 1522UP

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GATCGACAAT	ATTCCCCCAC	CAGGCGCAAG	AATCGAGTGC	ACACAGGCCA	CGCGCGCATC	60
CGGGCTCGGA	TCGGCGGGCC	TGGGCTGCAG	TGGGCGGCTG	GGGGGCGAAG	CACACTACCA	120
CAGTGTGCTG	TGGTGCGGCG	GGGACGCCAC	GCCGCGCAGC	TGCGGGCTGC	ATTCCAGCCA	180
CGCATGCACG	AAGAGCCGGG	TGACACTGCC	ACCGCTGGCG	TCGCTGCTGC	AGTCCAGCGG	240
CTACATGGGG	TTCAACAACG	AGCCGCGGGC	CGTCACGCGC	TCGTGTCTAG	GGGCGACACA	300
TCCCGAAGGC	CATTACGGCA	GGGACATGCT	GAGCAGCGCG	GTGGGGCACG	CCGCGTGTTA	360
CGTGGGGCGC	CAGAGCCCGT	TGCTACCCTG	GGGCGACGCG	ATTGCGCCGG	CGCTCCCACC	420
CAAGCCATCG	CATCGCTGCG	TCGCGGGGAA	CGCGCAGCTG	CGCCGGCCAG	TGCTGCCCAT	480
CGTGGGGCCC	GCGGCGTCCC	ACGCTACGAA	ACGAACAAGA	CATGCCTCGT	TTGTGGCAGA	540
CGATGTACCC	GTCCCAGCAC	GCTCAAGAAC	ACATGCTCAT	CCACACGGGC	GAAGTCTTTT	600
TCAGTGCAGT	TGGCCCGGGT	GCTCCAAGCG	GTTCAACGTC	AGGAGCAATA	TGAACCGACA	660
TGTGAACTCC	CACAAGCGCC	CGCTGATGAA	GGAAAGCAAG	AAGAAATCCA	GTTCTCCC	

## 1523RP

	GATCTTATCT	AAACCGCTCC	GCGATGATGC	TTTGGTAGCA	ACGGAAGCCC	GCATTTCAAA	60
	GTCAACATCA	GCGGAAGCTT	GGATAGATGA	GAAAATCACA	GGTGTACAT	GGCGCGAGAG	120
5	CTGAATTGGA	TTCACCGCTT	TGCTATCAGT	GGGTWAGAGG	CGTTCACCTG	GCTGTTCTGA	180
	ATTTGAACTT	CTGGAGCTAT	WCGAGGGGTT	ATGAGCAAGT	CCAAGTTCCC	GCGTGAAAAG	240
	CTGATCCTGG	TAATACTCGG	TGTAATCCAC	GCTTTTCTGC	CAGCAAAAAG	CTGGCGAGTT	300
	TGGAATCTTT	CCTTTATCGG	CGACGTCCGT	GCGTACATGG	CGTTCAATGG	TATTTGCTGA	360
	TGTAACCTGT	GGGAGAAGTC	GTAGGGAATG	TCTAGATAAG	GTTGACGCTG	AAAAGCTATT	420
	ACGTTGCAAT	AGCTGCGGTT	GAGAATGGTG	TACTTGGGCA	CAGCAACCTG	CTGCGCTGCA	480
10	TCTGGGTGAG	CTATTAAAAA	TCTCGGCCAC	CGAATAGAAG	AGCATCTTTG	GGTGAGCGCG	540
	ATTCAGTTCC	ATGAGATCAA	CAAAGGATAA	AATCCGGAGG	TTATCAAGGG	AGAATTTGTT	600
	ATCATACAAG	AGCCAATCAT	CACTGCAGTT	GGCTATATTT	GGATTATTGT	GATATTGCCT	660
	CACAGCAGTG	TTTATCCGGT	CTTTTTCGCA	GTCATATACC	ACAATGGATT	GT	

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## 1523UP

	GATCGACAGA	ATGAGCAGAG	CCATTCTGAG	AAAGCAAACA	CGGCCCATTG	CGGTTCTGGG	60
	ATCCCTGCCA	CAGAGCGAAA	TGGGCCCAGA	AGGTTTGTAC	TCGCCGATCA	AGGATCATCT	120
	GGCCTTAGCG	CCATGCGACG	TAGTAAAAGG	ATGGCATGGA	TGCTGGTCGG	AAATGCGGTG	180
20	CGACTGGCGC	AAGACATGGA	TTTTATCAAC	ACCAGCTCCA	AGATATTCTG	CGCAACACAC	240
	ACTTCGGAGA	CGAATTGCGC	AATGAACATG	GGTCAGAACA	GTACATTATC	CCATTCTCTG	300
	ATGAACGCAA	ATATTATAGG	CTCAGAGTCA	AGCACGGCCA	TTAGCAATCC	ACCTATGCCA	360
	TCTGAAACTG	AGGAACGTTA	CAAAAGTGTT	TTACAGAGAC	TCGGTAAGCA	TGTCCCTCGG	420
	GGTAGAGGCC	TATCTCAGCT	TTATAATGAG	TTTTTGGAGG	ACGAGCGCAT	CCTCTACGGC	480
	TTAGGTGGTG	GAAGTGAATA	TGTTGAAGCA	TACTGCCGATA	GTTTGGATCA	AACAAAAAAC	540
25	AATGTGAGCA	TCGAGACTGC	GTATGAATCT	TCTTTGCTAG	AGCGCGGGGG	CCAGCAGGTT	600
	TTTCTGTCTT	TCGCCCAACG	CCCGAAGATA	GAGCTACTGA	GGATCATGT		

## 1524RP

30	GATCTTTTGA	AACAAGTGAA	TTTCTGGAAA	TCGAAGTGCG	GTGACTTGGA	CAAAATTAAG	60
	CAGGACTTAC	TGGCCAACAT	GGCGACGAAA	GAGACGGACT	TCAACAATCG	ATGCACCGAC	120
	TATGAACGTA	ATATAGTTGA	ACTTCAGCGT	CAACTATCAG	AAAAGTGCGA	CGCTACAAAC	180
	GAACGCTCTG	TCACTCAAC	CTCTGCCGAT	GTACCTGGAG	AAACCAAAGA	ATATATTGAG	240
	TCTCTCAAGG	AAGTCAACCG	TAGACTGGAA	GAAGATATGT	TTGCTGTTTT	TGCGGGGAAC	300
	ATAGTGTTAC	TGGAGAACAT	CGGCCGCTT	CTTTCTAGAG	GCCCTGACAA	CAAGTTACAG	360
35	ATTATACCGG	TTAAAGGTTT	AAGGAAAAAC	ATAGATGATA	GTATAATAAA	GGACAGCAGC	420
	CCTGTAATAA	ATTCACATAT	GGTGAAAGAG	ACAGTTTTC	AGGATGTGAA	GAACCTTATT	480
	GACGAGCTTC	AACTGAGCCA	AGGTGTTAAC	GACCAACTCC	ATTTTGTTAG	TGAGCTGGAA	540
	CGCTTTTATG	AAGAGGATCT	ATTTCCAAC	TCCGTGATCA	AGAGGTTTAC	CGATGTAGAG	600
	AACCTGGCTA	AGAGCTCAGA	AAGGAAAATA	AGGCTAAAAA	AAGCGTATTG	AAAGACACCA	660

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## 1524UP

45	GATCTATCGA	AAGTGTGAAG	CTCCTAGACA	AGTTCGTCCA	TCCCAAACC	GGGAGAACC	60
	CTTTGTGCTA	CCGTATCAAC	TACCAGTCCA	TGGACAGGAC	TGTTACCAAT	GCCGAGGTCA	120
	ATGTCCTTACA	AGAGCAGGTC	AGTCGGGAAC	TAGTCAGGCT	TTACAACGTT	CAATTGAGAT	180
	AGCCCAATCA	GGCCGAGACT	AATAAACTTG	TATATACAGC	TTTGCGGACA	TCGCACCCAT	240
	GTAACGTATA	GTATGATATC	TGCTTACTCA	TATCGCACCT	GAATGCTAGC	AGACTTCGAG	300
	AAATGCCTTA	ATACGCAGCA	TATCCGATAA	CTAGTGCCTA	AAGCCAAGTT	CTTGGATCTT	360
	CACAGCTAAC	CGTTTTTCTT	TGCTCCTGAT	GGCAGCTACA	AGAATAGCAA	TCCTTTATGG	420
50	ATCTGAAACC	GGTACTGCAC	AGGATTTTCG	TAATATACTG	TCCCACCAAC	TACGTCGTTT	480
	TCATTACAAG	CATACGGTGT	GCTCTATTGG	AGAATATAGT	GCCCAGAATA	TCCTCGCATG	540
	TCAGTACCTA	TTTGTCAATT	GCTCCACCAC	CGGGCAGGGT	GCGCTGCCGC	AAAATGCGCG	600
	GCAGTCTCCG	CAGGGCAAGG	TGGAAGGTAC	ACCATGGAGT	GTGCTCAAAA	GAAGCTCTCT	660
	CCCACCAACT	C					

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## 1525RP

	GATCTTCTCT	CGCTGGAAC	GGTGATGCGT	CCAAAATTTT	AACTTAACAA	TTTTTCACCT	60
	TGACCTCGCC	AAGCATCTAT	ATCACGTGAT	TCCATCTGAC	CAACCTCATC	CCAAATGCAG	120
5	GCCATTGGCT	GCTGCATTAA	CGGTCTCAGT	GCCCGGCTAG	AGAACTAGCG	TTACGCTTTG	180
	GGGTTTACTA	GCAAGTGGCC	GTGCCGTGGG	ATTTCGCAATG	TGGGCGCGCA	CCTTATCCAC	240
	GCGACACAGA	AGTGGGTATT	TTCCGCTTGT	TACATAGATG	TCCAAAAACA	GTACGCGCAA	300
	AGCACCAAGC	AAGCTTCAGC	AAGACTCAGG	GAGGTGTTAG	AGGCGATAAT	CCAACTCTGTG	360
	CTGAATGGAG	CAGGCGACGG	GACCAAAGTG	GATATTTTGA	GGCGAAAGTG	AGACGATGGC	420
10	AGCGCAAGAG	GGCAATGGAG	TAAACGGGGA	CCTGGACGGC	GGCATGCGAG	AGACGTTCAA	480
	CCCCGTCAAG	CCGCTGGACT	TCAACGTGAA	TTTGGCGGTT	TACCGGGGCA	AGGCGGGGCT	540
	CGGGGAGACC	CTGAACGTGC	GCGCGGCGGG	GCAAAAGCTC	AGGGTCGGAG	GAGGAGACAG	600
	ATAGCGAAGC	GAGCGGGAGC	TCCAGCCGGG	GGCGGGGGAG	TGCAGACACG	TCTAGTCTGG	660
	AGCCCCCGAA	GGTGGACCGG	TCGTTGACGC	CTTGGCGGCT	GAAGTCGTCG	CC	

## 1525UP

	GATCATCGCG	ATTTTCGGTG	GCGTTGATGA	GAAAGGCCCT	CACTTATACA	TGCTTGAACC	60
	AAGTGGCGCT	TACTGGGGTT	ATAGAGGAGC	CGCTGCCGGA	AAGGGCAGAC	MAGCCGCTAA	120
	AGCGGAGCTG	GAGAAACTGA	TTGGGAACGA	TAAGTCAGAG	CTGTCAGCTA	GGGATGCAGT	180
20	GAAAGAAGCG	GCTCGGATCA	TCTACGTGGC	CCATGAGGAT	AATAAGGAGA	AAGAATTCCA	240
	AATFGAGCTG	AGCTGGTGCT	CCGCTTCGGA	GACGGATGGC	TTGCACAAGG	AGGTACCAAA	300
	AGAGCTATTT	GATGCAGCGA	TTGAGTTTGC	GAAGAAGGAG	ACCGGTCAGG	AGAGTGATGA	360
	TGATTCGAAGC	GATGACAACG	CATCTGGAGG	TGAAGAGTCC	TCAACAAAGA	AGGATGCTGA	420
	CGGTGATGTC	CAGCTTTTCT	GATAACAGCC	CGGCATTATG	TGGAGGTTCA	TTTCATGACA	480
	ATTGACGGAT	GTTACTAAGT	GTATATTAAG	TTAATCCACC	TATATAAATT	AATAACATGC	540
25	AAAGCAATTT	AGAATTTGTC	GGAAAGCAGG	TTAAAGCATG	TCTACTCTCC	TTAATCTTTC	600
	GCGAAGCTGT	ACATTTTCTT	CTCAAGTGAA	CGAATTCTAT	CCACCGGCTG	CGTCTGATTC	660
	TAATTTCTTA	CGTTCGCGTT	CTGTGTACCA	TTTCCGCGTC	AGC		

## 1526RP

	GATCTGGCCG	CGACCTTGAG	AGGCGTCTGT	ACCTTCTTTC	AGCACAACTA	TTGTGGGAGC	60
	TTGGTTTCCA	AAGTTCATCC	TGAGCTCGGT	GGTCTGTCAG	ATATGGTGGG	TGATGGCCTC	120
	GTCACGGTCT	GTCAGCTTCC	TGTACCGACG	ATGACGGCAG	TTTTTGCCAC	TAGGCCATTT	180
	TTTTTTTTCAG	CTCTAAGATG	GCAGACGGCA	AGGAGAATGC	TCCAGGACAC	CGGATAGAGC	240
35	TCCAATCTCA	GCAAAACATC	GCCTACTGGC	CCATTGCTGC	TGCTGCATAA	CACCTTCTATG	300
	GCTTAGTTTG	TGCACGTGGT	CGGCGCTTCA	CATTGTATCT	CGTGAATTGC	GTACCGGTAC	360
	TATATTACGG	TTGTGTGGCC	GAGCGGTCTA	AGGCGCCTGA	TTCAAGTGTA	TGCTTACAGC	420
	TGTTCCACAGC	TGAACACTCA	GGTATCGTAA	GATGCAGGAG	TTCGAATCTC	CTCGCAACCA	480
	ATATTTTTCG	GGGCGTTTTC	GGGGCGCCAG	CGAAACTGAA	CCGCACACTA	TTTCGTGGTA	540
	CCGTTGGAGG	TAAACTGTTG	GAATCCGACA	GTGGGGTACC	GAAACCATCC	CAGCCTCTTA	600
40	TTACTAAGCT	GGATCGTGCA	CTGCAAGCGG	TGATATTGGA	ATCGTCCCCA	CGTATTATTA	660
	CTAAGCCGCC	ATCTTGCCGG	CCATGAGGAG	GGTACCGAAA	ACCAATCCCC	AATTTGCATT	720
	ACTAA						

## 1526UP

	GATCGTCAAC	AGGTCCCCGG	TCCTCGGGAA	CGTCTTGCCA	TCGCCGCGG	ACAGTCTGTC	60
	GATCTTCACG	TTACCTTCGA	TTACCTCCGA	CATGCTCGTT	GCTGCTCCCG	TGGCTGCCCG	120
	AGAGTGATCA	AGTGCCTGTT	ATTAAGGCC	CCAACGCCAC	CCGCCGCGG	GGGTAACACG	180
	TGCCCCGCGG	CTCGCGCGGT	TGGGGCTGTG	CGGCCCGGCC	GCCCCATGCA	CCGGCAGCGG	240
	GGCCGGTGCA	CCGCGTGCGC	GCACTTTGCG	CCCGCGCGCG	CGCCCACTGC	CCGAAGCGGT	300
50	AAACTTAGTA	CGCAACCGCC	CAGCGCCCGT	CATAGCATAC	GGACGCCAGA	CGGGGTAAGG	360
	CCGTAGCCCC	GTGCGGAATG	CGGGCAGCAT	ACCTCTTTAG	GCAGGATACT	ATTTTAAGGC	420
	GTACAGGCGC	GCAGCCCATC	GTGCAGGCTG	CAGTAGCAAG	CTGAGACAGG	CTGGGCAAGT	480
	CTAGACCTGG	GACACAGCCC	GCAACCTAGA	GGCCGCGGTG	CGCCGAGGGC	GTGAGACATT	540
	TTCCGGTGCGA	GGGCGCGTGG	CAGCAGGACA	AAGAGCCGCG	AGAGAAGCAA	ATGCMCAACT	600
55	AAACGGGGAG	GAAGGGCAGC	GGATTTCTTT	TTGGGCTTCT	GTGCGAGGTG	GAAATTGTAT	660
	AAATAATGGG	AGCGGCGGCT	GGTCTTGCCG	GCTGAGACTG	T		

## 1527RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACAAC	GGGAATTAA	GCCCCTTTTC	60
	CAATATTTTG	AGCGTCGTGT	CATAGCTCGG	AAGACGCAGC	AGAAGCCCCC	CCAGTAGTGT	120
5	CTGTTTCATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTCGTCAGGA	TTACAGTAAA	240
	ATAATGGTAG	AACCGCGGAC	TCACAGAAGC	GACGACCGCT	CGAAATGAAG	TCGGCCCCGTA	300
	GAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTACACGGG	360
	GGACACCGTG	CCCATAACGT	GCTTCTGCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
	CCGCGCGAGC	TCAGTCTCAA	GCTCGTCGAT	CCGTCGCAGC	AGCTCCACAT	TGGGCGTCGA	480
10	GCTGAACAGC	TCCCCTGAGT	TCACGTCGTG	CGTAAACTCA	GACAGGTACA	CACACTCGGG	540
	CAGGCCCTTC	CCAATACATG	TATAGCACTT	CGGCCGCGCC	TTGTTGCACT	TGACGCGCCG	600
	CTTGCGGCAG	AACACGCACG	ACTTGCTGAC	CTTCCGCCCTG	GTTTTTCAAA	TCCTTGCCATC	660
	GGACTCTGCC	ATCCCGCCAG	CTTCAAGCAA	AATGATTAGG	CTATA		

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## 1527UP

	GATCGCGGAC	GTGGAGCACT	GGCCGGAGAT	GCGCGCGGCC	ATCCTGGTGG	TTTCTGCGGA	60
	CCGCAAGGAC	ACGCCATCGA	CGAGCGGTAT	GCAGCAGACG	GTGCACACGT	CGGACCTCTT	120
	CAAGGAGCGC	TGCGCGACGG	TGGTGCCGCG	GCGGTACGGA	AAGATGGCGG	CGGCGATCCG	180
20	CGCGCGCGAC	TTGCGGACGT	TTGCGCGCCT	GACGATGCAG	GACTCGAACT	CGTTTCACGC	240
	CACCTGCCTG	GACTCATTTT	CGCCGATCTT	CTACATGAAC	GACACTTCGC	GCCGGATTGT	300
	CAAGCTGTGT	CATCTGATCA	ACGAGTTCCTA	CAACGAGACC	ATCGTGCGGT	ACACGTTTGA	360
	CGCGGGTCCG	AACGCGGTGC	TCTATTACTT	GGCGGAGAAC	GAGGCGCGGC	TCTGCGGCTT	420
	CCTCTCTGCC	GTCTTTGGCG	CCAACGACGG	CTGGGAGACC	ACGTTCTCGA	CGGAGCAGCG	480
	CGCCACCTTC	GCCGCGCAGT	TCGACGAGTG	CGTGCGCGGC	AAGCTTGCGA	CGGACCTGGA	540
25	CGACGAGTTG	CACAGAGGAG	TTGCCCGCCT	CATCTTCACG	AAAGGTCGGG	CCAAGGGCCC	600
	AGGACACTAA	ATCCTCGCTC	ATCGACCCCG	AGACGGGCCT	GCCCCGCTGAC	GCTATTCTCC	660
	TGCTATTTTC	TGCTCTGTAT	ACCCTGCCAG	AACGCGCTAT	ATATATAGAA	TATGCATT	

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## 1528RP

	GATCACTGTA	TCGAATTTGA	CACCCAAGGA	AGCCAAAACA	TCGTGGGCGG	ATCCCGACAA	60
	TGTGGAACAT	ATGATATCGC	TTTCTGCAAG	GATGCGTGCC	TGAGCTTTCC	TCTTATTCAA	120
	TTCTCTATTT	CTATAATTCA	CCGCATTCCCT	TTCCCTCAGC	TCATCGCGCT	GCTTACCTAG	180
	CTCATTAAATC	TTCTTGCTCA	AGTCCCTCAA	CTTTAGCTGT	ATCTTAGATA	TCTCATCAGT	240
35	TGAGAGTTTA	CTAGTCGGCG	AACCATCCTC	TTTATTTCATC	ATATCCCTGA	GCTTTCTCCT	300
	CTCCGCTACG	GCGTCATGAA	AACCTCTGATC	TAAGTTTCGGA	TCGTGATTTA	TTTCGTACGA	360
	CTGATTCAA	GCTCGCTTGT	CAACCAGCTC	TTCCAACGTT	AGGTCTCTGA	TAGCAGCGTT	420
	AACCTGCATCT	GATTTACCAA	TCCGCACTAA	TTTTGGTTTG	AACAACCTGC	CGTCAGTATC	480
	GACCAAACCT	TCTCTCAGAC	GCAACACAAG	CTCGTCAACG	GCTGCATTAC	TGGGTGCACA	540
	TATCAGAACT	TTTTGTTTCT	GTAGTAACAT	CTCAGTAGAG	GTAGCGTTTC	ATTCTGTGGG	600
40	ATTTCTGATA	ACATTTGATG	GTAGTGCTTT	TGCGGTAGTT	AGGAAAAAGC	CGACGACACC	660
	AAGAATAGTC	TTAGTCTTAC	CAGTACCAGG	GGGTCCCTGG	A		

## 1528UP

45	GATCCAGCAT	TTGCGGGTAA	ATCGGCGTAT	TCCGCACGCG	AAGGTGGGAA	GCTTCAACGA	60
	GTTGATCTGC	ATGTGGCGGG	CGCAGATGGT	TCTTCCACTG	CTGCGAGACT	TTGATGCCTG	120
	CAAAGTATCA	GATGCTGTTA	TTCTGGCGAT	GTATGAGATA	CTGCTGAATC	CGCAGATGCT	180
	CCGGTGCTCG	CCGGAACCTA	AGTACTACTA	TGATCTAGCA	TTCAAGGGCA	TGTATGAGAC	240
	GGGACATAGG	CTTTTAGACC	ACACAAAAGA	ACAAGGTATC	AATCTGCTCG	TACCTGGAGT	300
	CGTATATTCA	CAGATGTACG	GCTGCCCTGA	ACAGAGTTCT	TGGGCAACAC	GTCTCTGCG	360
50	GCACTTCTTC	GAGAACGAAT	ACTCAATCAC	AAATGAAAAC	GTGACAAACG	AACTGCTTGA	420
	CGAAATCACC	TATCATTTTTA	TTTCAATTACA	GTTGAGCAGG	AGCAACAGCT	CGTATTTGAG	480
	CATGATTGGA	CTATTCTGGA	GCAAGATGTG	CCCGTTCTTT	GCGCTGATGC	ATGTTGATGT	540
	CTTAAAGGAG	TACTTTTATTG	AGCTCAAGAA	TATTAAGTCA	TTGCGGTCCA	CGACTAATGT	600
	TCATATTGAA	TCTGTTTTCA	AGGTATTTTA	TCACCATCTC	ATAATGCAGG	TAAGATCAAA	660
	ACCGTTGGAT	ATTCTGCTCC	GTATTTTGA	ATTATCCTGG	AAAACTAGG	G	

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## 1529RP

	GATCAAAAAG	AAGGCGATTG	CTATGGCGAC	GGTGA CTGCT	GCTACCGCCG	TCTACGCTCT	60
	ATATCCTTCC	TCTCCGATGT	TGGTTGACAG	CTCCGCGTTG	ATCAAGCTAG	AAGGCACCAT	120
5	TTCTCTCAGT	AGCAAAGGTG	CTACTAATGA	TACTGATGTT	TTCATATTAC	CAGAAAAACA	180
	TTCTGCTGTT	CCGGGCTACA	ACACAATCAT	TCGTTTCCTC	GTACCCGCCA	TGAATGCCTT	240
	CAGGCTTTAT	GGCAGGCCGA	AAACACTATC	GGCGAGCAAG	GATGACACAA	ACTCACTCCT	300
	GTTTAGTCTA	CCAGCGCTTC	CACATGTGCA	CTACTTGCTG	GTCTAGGATT	TGCTTCCATT	360
	AGTGAATTCA	GCCTCTGGCT	CATGGACGAC	GCAGGAGTGG	CGGAGACAAA	TCAAGGCTCT	420
	ATTACAACGG	AGGGTAGCGG	CTGGCTATCA	GGGATGTGGT	TCAAGCTCCG	GTCTATCCGG	480
10	CGCTCTGTCC	TCCCCTGCTC	TGGGTCCATT	GAGTCCTACT	TCTTTGTTCAT	CGCCGCATTT	540
	TGCTCCGTCC	ATTGCGTTTT	CGCCTACTGA	GTCCAAC TAC	ACTTTTATGT	CAAGTCACTC	600
	AAGAATAACT	TCACTACATG	ATAATATCCA	GAGACCATAT	TGAATACCGT	GGCCAGCACA	660
	TCCGATAATA	CWCTGCACCC	AAACAATATG	CTATCTCCCC	CAGGTCTTGC	CCCTGATGCA	720
	TT						

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## 1529UP

	GATCCCGCTC	AATGCCAAGT	AGAATGTTTT	TCGGGGGAGC	CCATACAGTA	CCGCCTCCTC	60
	CTCATCCCCG	CTCTCCTGCT	CCACGTCCTC	TCGTGCAACA	TCTAGCAGTT	TCCCGATAAC	120
20	ACTGGGGATG	GTCATGCTCA	CGGCTCCGGA	TATCAGCATC	AGCACCAAGG	CGCATACTAG	180
	AGACTTGAGC	TCAGGCCGCG	CCAATTGGAA	CAGTCTACGC	ACATCCTTGG	CACCTGATGC	240
	GTTGCCCGTC	GCCGTCGACA	GCTCGAGTCT	TTCTTGCTGG	GGTTTCTCTT	CCGTACTTGC	300
	CCGAGGGTTT	GCTGTTGAGT	TTAGCCTCGT	TTGAATTCTT	GTGATGCGC	TGAACGAAAA	360
	CGGGGTGCGT	TGATGTAGAT	GATTGAACGG	CGGCCATCGC	TGCATCCCAA	TAACAGGCCCT	420
	CGGCACCTGC	TTAACAGCTA	GCGATAGCCA	CATATATGTT	CTCCTCGAGG	TCATATTCCTC	480
	AGTTTTCTTC	TAACCTCACC	AGCCTTGTAG	GCCTCTCGAG	TTGCTGTAA	GTGGTGAATT	540
25	TGCCGATCGG	ACTCATTTTT	CATGGAGAAT	AAATAATTGT	ATTACAAAAT	AGAGATGCAT	600
	GCCGAGCTAG	TCGAGGCCAG	CTACTATACA	GCTCCTGGAG	CTTTGCAGTT	GTAGCGCACC	660
	GGTTTTTCGGC	TCCATGTGAC	TACAACATTT	T			

## 1530RP

	GATCCCTCTG	CTACAAACAC	ATACCTAGAT	TTCTCATATT	TTATACTGAA	TACATATAAT	60
	ATATCATTTA	ACTGTCTTCA	TTCATGAGAC	GTCGTCTAAG	TTCTGTGCTG	CTCAACTTGT	120
	TTTCCCACTT	GTCAGCCTCT	TCGCCCCCCA	GTACGTTTAC	CACATGCACG	GCTAGCTTCC	180
35	TCATTCCTTT	GCTCTCACGC	GTATCGTTGA	TTGTCTGGGC	ACCGGCCACA	GTTTCCTCAC	240
	TCACTACCAG	GGCTTCGATA	CCAGGTTTCG	TACCCGTGGG	CCCGCACACG	TCATGTAACG	300
	CAAATATTTT	GATTTCCAGC	CCCGGTTTCA	GCCTGTGAAG	GAAGCTGCAC	ACGTTATCGC	360
	ATCGTTTCGT	GAAGGACTGA	AGCTGCTCCC	TGTATTTCTT	GTTCCGCAGC	AGTTCTTCAT	420
	CTGTAATCCC	CACGATCAGC	CGGGACGCAG	TCACGAGCGC	GGCAACACTG	AGCAATATTT	480
	TATGTCCGTC	GTGTAAGTGG	TCGAAAGTGC	CTCCAGCGC	GCTAACAGCG	TACTTGTCTC	540
	TACCGCCACT	CTCGACCGGG	CCCGCAGCCG	CCATCGCCGG	ACTATCAAAC	AGCTCTATCT	600
40	GCCTGTGCGG	GAACGCATCC	TGCAGCAGGC	GATCGCTCAG	GAATACAACG	TCCCACTTCA	660
	TTCCGGCTGTA	CGCTTCCATA	CTGACGTTGA	ACAAAACATT	TATCGGGGTC	GTGT	

## 1530UP

45	GATCCTGGGA	CGACATCGAC	ACCATTTCTA	TCGGTAACGA	ACTTGTGAAC	AACGGCCAGG	60
	CGACCGTGGA	CCAGATGGCT	GGTTACATGA	AAACTGGCCG	CAAGTGCCTC	GCTGAGGCCG	120
	GCTACAAGGG	CCCAGTTGTT	TCCGTGGACA	CTTTCATCGC	TGTAATCAAC	AACCCTGGTC	180
	TATGTGACCT	ATCAGACTAC	ATGGCTGTCA	ACGCCACCC	ATACTTCGAC	TTCCACACTT	240
	CTGCTGCTAT	GGCCGGCCCT	TGGGTTTTGC	ACCAGATCCA	GAGAGTCTGG	AGCGCCTGCA	300
	ACGGTAACAA	GAAAGTTGTC	ATCACCGAGA	CCGGCTGGCC	TACTCAGGGT	CAGACTTACG	360
50	GCAAGGCCAT	TCCATCCAAA	GCCAACCAGA	AGATGGCCTT	GGAATCTATC	AAGGCCACTT	420
	GTGGTGATAG	CGCTATCCTA	TTTACTGCTT	TCGACGACTA	CTGGAAGCCA	GATGGGCCCTT	480
	ACGGTGTCTG	GAAGTTCTGG	GGTATGCTAT	AAGTTGCCGT	GAGGTTCTTT	ATGACCTGTC	540
	TCTTTATTTT	GCTCGGAACC	CTTACATGCA	GATGGGGGGT	GGCGGTGCAT	GGGCCTGCAG	600
	CCTCCGGGCC	TGCAAGTTTC	TACATCGCCC	TACTTTAGCT	GCCACGGGAC	TTTTGAATTT	660
55	CTTTGGCAGC	TGGTACTGCT	GGCATCCTTC	TCATAGAACA	CAGTGTGCCC	ACAGGG	

## 1531RP

	GATCTGCATC	CTCGTGATGG	AAAATACGGC	CATGCAGCTA	ATTTTGGGAAT	GGTTTCTGCA	60
	TACCGTAAGA	GAGATGGCTC	CAAATCATAC	CCAGTTACTA	TCCTTGTGAC	TAACTTTTCA	120
5	AAGCCGACAC	CTACCAGACC	TGCTCTTCTG	AAGTTGGGAG	AACTCACAAC	GTCTTTTCAT	180
	GAGTTAGGCC	ACGGCATACA	CGATTTGGTG	GGTTCCAATG	ACTTGGAGTC	GCTCAACGGG	240
	CCTGGGTCTG	TCCCATGGGA	TTTCGTGCGAG	GCGCCCTCTC	AGATGCTGGA	ATACTGGACG	300
	GCACGGCGTG	ACGTTTAAAC	TATGTTATCC	AAGCACTACG	AGACAGGTGA	GAAAAATCCCG	360
	AAGTCGCTGC	TGGATGCCTG	GTTTAGTGT	GGCGGCCTCA	ATTCAGGATT	GGCCAACTTG	420
	GGCCAACTGA	AACCTTGGCTT	GTTCGACATG	TATGTGCACA	CCCGCGATTA	CAAAGGAGCG	480
10	GAGGTACGGA	AATTATGGAA	TGATCTCACC	AGAGAGATCG	GGCTCATGAA	CTTAAAAAAC	540
	TACACTAGCA	CCGGCTATGA	CTCCTTTGGA	CATATTATGG	CTGGATATGC	TGCTGGCTAC	600
	TATGGCTACC	TTTGGTCCCA	GGTTTTTGCT	GCAGATATGT	ACGACACAAA	GTTCAAGCCC	660
	AACCCATTCA	ATGCTACGGT	GGGTGTGGAA	TACAGGGACA	CTATTTTAGC	TACCGGTGGA	720
	CTT						

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## 1531UP

	GATCCAATCC	TGGAGGCGGG	TTAAAGTGCT	CCTCAATGCA	GCGCAGCCGG	CACTGGAGTA	60
	TGGCACGGAA	ATCGCACTCT	GGAGGAGGCG	CGTGGTTGGG	AACTGGATCG	TCCACCTCGC	120
20	GCAGAAAGGC	CGTTTTCAAG	GCGCAGGCGA	GGACCGGAAT	GAGCATTAAT	AAAGAGGTAA	180
	CGTGCAATGCT	GTGAAGAGTT	TCACTTTATG	CGTTGCATT	CTCCCCCCT	GAAGACGAAA	240
	ACACGGCGCA	CATGCGCTAT	ATATACCCTT	CGTGTCTACT	ATTGTGCGCT	GCCCCGCTCTC	300
	ATGTCAGTTT	TTACTTTTTTG	ACGCCGGGAA	CGCGACATCT	GCCACAACGC	ACCAACGCC	360
	AGTGACCAGC	TCTATGCCGC	TTGCTCTGCC	AATAACCAGC	CCCCTACTAG	CCGAGCATTT	420
	TGCCTTAGTC	CACCCAGATAT	TCCATTGTTA	TCGTTGCTCG	CCAGCCTCGG	GCTGGGACAT	480
25	AAAGATCGGA	AGCTCCTGTG	CAAACCTGCA	CAGCGCGCCT	TCGAGAATAC	TCCGCAGGGA	540
	CCCCCCTCC	CATTAGTCCT	TGGCAGTTTT	TTGCTTTGTC	CCGCGATAAT	GTATCTAAAT	600
	ACAGAATATC	GATTACGGCG	AATAGGCAAG	TTTTGTGGTC	TGACATGCCG	AGTGTCAGTT	660
	CATGATTACA	TAATGTGTCTG	TGCCATATCT	GT			

## 1532RP

	GATCTKTTGA	AAGAGTAACC	AGGATCAAGC	CTGCGGTATA	GCCAGCGAAA	TATGCATATG	60
	AAGTCTTTCT	GCGTGGGCTG	TTTCAATGAC	TTCAAGTGATA	TCGCATGCCC	AGTTTCTATG	120
	TCAAACTTGC	GCGACTGCAG	ATAATCAAAT	ATCTCCTGCT	GCAACACTGC	CTGGTAGTTT	180
35	TTGTACCGGA	GAGGTGCGCG	GTCGCGGGTA	CTCTGCAGCG	CACCGTAAGC	TGACGGACCC	240
	CCGCCGGGAA	CAATCGAAGG	CCGCTGCGAA	GATCGCAGAC	TCCGCCGGAG	AGACTTTTCG	300
	ACCTCGGGCA	CAGGTCTTGA	AAGAGAGCTC	CGGCCGTTCC	GTGCCAGACT	CTTGTTTATC	360
	ATGTCCGTAA	GAGCAGCGTT	CGTGCCAGGT	ACGCCCTTCT	TGTTTCGTGTT	TCCACCAATT	420
	GATGGAATTT	GAGACGTGAA	CCTCTGCGGA	TTCAAGCTAT	TGAGCACACC	ATTGGCACCA	480
	CTTGAGCCCC	TTGCTCTGTC	CATCCCTAAT	CGTCCATACC	TACGGGCGGC	TAATAAGTTA	540
40	CTACCAGACT	CTGGCCCTCA	TCTGGGACTG	ATGTTATCGT	CTGCAGCCAG	ATCCTGTTTG	600
	TGACCCGATC	GAAATCATCG	AGTACGAATA	ACCACGTGAC	CATTATTAC	GTGATGAATT	660
	TGCGGTCCC	TGTGCGGAC	TCTTACTCCA	GGTTAACCAT	GACTIONATGG	GCATACCTCA	720
	GA						

## 1532UP

	GATCATCTGA	ACGCTCATGA	ACAGTTGCGG	GAACATCGTG	TCCACGACTA	TGCACTGCTG	60
	GATGTCCCTC	TGGCCGAAGT	ACGCGCGGTC	CGGAGCAACA	ATGTTGACCA	GCTTAGCAAC	120
	GACCGTCCGC	ACACCGCGGA	AGAAGCGTGG	ACGGGTGCGA	CCCTCCAGCA	TCTCGCTGAC	180
50	GCCAAGCACC	GACACAAACG	GCCCGCGCTG	CGCCTCGACC	TCCAGTGGGA	TGCCGCGCGG	240
	GTACATTTCC	GCGGGAGAGG	GAGCAAAGAG	CACGTCCACA	CCGGCCTCTT	CCAGCAACGC	300
	GCGATCCGCT	GCCAACGTCC	TGGGATAGCG	GTCAAGATCT	TCGTTGCGCG	CAAACCTGCGA	360
	AGGGTTTACG	AAGACTGAGA	CAACAGTAAA	GTCGTTTTC	GCGCACGATC	TCCGCACGAG	420
	CGTCATGTGT	CCCTCATGTA	GGCAGCCCAT	CGTTGGCACA	AACCCAAATCG	TCTGTGTCTT	480
	GCAATCTACC	GTCTGCTTGC	GCCATTGCGA	GACTTCCTGG	ACCTTATTTGA	GCACGTGCAT	540
	GAGGCGTATC	GCTTTGATGG	TTTACGCTTC	AAGTTTGTCT	GTGTGCATCT	CACAGATTAA	600
55	GGAAGCTTGC	GCACACTAT					

## 1533RP

	GATCACGAAC	TCCATCATT	CAAAGTCCAT	CGCGTCGATA	CGAAAACAAA	ATGCACAGCC	60
	GCTACCGACC	TTCCGAAACC	TCGAGAAGAT	CAACCAGCCG	CCAAAGAACG	CTGACCATGC	120
5	GTGGGAGTAC	ATAAAATCGT	GAATTATTGG	GGTTGTATGT	ACTATATACT	ATCGCTCTGC	180
	CGCCCAATGA	TGGTTACGCC	TCTTGCACGT	GCATTCTGGG	TGACGAGGTT	GTCTCCGTAC	240
	ACCTCTACTA	TTTCCAGGTT	GGGCGCACAT	TCGCTGATAT	GGGCGAGCAA	TTTGTCTGTA	300
	ACGCAGCGGA	CGAACCCTAC	ATTCAGTTGC	TGCAAGTTTG	GACAGGACAT	TAGCTGGAAC	360
	CCAGCTGCCG	TCAGGTTTCT	GGCTGAGTTC	AAGTTTAGCT	CTTTGAGGAA	TTTGGACAT	420
	GGATTCAACC	ATATCTCCGC	AATTGATGCA	TCATCCAGCT	GATGGCAGCG	CCTCAAGTTG	480
10	AGGTAGTGAA	GTCGGGGAAG	CTGGACCGAA	GAGAAAAATG	TAATGAATCC	ATCGGACGTA	540
	ACCTGGTCCA	ATTCTCTAG	GGAT				

## 1533UP

15	GATCCGGAGA	CAGACGTGTA	TCTGAGTTCT	ACCGCTGGGC	GCTGAAACGC	ACGTCGTTAG	60
	CGCACATCCT	GTGTGCTTGC	ACCGGCCCAT	AGCAACCAAG	TATTCTTATA	TTCTGTGAAA	120
	CTGCGGTAAAT	AACCATGTAG	AAGATTCCGC	GCCCGAATAC	CCGTTTTACC	CCAATATGTC	180
	CGTCATGTGA	GCTATTGGAT	CGAAGAGTTT	TTAATGACGT	ATCCCTTATC	ATAAAGCGGT	240
	GCTGGATTAT	TGGAGCATGC	ATCTGGTTCA	GCTCGGGCGT	GCCAAATATA	TGGTGCAAGA	300
	AGAACTATC	GTACCAACCC	CGTCTGTTCT	GACCTGTGTC	CTCTTAATCG	GCATGACTAA	360
20	TATGGGGTAT	CCTTAAACCC	TTTAAGATGT	TACCTCCGGT	CTCCAGGCGG	GTTGTCTAGT	420
	TTACAAGAGT	AAATACCACC	TTGCCCTGG	GAGGGTTCTT	ACTTTACAGT	AGGAAAGAAT	480
	CGATACCACT	GGTGGGGGGA	TTTGGTATAT	TTTGAAAGAT	GGATGGAATG	GAGGGCTCCT	540
	TATTGACAGC	AAAGCCACTC	CGACAGAATA	CCCACACCTT	GGATTTGGAA	GCTGCGGATC	600
	GACAGAACAT	GGTTACGTAA	TCGAATTGTC	CTGTCGGGCC	GCCCTTCCGG	TTAATCAAGA	660
25	AGAACAACCG	CGGGGCACGC	AGGGAACAT	TGAATTTCAGT	GCTGCCAAGC	CTAATTTATG	720

## 1534RP

30	GATCCACATT	GGAATATGGG	TATGGGACTT	GATGGTTGAA	CGCTTCGCTT	CAACCACTGC	60
	AACATTGGCA	AACCGTTTGA	AGTGCTGGAT	GATTTTCTCC	TTCTGGATCG	CAGTCAAGAT	120
	GTGGCCGAAT	CGTTTTTCGT	TGTATAGGCC	TTGCTCATCC	TGTGCTTCAT	CCTCATCAGA	180
	CGCTAATGGA	ACGTCTGGCA	CAATCTCGAC	GCCATCGCAG	GATGCGATAC	TCAAGGTATT	240
	GAGCATGTTT	AAGGCATGTT	CCCTTGCTAC	TTTAAACCCCT	GCAATCAACTT	CCTCCTCGTT	300
	TTTCCATAGG	CGAGGGACAT	CGTTTTGATC	GTAACGAAAC	TTACTTTTCAA	AGCGTTCTCT	360
35	CAGTATAGAA	ACCACATTGT	CTTCTTCAA	ATACTGGTGG	ATAATATCAT	ACAGAATAGT	420
	CCATGCATTT	GACCGGATCT	TCAGGTATAA	AGCATAAATTG	TCCTCCTCGA	TGAGGTCGAG	480
	CTGGAAGTCG	TAAGCGGTAC	TTTCATCGGT	GACATCCCCT	AAATTGGGTA	GTTTATACTT	540
	TAGAACTGAA	CGCGGGAATA	CATCATCAAA	GTGGTCCATA	ACAAGTTGCC	AGACGTTATC	600
	CTGTGGATGG	GAGAGTAAAGT	GGACAATATC	GTCTCTAGTA	TGTGTGAATT	GGTACTTTTT	660
40	CGCCCTCAAT	ATAATAGCTT	TCATCTCCTT	ACCACGCTCT	CTTTCCGCTA	GTTCACTATC	720
	TTCTCCA						

## 1534UP

45	GATCAGCGTG	GACTTGATCA	TGGTGTGTCT	CGTGCGGCCG	TGTGGTAGGC	GGGGGACGCT	60
	GCTGCTGTCC	TTTGTGCGGC	CCGCGGCGGC	GGCGATCAAA	GATCGCGCAC	CACGGTCGCC	120
	GCCGGGGGGG	CTCCAAGACA	CACGCGCACA	GCAGCGCGCG	CGTGCCGGGC	AATGCAGCGC	180
	GCACAGCTAT	CCTCGCGCCT	CGTACCGGTG	GCTGCCTTCG	GGCGGATTGC	GCTCGTCAGC	240
	GGTCACGTGA	CCCGAGATAT	GTTGCAAACC	AAGCCATCGA	TCGGCATAGG	AACGCATTAC	300
	CAGCCGATTG	GAAAACCCCT	ACAACCCGCC	ATCTGCTGGT	ACGACCACCG	CAAGTCGCTG	360
	GCATCGGTTG	CACAGTGGTA	AGGTCTTCGT	TCAAAATTAC	TCTGCCAGGG	CCGCTCTCAA	420
50	AACCTGTCAA	GTGCAGACGC	ACTGACAGTC	CGTCAAGATG	CGACATTACA	ATGCTCTGGA	480
	AGCTCTCCAG	TAGGTTCTCG	CGCGCGTCT	AGACAGTCAG	GGGCAGGCTT	CATCGACAAA	540
	GACGCGCAAG	GATGTCGCAA	TTCTGTCGCA	CAGTCCACTC	TAGGGTCGGA	CGGGAAAAAC	600
	AGCGTACTC	TGCGTTGACT	GGGGCGAGAC	TGGTAGCCGG	CTGCGTGGCC	TCAATGAGGA	660
	CAGACCAAGG	TGATCATGAT	AC				



## 1535RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACAAC	GGGGAATTAA	GCCCCTTTTC	60
	CAATATTTTG	AGCGTCGTTT	CATAGCTCGG	AAGACGCAGC	AGAAGCCCCC	CCAGTAGTGT	120
5	CTGTTTCATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTCGTCAGGA	TTACAGTAAA	240
	ATAATGGTAG	AACCGCGGAC	TCACAGAAGC	GACGACCGCT	CGAAATGAAG	TCGGCCCCGA	300
	GAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTACGGG	360
	GGACACCGTG	CCCATAACGT	GCTTCTGCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
	CCGCGCGAGC	TCAGTCTCAA	GCTCGTCGAT	CCGTCGCAGC	AGCTCCACAT	TGGGCGTCCA	480
10	GCTGAACAGC	TCCCGTGAGT	TCACGTCGTG	CGTAAACTCA	GACAGGTACA	CACACTCGGG	540
	CAGGCCCTTC	CCAATACATG	TAGAGCACTT	CGGCCGCGCC	TTGTTGCACT	TGACGCGCCG	600
	CTTGCGGCAG	AACACGCACG	ACTTGCTGAC	CTTCCGCCTG	GTTTTACAA	TCTTGCCATC	660
	GGA						

## 1535UP

	GATCGCGGAC	GTGGAGCACT	GGCCGGAGAT	GCGCGCGGCC	ATCCTGGTGG	TTTCTGCGGA	60
	CCGCAAGGAC	ACGCCATCGA	CGAGCGGTAT	GCAGCAGACG	GTGCACACGT	CGGACCTCTT	120
	CAAGGAGCGC	GTCGCGACGG	TGGTGCCGCG	GCGGTACGGA	GAGATGGCGG	CGGCGATCCG	180
20	CGCGCGGAC	TTGCGGACGT	TTGCGGCCCT	GACGATGCAG	GACTCGAACT	CGTTTCACGC	240
	CACCTGCCCTG	GACTCAATTC	CGCCGATCTT	CTACATGAAC	GACACTTCGC	GCCGGATTGT	300
	CAAGCTGTGT	CATCTGATCA	ACGAGTTCTA	CAACGAGACC	ATCGTGGCGT	ACACGTTTGA	360
	CGCGGGTCCG	AACGCGGTGC	TCTATTACTT	GGCGGAGAAC	GAAGCGCGGC	TCTGCGGCTT	420
	CCTCTCTGCC	GTCTTTGGCG	CCAACGACGG	CTGGGAGACC	ACGTTCTCGA	CGGAGCAGCG	480
	CGCCACCTTC	GCCGCGCAGT	TCGACGAGTG	CGTGCGCGGC	AAGCTTGCGA	CGGACTGGAC	540
25	GACGAGTTGC	ACAGAGGAGT	TGCCCGCCTC	ATCTTTCACGA	AGGTGCGGGC	AGGGCCCAAG	600
	ACACTAAATC	CTCGCTCATC	GACCCGAGAC	GGGCCTTGCC	CCGCCITGAC		

## 1536RP

	GATCATTTGT	CCTTGCAGCA	CAAACATCCA	CAGCTGTGCG	ATTTGCAGTT	GCAATCCGGA	60
	GCAGCAGCTC	CTTCGCAGCA	TTTGCAAACG	CCAGGCTCTC	CCACCTCTTT	CGCATGTTCT	120
	TCTGACATTT	TTGTTTGTTT	TAAATCGTGA	TTTTGAGTCG	ATGGTTCCGA	GACCGCCGCA	180
	GCTGACTATA	GGGGGGACCA	AGACCCTTTA	TATATTTTCG	CAACCAGATA	CATTAATGCG	240
	ACGCCAAAAC	ACTATCAAAA	ATAAGGTATA	GCCTCATTTT	TATTGTGACC	CATGGGACAT	300
	GCTGTAATCG	GATTATTCTA	ACTAAGCTAG	TATTATGTGCG	GTATCCTTTT	ATTAATTACA	360
35	ATCACTGCTG	AGTTCCGGTA	TCGTGCAACT	GCACACGCAG	CTCATCAGTG	GTTTCGTTCC	420
	CGCGCAGATC	ACGTGCCTGC	GACATGGCGA	CTTCATCCAC	TGGCGCCCAG	CTACGTGGTA	480
	TATGACATTA	TGGCCGAGAG	GTAAAGGCGT	GAGACTCGAA	CTAAATTGAG	GGATCTCTTG	540
	GGCTCTGCCC	GCGCAGGTTT	GAATCCTGCT	GATGTCGTTA	TTTTTTGCTT	GCGCGGCCTA	600
	CGGGGGGCTG	TATTTGCTTG	TTGCTATTTA	GATAAACGAG	ATACTAAACT	ATGGGTAGAA	660
40	CTCGCGGTAC	TTCCCGTAGT	AGTAGGCTGT	GCCGAAACCG	CCGAGGGCGG	TGAGCAC	

## 1536UP

	GATCAGCTCG	GTACTGGAGA	AACAAGGCTA	CTGTCCCTTG	CCTTGACGAA	GTTACGCGAA	60
	ATCGAAAGCA	GCAGCAACAA	GCAACATAGC	AAGACCGCTA	AATACATTCT	CAAGTCATTG	120
45	GAATAAGCTC	TAAAACATACC	GATACGTATA	TTTACTGCGT	TAACGTTTAT	ATACATATAT	180
	CTAGGCGTGC	GTATGGGTGT	TGTACGTGTA	CATCTAACCA	AATAACTCCA	CTATAGCTGT	240
	AGTACATGGC	ATTCCCTTGT	AAGCAACTTC	AGGTCTTGGA	CTACCCAATT	GCTGTCCCGC	300
	ATCCAGCCT	TGGGGTCGTG	GCCCTGTGTT	GACCTCAATT	TAGCGAAGAC	CGACTTGTAG	360
	TCGCTCTCAT	ACTGCTTGAA	TTGCGGAATG	ACGCGGTTAG	AGTCGAACTC	AACATACACG	420
	CGCGTATCGA	CTATCTTGAA	GAGGACATCG	TCCACACGCA	GGAAGAAACG	ACTCAAAATC	480
50	AGCATACACT	GTTCCTTACAC	TCTCACCTTA	ACATTACAGAA	TGCTAATGCC	ATTGTCCGCT	540
	AGTTGCTCCT	CAAAATAAAAT	CATGTGCTCG	TAGAAAAGAA	TGGGGTCCGG	GCTCGAAAAG	600
	CTTCGCCAGA	GGCAGCTCCA	CGCTGTCGTC	TCTGACCATC	GCCCTGCCAT	CTATGGTGCC	660
	CTGGTAGAGC	GTCGTGTACG	TCCAGTCGTA	CTGGTGGGAT	ATGTTTAGGG		

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## 1537RP

	GATCTCCGTA	CTTTAGGATG	GCTTTATAGA	GGGCACGAAT	TTCCCTTTTCG	CCTATAGAGT	60
	TCAGGTTGTT	GGATTTTCGCA	CGTTTTTTTGG	AGCGTGAATC	CTCTTTGTGCG	CTTAAGCTCT	120
5	GAGCTCCATC	TCCATTGACG	CTATTTTTTA	TCTTATTTCAG	AGCAACATTTC	CTACGATTCA	180
	TCATTTGCAG	TTGTTCCCTGG	ACATACTCTT	CATCCTTCCG	CTTCTGTTCT	TCGTCTTTGA	240
	GTTTGCCTAG	CTCGTCTTCC	GGAATGATAT	CATCCCATTTC	CACGTCAGCT	TTATAATCGG	300
	TGACTTCAAA	CTGTTTTAGG	AATTCCCTCAC	CTCCGAGATG	AGACTCTCCC	AAATCTGGTG	360
	TGGTGACGTG	ATCTTCCGCA	TGATTCAAGA	CATCATCCAA	GTTCAAATCT	TCAAGCTTCT	420
	TTTGATTATC	ATGCGCTTTG	AACATATTGC	CTGCACCAA	CTTGAGAATC	TCAGACAGCT	480
10	CTCCTGCACT	AGGTTCGGCT	TTGCTCTTGC	TCGTATATTT	ATTCCCATCT	GTAACACCTA	540
	ACGAGATGAT	AGCATACTCC	AAGATCATCT	TTTTGCGTGC	TCTTTCTAAG	ACTTCTTCTT	600
	CAACGGTATT	CTTAGACACA	AAACGGTAAA	CCATAACATG	ATTCTTTTGA	CCAATTCTAT	660
	GCGCGCGAGC	CATTGCTTGG	AGATCGGCCT	GTGGATTCCA	GTCGGAATCA	AATATGATCA	720
	CAGTGCTGTC	CGTCATC					

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## 1537UP

	GATCTAGACC	ACCCGGGCTC	GTTACCCGGA	TACGAAGTAA	AAGCAGTCGG	GAGCGGTCTT	60
	CTGGCAACGA	CGTTTTCTTC	TACACACCTC	CTCGCACAGG	ATCCAGCATC	CTGCCGCATA	120
20	ACGTCAACGC	CGGCGTTGTG	ATGGTTCCCA	GGTGCCACTG	GCGCCAAGCG	CTGCGTGAGA	180
	AACAGCAGCG	CTGCACTTCG	CTGCTTCCGG	GAGGCTCCTG	GGAGTGGTCC	GGGGGTTTTCG	240
	CCACCGCTCA	ACCTAGCGGG	GCGTCGCTGT	GCCGGGCTCT	CCATGCAACT	GGGGCGCTCC	300
	CATGATGGCG	GGGGCCTTAC	CAGGGTGGTG	TTTGGGCTGC	CTGGCTGTGC	GTGGCCACAC	360
	GATGGCCTGC	TGGAGGAGCT	GAACCTGCTT	CCGTGGTGCA	AAGGTGTGTG	CGACAGCGCA	420
	CCTGCGTGCA	AGCTGTGCCT	GCGGGGGCGT	GTCGATTGCT	GCGTCCGCGG	GTGCAACTGT	480
25	GGTGACAGCG	CTTTGCAGGC	ACGTGATGGT	TGGTGCGGGG	CCCAGACGTG	CTCGGTGTGT	540
	CTCAGACAGC	TTTTCCGCGG	GCTGCGGGCG	CGCCGTTGCC	GCCATATGAT	TGATTCCGTC	600
	TCGATTAGTG	CATGGTGGTC	AGCTTCCAGA	TGGCCAGGCT	GTACTTGTGC	TTGCCCCGGG	660
	CCGGCAGGCT	CTTTGGCTGT	GCCGGTGGGT	CTTGCTTGTC	GGGCTGGCGC	CGTTCT	

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## 1538RP

	GATCCCTCTG	CTACAAACAC	ATACCTAGAT	TTCTCATATT	TTTACTGAA	TACATATAAT	60
	ATATCATTTA	ACTGTCTTCA	TTCATGAGAC	GTCGTCTAAG	TTCTGTGCTG	CTCAACTTGT	120
	TTTTCCACTT	CTCAGCCTCT	TCGCCCCCA	GTACGTTTAC	CACATGCACG	GCTAGCTTCC	180
35	TCATTCCCTT	GCTCTCACGC	GTATCGTTGA	TTGTCTGGGC	ACCGGCCACA	GTTTCCCTCAC	240
	TCACTACCAG	GGCTTCGATA	CCAGGTTCCG	TACCCGTGGG	CCCGCACACG	TCATGTAACG	300
	CAAATATTTT	GATTTCCAGC	CCCGGTTTCA	GCCTGTGAAG	GAAGCTGCAC	ACGTTATCGC	360
	ATCGTTTCGT	GAAGGACTGA	AGCTGCTCCC	TGTATTTCTT	GTTCCGACAG	AGTTCTTCAT	420
	CTGTAATCCC	CACGATCAGC	CGGGACGCAG	TCACGAGCGC	GGCAACACTG	AGCAATATTT	480
	TATGTCCGTC	GTGTAAGTGG	TCGAAAGTGC	CTCCCAGCGC	GCTAACAGCG	TACTTGTCTC	540
	TACCGCCACT	CTCGACCGGC	CCCGCAGCCG	CCATCGCCGG	ACTATCAAAC	AGCTCTATCT	600
40	GCCTGTGCGG	GAACGCATCC	TGCAGCAGGC	GATCGCTCAG	GAATACAACG	TCCCACCTCA	660
	TTGCGCTGTA	CGCTTCCATA	CTGACGTTGA	ACAAAACATT	TATCGGGGTC	GTGTACAGCT	720
	TCTGCTTCAG	AAG					

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## 1538UP

	GATCCTTGGG	ACGACATCGA	CACCATTCTT	ATCGGTAACG	AACTTGTGAA	CAACGGCCAG	60
	GCGACCGTGG	ACCAGATGGC	TGGTTACATG	AAAACCTGGC	GCAAGTGCCCT	CGCTGAGGCC	120
	GGCTACAAGG	GCCCAGTTGT	TTCCGTGGAC	ACTTTTCATCG	CTGTAATCAA	CAACCCCTGGT	180
	CTATGTGACC	TATCAGACTA	CATGGCTGTC	AACGCCACCC	CATACTTCGA	CTTCCACACT	240
50	TCTGCTGCTA	TGGCCGGCCC	TTGGGTTTTG	CACCAGATCC	AGAGAGTCTG	GAGCGCCTGC	300
	AACGGTAACA	AGAAAGTTGT	CATCACCGAG	ACCGGCTGGC	CTACTCAGGG	TCAGACTTAC	360
	GGCAAGGCCA	TTCCATCCAA	AGCCAACCG	AAGATGGCCT	TGGAATCTAT	CAAGGCCACT	420
	TGTGGTGATA	GCGCTATCCT	ATTTACTGCT	TTTCGACGAT	ACTGGAAGCC	AGATGGGCCT	480
	TACGGTGTCC	AGAAGTTCTG	GGGTATGCTA	TAAGTTGCCG	TGTGCTTCTT	TATGACCTGT	540
	CTCTTTATTT	TGCTCGGAAC	CCTTACATGC	AGATGGGGGG	TGGCGGTGCA	TGGGCCTGCA	600
55	GCCTCCGGGC	CTGCAAGTTT	CTACATCGCC	CTACTTTAGC	TGCCACGGGA	CTTTTGAATT	660

TCTTTGGCAC GTGGTACTGC TGGCATCCTT CTCATAGAGC ACAGTGTGCC ACAGGGTATC  
ACTGG

720

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## 1540RP

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GATCTTTTCT	TTGTCAAAGT	TCAACACCTG	TAAGCCGCCT	CTAGATACCG	CTCTAGAAAG	60
GGCCACATAC	GCTTGGCCCT	TTTCAAAAAC	ACGTCTGAGA	TCCACTTTCA	CTTTGTTTAG	120
TGTTTGGCCT	TGAGATTTAT	GAATGGACAA	GGCCCATGCA	AGCATGAGTG	GCAATTGAAC	180
TCTCGTTACT	AGAGGCTTCT	CATTTTCGTC	CTCGATAGCC	CATGCCTCTT	CTCGAACTAA	240
AACTGTTCTG	GTGGTATTGT	CGGGCTGGAA	GAATTGCACT	AATGGCAACT	TCTTACCCCT	300
TGAGCTCATG	TGAACCTCCT	GTAAGAGCTG	CTTCTTCCGT	TCTAGATTGG	CCTTCACTTC	360
AGGATCTGTG	ACTTCTCGAT	CATCCTTTAA	GAAATCGAAT	ATCGTGTCCG	CCAAGTGGTC	420
TACAGTGTCA	TCTGTGTCTA	TCGTCCCTAA	CTTCTCTCGC	AGAGCTTTCT	TGACCATGCT	480
TGTGCGGGTC	TCCTTCTTGG	GCTCCTCATC	CTCATCAAGC	TCGGGGGCGT	TCCAGTCGTT	540
TTTCGCTAAT	GCATCCCAGT	ATTTCTCCCA	TTCTGCAACG	TCAAGATCAT	CATCGCGAAC	600
ACTTTGATAG	AACATAAATG	TTGCCTCATC	GATGAAGTCA	ATGACCTTCC	CCAGTGATCC	660
GTTTACGAGT	GTATCATCGA	AGTTCTTAAT	GTTCATAACC	TGTGCGCCGA	CTTTAA	

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## 1540UP

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GATCTCCTGC	GCGAAGAGCA	CGCCCTGCGC	CCATCCGGCA	TAGGGGCCCC	ACTTTTGTAT	60
GAACATTTCC	CGCACAAAGCT	CCAGCTCCAT	GTTTCAGTTT	TTGCGCACAC	TGGGAAGGTC	120
CTTGATTCGC	GCTTTCAGCG	CAGCGATCTT	CGCTGCCGAT	GCATTGAACT	TGTAGTCTCT	180
TTGTGCGATC	CTGTTGATGT	GCACGTCTAC	AGGCACATGG	TCGTCCATCT	GCATGCCCCT	240
GAGGCAGACG	CAATCTGCGA	CCTTCGGACC	CACCCCGGGA	ACCTCCATAA	ACCGCTGACG	300
GATCTCCTCC	CGCGATATCA	TGTCTAGCCA	GGATTCCAGG	TGTTTCAGTAT	CGCTCATGTG	360
TGCCGGTTTA	CTTGAATCCA	TCCATTCTGC	CGCAGCCATG	ATATACTTGG	CGCGATACCC	420
AAACCCCAAA	TCCCGCAGTG	CGTCTCTGCT	AGCGCCTTCC	ATCAGCTGCT	TGCTGGTGGG	480
GAATGAGTAG	TATGGAGTAC	CGTCGAGCTC	GCCGAGGAAG	CTCCCGTACT	GCGAACACAG	540
TGCATGGCAC	ATCTTCGTGA	TGCGCCCGAT	ATTGTTGTTG	CTAGAGCAAA	TAAACGAGCA	600
CAGTGTCTCC	CAGGGTTCTT	GTCGCAGTAT	TCGCACGCCA	CGA		

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## 1541RP

	GATCGAACAA	CCATACTTTA	GGCCACACG	ACCGTTCCCC	TCGGGGATAT	CCTGCCGCCC	60
	CTCTACAAGA	TTGGATTCAA	TCATCACCCC	ACAAATGGCA	TTCTCACCTT	TACTCAGCTG	120
5	CTCATAGATA	TCTTGGGCGA	CTTTCGGCTG	GTTGCGGTAA	TCCTTGTTGG	AATTTCCATG	180
	CGAGCAGTCA	ATCATAATCC	TCCGCTGGAC	CCCAGCGCTG	TCAACTAGCT	TCGCATTGAC	240
	CAAGTCCTGC	TTAGCCTGTT	GTACACTGGC	AGCGTCATAG	TTTGTGCCAT	CTTTACCACC	300
	GCGTAGAATG	ATGAAGGTGT	CCTCGTTACC	TTTCAGTCCCA	ACAATCGCAG	TCACTCCAGG	360
	CTTGGTAACC	GAAAGAAAGT	AATGAGAGTG	AGCAGCGGCA	CGCATAGCGT	CAATAGCAAC	420
	CTGTAAGCAG	CCATCTGTCC	CGTTCTTGAA	TCCGATCGGG	AACGATAGTC	CAGAAGCCAG	480
10	CTCACGGTGC	AGCTGCGATT	CTGTCTGTCC	GGCGCCAATG	GCGCCCAAGG	AGAAGCAGTC	540
	GCTTAAGAAC	TGCGGCGATA	TGGTGTCTAG	CATTTCGCC	GCAATTGGAA	TGTGCTCCAC	600
	CAGCTGCGTG	TACATCTCCC	GCGAGATACG	CAATCCCTTG	TTTATTTGGA	ACGAATTATC	660
	GATGTCCGGG	TCGTTGATGA	GCCCCTTCCA	CCCCACCGTG	GTCCGCGGTT	TTCCAGATAC	720

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## 1541UP

	GATCAGCTGA	TGAAGATTGT	ACGTCATCAC	TGCTATTTAA	CACAAACATA	ACATAATTCA	60
	TCCGCGATAG	TTTAATGGTT	AGAATTCGCG	CTTGTGCGCG	GCGGGATCGG	GGTTCAATTC	120
20	CCCGTCGCGG	AGCTTTTTGT	GACATTTATT	GAAACGGTTG	TCGTTATAAC	CGTTCGGATG	180
	GAATGTGGCA	GGACCCTGTA	ACGGCGACGT	ATCCTGCAAC	TTCGACGTGT	TGTCGCGTCT	240
	ACGCCAGGGC	TTGGGCTTCC	AGAAATTGGC	TTTCCCGAG	CCCGAGTTTT	TGTGACCCAA	300
	TATTTGAGCT	GCTGATCATC	AAGCTCTAGT	CGCACACAGG	GGGCCCAGAT	ATCCATTGAC	360
	AAAGGTGCGC	GCAACATCCG	ATCGCCGGGT	CCCTTTATAT	ATAAATATAC	ACTAATGACA	420
	CATGCGAATA	CCCCACTGCC	GTGGATAGGG	GACGTTTGAG	GCCTCATACC	CCTCAATACA	480
25	GATAACAAAA	TTGGAATATA	GGAGAAGAAA	TGTTTCGAGG	GCTAAAACTT	AGGTTCCGGC	540
	GATGCAGAAG	ACTCAGAGCC	AACCGTTTAG	CAGACGTTCC	ATACCCGAAT	CCCACGTTGA	600
	ATTCCGCAAT	CATTTCCAGA	ATCGACACAA	TCACGGTGTC	AATCTCGGGT	CGCTATCGTC	660
	CTTGAGAAGT	GGATATCGAG	TCGATGTTCC	AATGTGGCGG	CGAGACCGAG	CATGCGGGGA	720
	TCAGGAAGAT	GA					

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## 1542RP

	GATCATGTGG	AGGAACTCGG	GCAGCGTCTC	GGAGCCGGCG	TAGTGGGCTA	CTGTGGCGGC	60
	GCGGGCAGCC	GACTGTCTCG	GGTATTCGGG	CGCCGGCGCA	GCGGCGTGTG	AGCCGATGCT	120
35	GCCTCCGGGG	TGGCGGGCGG	CGAAGGCGTC	TGCGCGGGCG	CGACGGGCGC	AGGGCGAGCC	180
	CCCGTCGGAG	AGCGCGAGCA	CAAGGCAGTC	GAGGGCGAGG	AGCATGAGGG	TGGTGGCGAT	240
	GGTGGGGGCG	TTGAGGCCGT	CCTGGACGAC	GCGCTCGCGC	AGGTGGGGGG	GCTGGAAGAC	300
	GGTGATCAGC	TGATGCGCGC	GGCGGGCCAG	CGTCCAGGCG	GGATCGCCGG	TGACGGCGAT	360
	GAGCGGGCTG	GCGGGTGCGA	AGCGCGCGCT	GCGCAGGTAG	GCGGCGAAGT	GCAAGAGCTC	420
	GTCAGTCTCG	CCGGAGTGGG	AGCAGAGCAG	CAGGGCGTGC	CCGTGCGCGA	CGATGCCGAT	480
40	GTCGCCGTGC	ATGGCCTCCG	TGGGGTGGAA	GACGGCGGCG	GGGATGCCGA	ACGAGTGGCA	540
	GGTGGCGACA	GTCTTGCGGA	TGATGCCGAA	GGACTTGCCG	CAGGCGACGA	ACACGAGCTT	600
	GCGGCGGTCC	GCGA					

## 1542UP

	GATCATTTAC	CTACGCATCG	GCCTGCCGCG	CATTGCCGCA	GACGGATCGC	TGCGAGACGG	60
	CTACCTGGAA	CACTACTACG	AGAACGCGTA	CGCCGCGGCC	CTTCTGGACG	GCTGCCGTGT	120
	GCAGCGCCTG	ATAGGACTCC	ACGCGCTGCC	GCTGTAGCGA	GTCATGCCGC	TGTGCCGGAC	180
	CCGAGCGGTT	TGCCGTCTCG	GGAGCCTCCG	GGTTTCGCACC	GCTGGAAAAA	GGAGGGCCAC	240
50	GCTGGTATAT	AAACGGCACA	CGAGCCATCC	GGCGTCAGGA	ATAGCGTGAG	TCGACAAGAT	300
	GGGTGCGGAA	CACGGTCCTA	AGGACCTTCA	GAAGAAGCCT	GTGAGCTTTT	CCAACATTGC	360
	CCTGGGAGCG	GCGTTGAATA	TGTGCGAGGT	CACGACGCTT	GGGCAACCGC	TTGAGGTCAC	420
	CAAAACGACC	ATGGCCGCAA	ACCGGCAGTT	CGGCTTTTTCG	CAAGCGGTGC	GGCACGTGTG	480
	GTCCCGTGGG	GGCGTGTTCG	GCTTTTACCA	GGGGCTGATT	CCGTGGGCTT	GGATTGAGGC	540
	GTCCACCAAG	GGCGCGGTGC	TGCTGTTTGT	TTCTGCCGAA	GCCGAGTACC	AGTTTTCGGCG	600
55	GCTTGGTCTC	AGCAACTTCG	GTGCAGGCAT	CCTGGGCGGG	TGTCTGGCGG	CGTA	

## 1544RP

	GATCTCAACA	AGATCAATAG	GCATATCCTG	CCGGCTAGGG	ACACCACTGA	ATTTTATGAC	60
	GAGAAGGCCG	AAGAGTTCGA	CCGCAGTGTG	AGAATGGAAG	AAATGGCCAT	TCGGATGGGC	120
5	AAACGGCGCA	AGTGGCTGAT	GAAGCACTGC	GAGGGCGATG	TGCTAGAAGT	TGCATCTGGT	180
	ACTGGTAGGA	ATATAGATTA	CCTAGACTTG	AGCAAAATCG	ACACAATCAC	CTTTCTGGAT	240
	GCGTCTAAGA	ATATGATGAA	GATCGCCAAT	AAGAAGTTCA	GAGAAAAATA	CCCACACTTC	300
	AAACAAGCTG	CATTTCGTAGT	TGGAAAAGCA	GAAGATTTAG	TGGACCTGGC	GACTGGGCAT	360
	TCGCCTCAGC	AACAGAATCT	GGAATTGGTC	AACTCTCCTG	AGCAGGTGAT	CCCGGAGTCC	420
	AAGCCCAAGG	TTAAATACGA	TACCATCATC	GAAGCCTTCG	GTCTGTGCTC	TCACCATGAT	480
10	CCTGTACGGG	CATTGAAAAA	CTTTGCGAAA	TTGCTAAAGC	CTGGCGGAAG	AATAGTTCTG	540
	CTTGAGCATG	GCAGAGGGAC	CTATGACGTT	GTGAACAAGA	TTCTAGACAA	GAGAGCCGAG	600
	CACCGTCTCG	AGACCTGGGG	CTGCAGATGG	AACTTGATA	TTGGCGAAAT	TCTAGATGAC	660
	TCTGATCTAG	AATCGTCACC	GAAAAA				

## 1544UP

	GATCAAAATTC	CAATCTCCGT	CAGCGTCAGG	CAGCCGCGTT	ATGTGTTGAA	CTCTTCGCTG	60
	CTTCTCTTCT	CTTCGCTGAA	CCCAGCAAGAA	AATTCCACCT	CACGCCGAAC	CAGAGGCCGAA	120
	AAACTGAAAA	TGAAATAAGG	CGCCGGCTTC	CGAGGACGTT	GCGGGCTCGT	GCAGCTCTAC	180
20	TTGCAATACC	CGCAATAGGA	CTACCAGACC	TTATTAGACA	CTGTAATATG	TGGGCAGCAG	240
	TAGGTGCAGT	CTACAAACTT	TTATAGCGCA	GCCGGGCGTA	TTACTCTTTT	CTGCTCCCGC	300
	GTCCGCGATA	AGTTGTGACT	CACAGTCCCG	CGGACGGAAC	GTGCGACCGA	GTGCGGCGAA	360
	TAATGAGTAA	TGTTCTATGT	ASTGGTTGCT	AGGGGGCTGA	AGGCTATGCT	CTGGGGTAGC	420
	TGGAATGTCA	CGCAGAACAT	GGGCTTCGTA	GGTGCCACTT	TGCGCACGAG	GTGGAACGAC	480
	AGCGCAGTCA	TGGGCAGGAT	GTCTGCGCTG	GTGTGCATTA	TCTCGAGCAC	ACGGCGGTGT	540
25	ATGCGGGCGT	GCAGGTCTGC	TGGCGCGGGC	TCGGGCTCGT	CGGGGCTGTA	TTTCTCGAAA	600
	CAGTGACAGT	GGATGTAGGG	CAGCACCAAW	TGCTGGGTCG	GCAGCGGCGT	CCTCCGAGAT	660
	CCGTGGCGCG	AGTACAGCCC	GGC				

## 1545RP

	GATCATTAAT	CAGCCATCGC	ATACCCGGGC	AAGATGACCA	TTAGCTCCTG	CTTTCGACAG	60
5	AAACAACGGA	CTATGGGTAT	AGAACTTGAT	GATAGAAGGT	TGAGGCATTT	AAAAAAGTGG	120
	CTAGACCGGG	CTTTAGATCC	GCCTACGACA	GACGAGAGCG	TCACAGCCCT	TGTGAAGGAC	180
	TATGTACTAC	AGGTACTACT	AGAGTGCAC	ATCGCAGCTG	TGAAGGGCCG	AAAGAACGAG	240
	TTCTGCGAGC	AGATGAGCCA	GTACCTGGCA	GGTATGGTGA	AGGACCACAG	CTGTCTAGAT	300
	GGGTTGTTTT	ATCAGCTAGT	GGACTTAGGC	GAGCCTCCCG	CGGGGAATAG	TTGCGGGCGA	360
	CAGCTGCGTG	TCCTGAAAAT	CCCAGCGGAC	CGGCTTCGCT	GGGAAACCTT	GCGTGCGGAG	420
	TTTGCGCCTT	TTGGAGCGGT	CACCAGGGCG	AGGATTGATT	ACGTGCATCG	TGAGGCATTC	480
10	TTGGAGTATG	CGGATGCGGC	CAGCGTCGTC	CGATGTTGTT	CGGTCCGGAA	GGCTTTCTTG	540
	GGGAACCGGT	TCGTTGAGGT	GCAGCCCTGC	TCGCGAGGCG	TGGGAATCAC	TAAGCGGTGT	600
	CGACGTCTGG	CCGCCGGATC	ACGAAACAAC	TGTGCCCGAG	CATGGATCAT	CTGGGGTGCC	660
	TCCGCGAACT	GGTGTGTCT	TGGATCGTGG	ACGTGCGCCT	CCGCCTGTCA	TCTT	

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## 1545UP

	GATCATCTTG	CAGGGACCGC	WCCACGTGGC	GTAGAAGTCC	ACGACCACGA	GCTTGTCGGA	60
	GGCCACGGCG	GACTCAAATT	CAGAAAGGGA	CTTGATTTTCG	GACACCATTG	CGTTCTGTGT	120
	GGCTGACTGT	ACCTTGTGTA	TACGCAGTAC	CCAGGAAGCC	GGGCGGAGCC	CCGCCTTTTA	180
20	TACCCGGCCG	CCTGCGGTCA	CGTGTCACCA	CGTGCGGGGT	CTCCCCCTCA	TTTCCGCTCA	240
	GGAGATAAGG	ATGACAAACG	CGTCCCTCGC	CGGTCCGCAT	TGACGTCTTC	GACAGCAATG	300
	GAACCTCTGC	TATAAGCGGT	GTCTGCGCGC	CGAGCCTTCT	CAATCGTCCG	TCTCTCTGTT	360
	CGCTTTGTGT	ACGCCAGGCG	CGGGTTTGT	TACGTTTCGG	ACGGGGTTGG	ATCTCCAACG	420
	CACGGTCGAA	TAACGAACAT	GAAAGCCAGT	TGTACAGTAG	CTACACCCCA	GCAGACGAAG	480
	CATCAGCAGG	CAGTTGAGAG	CGCGTACGAG	AAGTTCCGTT	ATAGAGCACA	CTCGAGACCA	540
25	TAGAGGTCAT	CCGCTAGGCG	GTACTTCAGG	TCAGGC			

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## 1546RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACAAC	GGGGAATTAA	GCCCCTTTTTC	60
30	CAATATTTTG	AGCGTCGTTT	CATAGCTCGG	AAGACGCAGC	AGAAGCCCCC	CCAGTAGTGT	120
	CTGTTTATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTCGTCAGGA	TTACAGTAAA	240
	ATAATGGTAG	AACCGCGGAC	TCACAGAAGC	GACGACCGCT	CGAAATGAAG	TCGGCCCGTA	300
	AAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTTACGGG	360
	GGACACCGTG	CCCATAACTG	GCTTCTGTCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
35	CCGCGCGAGC	TCAGTCTCAA	GCTCGTCGAT	CCGTCGCAGC	AGCTCCACAT	TGGGCGTCGA	480
	GCTGAACAGC	TCCCGTGAGT	TCACGTCGTG	CGTAAACTCA	GACAGGTACA	CACACTCGGG	540
	CAGGCCCTTC	CCAATACATG	TAGAGCACTT	CGGCCGCGCC	TTGTTGCACT	TGACGCGCCG	600
	CTTGCGGCAG	AACACGCACG	ACTTGCTGAC	CTTCGCGCTG	GTTTTCACAA	TCTTGCCATC	660
	GGACTCTGCC	ATCCCGCCAG	CTTCAAGCAA	AATGAGTAGG	TCATATTATT	TACCTGCTGG	720
40	TAATCTTGAA	TAATGCTCAC	T				

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## 1546UP

	GATCGCGGAC	TGGAACACTG	GCCGGAGATG	CGCGCGGCCA	TCCTGGTGGT	TTCTGCGGAC	60
45	CGCAAGGACA	CGCCATCGAC	GAGCGGTATG	CAGCAGACGG	TGCACACGTC	GGACCTCTTC	120
	AAGGAGCGCG	TCGCGACGGT	GGTGCCGCGG	CGGTACGGAG	AGATGGCGGC	GGCGATCCGC	180
	GCGCGCGACT	TCGCGACGTT	TGCGCGCCTG	ACGATGCAGG	ACTCGAACTC	GTTTCACGCC	240
	ACCTGCCTGG	ACTCATTTCC	GCCGATCTTC	TACATGAACG	ACACTTCGCG	CCGGATTGTC	300
	AAGCTGTGTC	ATCTGATCAA	CGAGTTCTAC	AACGAGACCA	TCGTGGCGTA	CACGTTTGAC	360
	GCGGGTCCGA	ACGCGGTGCT	CTATTACTTG	GCGGAGAACG	AGGCGCGGCT	CTGCGGCTTC	420
50	CTCTCTGCCG	TCTTTGGCGC	CAACGACGGC	TGGGAGACCA	CGTTCTCGAC	GGAGCAGCGC	480
	GCCACCTTCG	CCGCGCAGTT	CGACGAGTGC	GTGCGCGGCA	AGCTTGCGAC	GGACCTTGAC	540
	GACGAGTTGC	ACAGAAGAGT	TGCCCGCCTC	ATCTTCACGA	AGGTCGGGCC	AGGGCCCCAA	600
	GACACTAAAT	CCTCGCTCAT	CGACCCGAGA	CGGGCCTGCC	CGCTGACGCT	ATTCTCCTGC	660
	TATTTTCTGC	TCTGTATACC	CTGCCAGACC	GCGCTATATA	TATAGAA		

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## 1547RP

	GATCCTCCGC	CTACACCAGA	ATATTTCTGG	CCAATTAGTT	GTTCAACATC	GCCCCGAACG	60
	TTGGTGAAGC	CACGGCCATA	CGCTGCCATG	CCGAGTGCAA	TTTTTC1TGG	GCTGACCTTA	120
5	AATTGTTCCG	TCATCATGAG	TATCGCATCA	TGTGCATTCA	ACTCATCAAA	GTTGTCAATA	180
	CCCATATCTT	CATACCGACG	CTTATCTAGG	TGCGATTTGT	ACGGCGAATT	CGTAGCATTG	240
	TACAAGTTGC	TATGGTAGCC	TGTTGCTCT	GACCATGCAC	CGTGGTAGTC	GTATGTCTATC	300
	ATATTCCACA	TGCTGAGATA	CTTGTTTCATC	TCCTCAACCG	GGAAAATGCC	AAGTGTCGA	360
	GGAAAGGCCG	GTGCTGCCAT	GCTTAAAGTG	AAGCGCGGTT	CTGTAGTCCC	GCCGGGGCCC	420
10	CAGATATTGT	CTTCCAATTC	GTCCATCTTG	TGTCGCAAGC	GGCTACACAT	TTCTAGATAC	480
	ATCTGGGGTT	CGTAGCCATC	ATCCTTAGGG	AACTCCAGT	CAAGATCTAT	CCCATCGAAG	540
	CCGTACTCAA	ACATTGCGTC	GATCGCCGAG	TCGATGAAGT	TGTTAAACTT	CTCCTCGTCA	600
	CGCACAATTT	TATGGAACGG	CTCCCGATTG	GAACAGCCGC	CAACGGGCAT	CATGAGCTTG	660
	AAATCGGTCC	CTGGCCGCGT	CTTGAGGTAA	TTAAGCTTCG	CCTATTGCC		

## 1547UP

	GATCTCTGAG	GGTTCCAAGG	CAAGCCCGCC	GGAGCTTGCC	CAAATTGTGT	CACCCGCTCT	60
	CGAGTAGATG	GTGGCCTTGT	CGACCTTCCC	GGTTGCTAAC	AAGTTGTCAG	TGTAGGCTAA	120
	AGCTCTAGTT	AGTACCCACG	AACGGGGCCAC	GAGCAGAACA	CGTAAAAACA	CATACCTTGC	180
20	CAAGACATGA	TGCGTTCGCG	ATGAAATCTG	AGTTAGTGCT	AACACTCGCA	GATGCTCTGG	240
	TGAGTGGAAT	CTAGCTATCA	ATAGTATTGA	TTTGTCAATA	AATATACCTT	GGCTTTTGTG	300
	AATCTTTTTA	TATAAGGGGT	TCCGATCTGC	TGACATCATA	GCACACGAAT	TAAGTATCCG	360
	GGTAACGAAC	TGCCCCGGTA	ATGCGGGGCA	CAGGGCAAGT	GCCGGGTAAC	GGCATCCACA	420
	TACCGCAGAG	ATGCACTGGC	GGCTACATAC	TGTACACAGG	CTCGCAGCTA	CTCGTCTGCT	480
	GAGTCGAGAA	CAGCCACCTT	GCGACGCTTG	AGAGCGACCT	CTTCATCTGC	GCGCGGGGCC	540
25	GGCGGGGCAG	CAGCGTACTT	GGCTGCGCCC	TCGCGTTTCA	GCTGCTGCAG	ACGCGCGGCG	600
	TTTAGGTC						

## 1548RP

	GATCATCATT	GCTCGGTTAG	CGATTGCCGG	CAATTTTACA	GCTGGTTCAT	CGCTAGGCGG	60
	TAAGGCGACC	GCGGGTAGTT	TCCTGTCCTA	CGGGTCCGTG	GTGTTTGGTT	TTGCATCGGG	120
	ATGGACAACA	TATGCTGCAG	ACTACACTGT	CTACATGCC	AAAAATTCTA	ACAAATACCG	180
	CATCTTTTTT	TTTCATGATTG	CGGGTCTTGC	GACCCCGTTG	CTGTTACGCT	TGATTCTTGG	240
	AGCTGCTGCC	GGGCGCTGTG	TGCACACAAA	TCCTACGTGG	GGCGAATATT	ACAAAAACA	300
	TTCCGTGGGA	GGTCTGTGCT	TTGCTATACT	GGCTGAAAAC	GCTCTGGGCG	GGTTTGGGCA	360
35	GTTCTGCTGC	CTGTACTGG	CCATGTCCAC	AGTTGCAAA	AATATTCCAA	ACATGTATT	420
	CATCGCTCTC	AGCACCCAGG	CGCTGTGGAG	TCGTTTCGCG	CGTGTGCCAC	GAGTGTTCG	480
	GACCTGGGTC	GGCAACGCAT	GCAGCTTGGT	CATTGCAATC	GTTGCGTACT	ACAAGTTTGA	540
	GACCTTCATG	ACCAGCTTTA	TGGATTCAAT	TGGCTACTAC	CTCTCCATAT	ACATCGTAAT	600
	ATGTGTCACT	GAGCACTTCG	TCTTCCGCAA	GGGCTTCCGT	GGTTACACGT	CAGCCACTGG	660
40	GAACGTCCCG	ATCTTCCTCC	AGCTGGTTAC	GCTGGCTGCG	CTGCGC		

## 1548UP

	GATCGACAGA	TTACAGTTAC	AAGCGAGAGT	TCGGCCTATT	TAAGGAACAG	AACCTATACC	60
45	ACATTTGAAG	CTCGAGTTTT	GGCACGCCAA	GACCGATTTG	CGGATTAAGT	ATCTTGAAGT	120
	TTGCACTCAG	ACTCAAGAAC	TACTATTACG	ATACTATAAC	AAAGACGATG	ACTAGCACAG	180
	CCGACCACAA	GCAGCCCAT	TCGTTGAAGG	TTAACGGGGG	TCTATTTCGAC	GTCGACGGGA	240
	CCATCATCAT	CTCGCAGCCC	GCGTAGCCGG	CCTTCTGGAG	GGAGTTTGGC	AAGGACAAGC	300
	CGTACTTCGA	TGCGGAGCAT	GTCATCAGTG	CACCCACGG	CTGGAGAACC	TACGACGCCA	360
	TCGCTACCTT	CGCGCCAGAC	TATCTGAGTG	AGGAGTACGT	GACGAGACTG	GAGGGCGAAA	420
50	TCCAGACAA	GTACGGCAAG	TTCTCCGTGG	AGGTTCCCGG	CGCTGTTACG	CTCTGCAATT	480
	GCCTTGAACR	AACTTCGAA	GGAAAATTGG	GCCGTTGGTA	CTTCCGGCCC	CTTCCAGATG	540
	GCACCAAGTG	GTTTCGATGTC	CTCGGCATCA	AGCGTCCTAG	CACCTTCATT		

## 1549RP

	GATCTGCTTG	GTCTGACCAC	CGAAACCGA	CTGCTTACGG	TCATATCTTC	TCTTACCCTG	60
	AGCAAACAAG	GAAGCCTTAC	CGGCCTTGTA	CTGGGTCACC	TTGTGCTGGG	TGTGCTTGCG	120
5	GCAGGCCTTG	CCCTTGCAGT	AAGTCTTTCT	GGTCTTTTGA	ACGTTAACTG	CACACGTTAG	180
	TATACGTCT	CTTGGCGAGT	CCCTTTTCGA	TCTGCAGCCG	CGCCGTCAGA	AGGCCCTGCT	240
	GTAGCGAGCC	GTGGCCCCCT	GGCGGCGCTC	CGCGCTTCCC	CTCCGTCATA	TTGAACATAC	300
	CCATTGCGAG	AAGTAGCTTC	TGTGATGCTC	TGTGCTTACT	ATCAAGCAGG	ATGACACCCG	360
	GCCTTGAATC	CTGAAATTTA	CCATGTTTTT	CGCTTCGCGA	GCTCGGCCCG	CGGGCCGGCC	420
	GGCTGCCGCG	CCGGAAGGTC	CAGTGCTGCC	CGGCCTGCGT	CGCCCCAGTT	CACCCGGGCC	480
10	ACCACGCAAG	GTGGTGATGC	ACGCATGTGC	AGTATGTGTG	GGTGTGTAAT	AAATAGATGT	540
	ATGGGTGTAG	TCACATGTTT	GTCACAGGCA	CTCCTCCGCG	GCTAACGCCT	CGAGATTGGC	600
	CAATGCGTGT	GGCGGCATAG	GCGATGGCAG	CCATGCCTTG	AGCTCTGCGC	GGGGTTAGAG	660
	CCCAAGTCAT	TAGACTGCGG	CACTGCAAGC	GTCTGACCGG	CAGGTTTTAA	GCTGGTGTGT	720
	GGCCCTGCGC	TACGTT					

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## 1549UP

	GATCCATGTA	TAATCACCCC	ACAGCACCTT	TTGCAGGTTT	TCGCGCTTGG	CCCCAGCTT	60
	CTGCTCGTAG	AACCTTCGAA	ACAGACTGAC	GTTGAACCCC	CACCCATCTG	CAGCAGAGGC	120
20	AAAAATCACA	TTGTTCCGGG	ACGGGTCGAA	GTATATGTCC	GCATCATCCC	GCTCCACATA	180
	CTCGGCCTGG	GCGTCTTGCT	CCAGTTTCTC	TCTCCACGAG	AGGTCATCCA	GCAGCCGCTC	240
	CCCGGCAAG	AAGGACCCCA	GTACAGAGTT	GACCTGTTCA	ATCGTCTTCG	ATAGATGCAC	300
	GTAGGCCTCC	TGTGGCGTCA	GCTGGAGCTC	CGTGATCAGC	CGATCGATCT	TGTTTCAGCAC	360
	CAGGATTGGT	CTCAGCTTCT	CCGTCCAGCA	CTGCCGCGAG	ACCGTAATCG	TCTGCGAACA	420
	CACACCCTCG	ACCACGTTCA	CCAGCACGAT	CGCGCCATCA	CATAGCCGCG	ACGCCGCGCT	480
25	AACCTCGCTG	GAGAAGTCTA	TGTGGCCCCG	AGAGTCGATC	AGGTTGATTA	AATGTTTCGTT	540
	GACCAGCGGC	TCGCTGCTCC	CCTCCTGTTT	GTGAAGCACT	CCGAAGTTAC	AGAGAAATCG	600
	CACTGGACTC	CATCGTGATG	CCTCGCAGCT	GCTCATCTGG	CCCGGAGTCT	AGGAATCGCA	660
	CTTTCCCCGC	TAACCGCTGT	GAGATAATAC	CGTTGGATGC	GAGGAGG		

30

## 1550RP

	GATCGAGTAC	ACAAAGTACA	TGGATGCTGC	CAATAACTAT	AGTCTGAAAT	CAATGCGTTT	60
	CTTAGCGAAT	GCAGATGAGT	TGGCGCAGCT	GGCATCATTT	AACTCCATCA	GCCATTATTT	120
	ATTGGCTGAA	TGCCCATCTG	TCCAGACACT	ACAATTTTTA	TAAAGCTCAT	CTAAATTGTA	180
35	CCCAAAATTA	ACGAAGGAGA	ATCAAGAATC	TGCAATTATC	GAAACACTGC	TGTCTCTCAG	240
	TGAATTTACG	TTGCTGCACG	ACTTCTCTCT	CCAGGCAGGT	TTCCAGGTTC	AAAAATCGGT	300
	CATTTTGAAG	TACTTTTGGC	GCTTTTTTCA	CAGCGCACCA	AATGGGTCCA	GGGGACCGGC	360
	CAGAAATGAC	AAAGGCGAGG	AACAATCTTC	GCTTACTGCC	CAAAAAGGAC	TATTATTATC	420
	TTGAGACTCT	TCTTGATGTC	GCAGACGCCT	TGGCAAAGTA	TTGCTAAGC	TACTCACGTG	480
	GACAACCCCT	CAGACCATCG	CATATATTGG	ATCTCAAAGA	TGATCCATTG	AGAATCATAA	540
40	GCAAACTGCT	AGAAACGAAT	CCCAGTCTGT	ACCGTGACGT	TGAAACGACT	TTCGAAATCC	600
	TCAAGCAATT	ATATGAAGGA	TTGCAACTGC	AGCCTCATGA	TCCAAAGTAC	ACAAGTGAAT	660
	ATACCCGTTT	GCTAGTCTGT	CACATTGATT	GTGCATTGGC	AAATAT		

## 1550UP

	GATCTCCTCC	CGCGATATCA	TGTCTAGCCA	GGATTCCAGG	TGTTTCAGTAT	CGCTCATGTG	60
	TGCCGGTTTTA	CTTGAATCCA	TCCATTCTGC	CGCAGCCATG	ATATACTTGG	CGCGATACCC	120
	AAACCCCAAA	TCCCGCAGTG	CGTCTCTGCT	AGCGCCTTCC	ATCAGCTGCT	TGCTGGTGGG	180
	GAATGAGTAG	TATGGAGTAC	CGTCGAGCTC	GCCGAGGAAG	CTCCCGTACT	GCGAACACAG	240
50	TGCATGGCAC	ATCTTCGTGA	TGCGCCCGAT	ATTGTTGTTG	CTAGAGCAAA	TAAACGAGCA	300
	CAGTGTCTCC	CAGGGTTCCT	GTCGAGTAT	TGCGACGCCA	CGATGTGTTT	TCCCGATGAA	360
	ACGTGTGTCT	GCTTCTTGCC	ATTCTGCTAA	CAAAGCCTCT	AGGTTACCTT	CCATCCGTAG	420
	GTAGCGCATC	AGCCATTGTC	GTGCCGCCCC	GCTGCAGTCG	TCATCTTTAT	TCCAGCTAC	480
	GCTGAATTCA	ATACTGCACT	GATCGGGCTG	CTTCAATACA	ATAATACGAT	AGCCAGCTTT	540
	GTCATTTAGT	AGCATGCTCG	CGGAATAGTA	CCTTTTCTCA	TGATTCCAGA	TCCACCTGAA	600
	CGCTTGACCA	CATTGCAATA	CATGGTCCAG	GACTATTTCT	CCCTTTGGGA	ATATCAATCT	660
55	GTTAAACTTC	ATAACTGTGC	ATACAGCACT	GACCTCGCTC	TAATAATCAG	CGTCACGGCG	720

CTGGCTCGAG CATGTT



## 1551RP

	GATCTCACGT	GAATCGGATA	TCTGCTCAAC	GGCCAATTCT	CGTATATTCT	GACGAGATCT	60
	TGGCGTCAAT	TACGTGCACT	TTGGCCGAAG	CCTTCGCACG	AGCTTCTACG	ATACAGAATG	120
5	CTGCCAGGTG	CATCTTAAAA	AGCGGGTTTA	CAGTGAGCCC	TCCGTCCTTC	AGGGCACCAG	180
	CCCCTAACTG	TACATAGTTT	CTGTATAGTA	GTTTGCCTTT	CCTCGCGATG	CCTGCCTCTT	240
	GTGGAACAAA	AACAGGCGGT	AGAAGGAAAT	TCCCGTGCGT	CATCGGTATC	GGACGGCGTC	300
	TGCCTGGATC	TGCGGAGTAG	CTTTATGAGC	CATTAGTGAG	GAACGCCAGT	TTCGACGACA	360
	GATTTAGTCT	TTTCTGTGTT	CCTGCAAAACA	GGCTTGGAAT	GTATCAGCGC	GCTGGCGCAG	420
	CGACAGGCGA	CACCGCTTCA	CATAGGGAGA	GGCCACCCAC	TGAACACGCG	GTGCACTGTC	480
10	AGGGGGCGCA	GCGTACTGCC	TACAATGGTA	TCGTCCGCAA	ACGGCAGGCC	AACCGGCAGA	540
	GCGGGCATT	AGATCTAAAT	TTATCAGCCC	ATGGACGGAT	GGATTACGG	CAGCGTGTCT	600
	CCGCAGCAGC	GGGCACGCCA	GACTGCGAGG	TGGCAAATAA	TTACACATAGC	AACCTGCATT	660
	ATAAACATCC	CAAGTCATTA	AACCTACTAA	ATATTGTTGC	GT		

## 1551UP

	GATCCCGGTG	AAGCTGCGCA	ACTGACCGGT	GCGCTACGAG	GACCCGGGCG	GCGCAGTGGA	60
	GCTGGCGCAC	TACGACTACT	CGAGCGAGCT	GGACCGGTAT	CTGAAGGATA	TCGAGGTGGA	120
	GTACGAGGTG	CTGGCGTACA	ACTGGCCGAC	GTTTCTGGCG	TACGTGCAAG	AGCTGGAGGA	180
20	GGGGGAGTTC	CGCGAGTTCT	TCGCGGAGCT	CTGCGCTTAC	GCCGCGGAGA	ACGAGGTGTA	240
	CGGCGCGAAG	CTGTGGGCGG	GGCTCGTGAA	GGAGCGCTCG	ATGCAGGAGC	TGATCACGCG	300
	CAGAAAGCGC	TCGTCACTCA	CGCCTGTGTC	CGCGCGAGGA	GGAGACGCAG	CGACGGCAGG	360
	TGGAGGACGA	CTGGCACAGC	AAGCTCGACG	AGCGCGACCG	CTTCTGCGG	CTGCGGAGCA	420
	AGCTCGTGCG	CAAGCGTGCC	AAGAAGACCA	AGGACGCGCT	GTGGACGGTG	CTGTGGGAGC	480
	GCTTCCAGAG	CGACGCTAAG	ATCGAGAAGA	TGCGGCGCCG	CAACGAGGCC	GCCACGCCCCG	540
	AGGCGGGCGG	CGACGAGCTC	CTGACGCCCG	CGGAGCGCTA	CGCGCTGGAG	CAGGGGCAGG	600
25	GCTTCCCTGG	CGCCTGTGCT	CCCTGTGCGG	GAGCCGGCGC	CGGCCCTGGC	CGTGCCCTGC	660
	AACGAGCTTC	CCGATGAATA	CTGCATCACC	AAGACTGACT	TCGACCGGCT	CGCTAGCCAC	720
	GGCATCCCGG	TCGAG					

## 1552RP

	GATCGTCGGC	TCATGCCACC	ACAACCTCCA	CGTCCACTGC	ATCTACCAGT	GGCTCAACAC	60
	CTCCACGTCC	AAGGGCCTCT	GTCCGATGTG	CAGGCAAGCG	TTTTCACTCC	GGGAGGGCAT	120
	CCGCATTAAC	GAGCCCCACC	GCGACAAGTT	CGAGAAGGTG	TTGATGAAGG	CGCGCCAGCA	180
	GAGCGTGGTG	AGCGTCGCGG	GCGCCAACCC	GGTCGGGCGG	GACCAGGACG	ACGTCAATCAT	240
35	CKACCAGGAG	TTTATCCGCT	GACACTAACT	AGCCTGTGTA	CCCATGTAAA	AATAATGCTT	300
	CCAACCAGAT	TCGAACGTAT	GATCTCCACA	TTACTAGTGT	GGCGCCTTAC	CAACTTGGCC	360
	ATAGAAGCAA	TACGAGCGTC	TAGCGGACTG	CGCCGGGCTA	TATGCGCCGG	GCGTGACCGC	420
	GACGAAACGC	TGGCGCCCAA	ATACCTGATC	CCAGGTTTCC	AACGCTGGTC	ACGCAACTTC	480
	TGCCACGTGC	ACTGCACACC	ACGCCAGCAC	TATATAGCCC	CGCACCCGCC	AGGCGTTCTT	540
	GCCAGGTAC	CGCGTCCAGC	TGTGCTGCA	GCATTCCACC	TGAAAAagTT	TCACCAGCAG	600
40	AAAGACTTTT	CCACTTCTCA	ATAGCACTTC	TATCCCTTAT	TTCTCTAGCA	GTTTTGCAAT	660
	GAGCTACaCT	ACCAGACAGA	TTGGAGCTAA	GAACACCTTG	GACTACCGGG	TGTTTCATCGA	720
	GAAGGCGGCA	AGGTCGTCTC	GCCGTTCAC	GACATCCCAT	TGTaCGCGGA	nGAGaAACC	780
	aATCTTCnAC	aTGGTGGTGG	AnAT				

## 1552UP

	GATCTTGCAG	ACACGCCTGC	GCCCGTAGTC	CGTGCAGAGT	CAGACTGCGT	CGCCGAATAA	60
	ATAGCTTTGT	GCCAGGCGGT	CGCCGAGGCG	TTGCGGGACT	CACCGCATAA	AAGAAACACG	120
	CTGCGGCCGC	GCGGCCGCAA	AGCAGCCAGG	CGCAACGGGC	GCGCCGCAAA	AGCAACCGTG	180
50	ACACACGATA	TGGCAGATT	ACRTACATAT	TATACATAGC	CGGCCGCGGC	ACGCGGCTCA	240
	GCCGCCGAAG	CCGTACAAAT	TGCGGCCCTG	GCGCTTGAGC	CGGTACACGA	CGTCGAGCGA	300
	GGTGACGGTC	TTGCGCTTGG	CGTGCTCGGT	GTAAGTGACG	GCGTCGCGGA	TGACGGACTC	360
	CAGGAACGAC	TTGAGCACCG	CGCGCACGTC	CTCGTAGATG	AGGCCGGAGA	TGCGCTTGAC	420
	GCCGCCACGG	CGGGCCAGGC	GCGCGATGGC	GGGCTTGGTG	ATGCCCTGGA	TGTTGTGCGG	480
	GAGGATCTTG						

## 1554RP

	GATCAAACTA	GGAATTTTGT	ATAATACTGA	AGAAGGTCCC	ATATTCAAGT	CTCTATCCAG	60
	CGATGATGAG	GAAGTGGGTG	AGATTGTGCT	GCACGACCTG	ATGAACAATC	TCGATTTTCAT	120
5	AACTATGGAT	CATCCTGACA	GATCGAGAAA	CCAAACTCAT	CAAGATAGAC	CGATGATGAT	180
	CAAGAAGTAG	TTTGAGATCC	CTCTGCTACA	AACACATACC	TAGATTTCTC	ATATTTTATA	240
	CTGAATACAT	ATAATATATC	ATTTAACTGT	CTTCATTCAT	GAGACGTCGT	CTAAGTTCTG	300
	TGCTGCTCAA	CTTGTTTTTC	CACTTGTCAG	CCTCTTCGCC	CCCCAGTACG	TTCAACCAT	360
	GCACGGCTAG	CTTCCTCATT	CCTTTGCTCT	CACGCGTATC	GTGATTGTC	TGGGCACCGG	420
	CCACAGTTTC	CTCACTCACT	ACCAGGGCTT	CGATACCAGG	TTGCTACCC	GTGGGCCCCG	480
10	ACACGTCTTG	TAACGCAAAT	ATTTTGATTT	CCAGCCCCGG	TTTCAGCCTG	TGAAGGAAGC	540
	TGCACACGTT	ATCGCATCGT	TCGTGCAAGG	ACTGAAGCTG	CTCCCTGTAT	TTCTTGTTCC	600
	GCAGCAGTTC	TTCATCTGTA	ATCCCCACGA	TCAGCCGGGA	AGCAGTCACG	AGCGCGGCAA	660
	CACTGAGCAA	TATTTTATGT	CCGTGCTGTA	AGTGGTCGAA	AGTGC		

## 1554UP

	GATCACTGAG	GAAATCAAAA	CCTTGAGCAG	CTTCCCTGTG	TTGCGGTGTG	ACGGTGTGGA	60
	CTGTGCCCAA	GTGAGACTG	TCCTCCAGGC	CAAGGCTCCA	GGCCAAAAGC	TCTTCCTAGG	120
	TATCTTCTTC	GTCGACCAAA	TTGAGGCCGG	CGTGAAGGCC	ATCAAGGAGG	CTGTTTCAGAA	180
20	GCATGGATCC	TGGGACGACA	TCGACACCAT	TTCTATCGGT	AACGAACTTG	TGAACAACGG	240
	CCAGGCGACC	GTGGACCAGA	TGGCTGGTTA	CATGAAAAC	GGCCGCAAGT	GCCTCGCTGA	300
	GGCCGGCTAC	AAGGGCCCAG	TTGTTTCCGT	GGACACTTTC	ATCGCTGTAA	TCAACAACCC	360
	TGGTCTATGT	GACCTATCAG	ACTACATGGC	TGTCAACGCC	CACCCATACT	TCGACTTCCA	420
	CACTTCTGCT	GCTATGGCCG	GCCCTTGGGT	TTTGCACCAG	ATCCAGAGAG	TCTGGAGCGC	480
	CTGCAACGGT	AACAAGAAAG	TTGTCAATCAC	CGAGACCGGC	TGGCCTACTC	AGGGTCAGAC	540
25	TTACGGCAAG	GCCATTCCAT	CCAAAGCCAA	CCAGAAGATG	GCCTTGGAAT	CTATCAGGGC	600
	CACTTGTTGGT	GATAGCGCTA	TCCTATTTAC	TGCTTTTCGAC	GACTIONTGA	AGCCAGATGG	660
	GCCCTACGGT	GTCGAGAAGT	TCTGGGGTAT	GCTATAAGTT	GCCGTGTGCT	TCTTTATGAC	720
	CTGTCTC						

## 1555RP

	GATCATACAC	GCATTGCAGG	TATACATTAT	AGTGCTCATA	ATTATCGGAT	TGCAAATAGA	60
	ATGGGGCCCT	TACCGTAGTA	CTGTCTTGGT	AATGCAGCGA	CGCTCAGGCT	TAAGAAGCTT	120
5	TTTGTCTCC	GTGTATTACT	AACAAAATAA	TTTCCTCGAG	CACAGGGAGT	AGAGATGAAT	180
	TACATAATCC	ATATGGACAC	CTCGTCACCT	TCCAGCGACA	TTAACATTTC	CTTATGAATG	240
	CCCAATAATG	GTGCCTAAAT	GATGTGCTTG	GTGTAATGCG	CATTATAAAA	TGTATGTGGA	300
	TTATATATTG	TTTGTAGCAT	CTAGTAAAC	CATGGTAGCG	AGGTCTTTGG	CCATACCCTT	360
	CTGAAGAGAG	ACATAGCAAC	AGTGTCTTGT	GCAGACAGT	TGCCGTCGAA	TGTTGCCTTG	420
	AAGTAACCAT	GAGTACCAAG	ACTCTCCTTA	ATGAAGCCAG	AGCGTCCAGA	TTTCGTGAAT	480
10	AGTGGGATCG	ACTTGAACCA	CTCGACATCT	TCTGGCCTAA	AGAACATATA	GCGCACTGTG	540
	ACGACGCGCT	TGTGGAACCT	GAATGGATGG	GCAGTTAATA	TGATTCTCTT	GGCCAATATC	600
	CGTGTGTGGT	CTGCGTTTCA	GAACGTGCCG	TGGCCACGA	ACGTCAGGCC	CTTTGGATCA	660
	GAAGGGTTTT	CTTTGAAGTA	GATGGCCGGT	GACTGGGTCA	GGTCCAAGGG	AA	

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## 1555UP

	GATCTGGGAA	ACAAGCATTC	CAACCTAGTT	GGAATGGCTG	GCAATTAGCA	GCTGCGGCAA	60
	GGCAGATAAA	GCTAACTGTG	GCATAGTTTC	CGTGAGTTTT	GATTGCGTTT	CTCAAGCAGG	120
	AATACTTTGC	TGGCCGCCAC	GGNCGCCGTT	TTTATACTGT	CAGGCCAGCC	CGCGGCCTGC	180
20	CGGGTAATGC	CTGGCAGACC	CGCTCTAGGG	CACGCGAAT	CGCCCGTGAC	AACGCCTGCC	240
	GCCGCAAGAT	GAGCACCTAA	AGGGCCGGCA	GCCTCCGCTA	GACAACCTGA	TGGTAACGTC	300
	GTATTGTAAT	ACTTAACTTA	TACAGGGTTT	ATTGATTATA	TTACTCAGAA	ACTGCCGTGA	360
	GACCCACAGC	CCGCCCGCCG	AATTGTGTAC	AGTAGGCGGC	AGCGGGCCGC	CCGCCGCTCT	420
	TAACGGTACT	TGTGGAAACC	AATGTCGTTG	GCCTTCTCTC	TGAAGCACTG	ACGGCAGATG	480
	TTCAAGCCGT	ACTTTCTGAT	CAAACCAGAG	TGCGAAGCGC	ACACGCGGCA	CTGGCGGGAG	540
25	CCCTTACCGT	AGTTTCTTGG	GTGGGAGAAC	CAAACGTTTT	CGTGAGCCAT	CTTGCTTGCA	600
	ATGCGTTAGT	ACTCTGTCTG	ACCGCTTGGA	AACGCTCCGG	CCCTCGTTGA	GCTGCCCACA	660
	CGCTCGGCGT	CTGCGGCGTC	CTCATTGCC				

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## 1556RP

	GATCAACCAG	TCGGCCGAGT	CCTATACGAC	CGGCATCAGC	CTGGTGTTCG	AACTTCTCGG	60
	TGACCCTCCG	ACGTACCTGC	CTAAGGATAG	TTTGCCGCCA	GAACACCCTG	ATGAGGGCTT	120
	CACGAGTGCT	TCTGCGTCCG	AGCTGCAGCG	CCGCTTTGCA	TTCAAGTGTC	AAAATCCACG	180
	AGTCACCCTC	GTAAATGACT	TCACGGTAGA	CGTATACCCG	GCCTCAACCT	TCCAGCTGCT	240
35	CAATGATAAT	ATCTGCTTGT	GTTTTGATAT	TCTGAGAAGG	CAGAAGTGGT	GGCACACCGT	300
	CTTATATCCT	ATTTCCCAAC	TTTGTCTGCA	TCAAGGCCAG	GATTCTGCGG	TAGGAGACGC	360
	CCGAGCACCC	GCAGCCCAAC	CCCCGCTCCA	CCGCCGCCGA	TCAAGCAACA	AGGGCTGTG	420
	CCGAGCAAGT	GCGGCCGAGT	CAGCCACGCT	AGGGGACGAA	AATATGCACC	AACCTTACCTT	480
	AACGGAATTT	ATGAACAAGT	CTGTGATTCC	CGAAGATGAC	CGATGATGGA	TGACCGCATT	540
	GAGCTCTATG	TTAACGAGAA	CTACGTCTAT	CTGGGGACCA	GGAGGGTTGC	AGCTTCTATA	600
40	ACGATCCGAT	TGAGAGGTGG	GAGGCGTTTG	TAGAGTCACT	AAGACAGATG	CTTACGTAGG	660
	TATATAATTC	TCATCTCACG	CCTGGTATGT	ATGCGCTTGT			

## 1556UP

45	GATCCGAATA	ACGTCCACAT	AAGGGAGAGA	CTAGAGGCTT	TGACTGCCCA	GCTAGCCAAC	60
	CCAGGGGCCC	AGCAGCCTCA	GCAGCAGCCT	CAACAGCAAC	AGATGCAACA	GCCTAGAGGG	120
	CCAGCACCCA	TTATGTTGCA	GCCAACATTG	CAGCAGCAAG	ACCAAACAAA	TCCGTTGAAT	180
	AACAAACCTG	CGTTCTACCG	GTCTCTCC	CACGGAGTTG	CGGTTGCCGG	AACAGAGTCC	240
	GCAGGCCACA	CACCAATGTC	AGGACGGCCT	CAGCCGTTGC	AGCAGTTGAA	CAATAACGGA	300
	AGTATCCTGG	AACCGTCATT	GTTGCCGCAA	AAGAGGCCCTA	TGGAGGGTGG	AATGGATACA	360
50	TTGGTAAATG	CCATTTTCGCA	GCAGGAGTTG	CAGCAACATC	AGAAGAAACA	TATGCCTTCT	420
	CAGAACCATC	CTAGTPTGGC	CCTGGCTACA	GGACAGCCGC	AGCAGTTACC	ACCCGATGCC	480
	GCTCCCATAA	TACCGCCCGA	AAAGAAAGGT	GCGCCTCTCC	CCCAGTTTCA	GAAAACGTAA	540
	CCAGAGCATG	CGGCAAAAAG	ACTGAAGCAC	GAGCAGAATA	ACGTTTAAAG	GCAACCGGTC	600
	CCGTCTCGAA	TATACCTTCG	ATTACGCACC	CAGCTTCCAT	GGAACATTCT	GGTCCGGGAG	660
	ATCAGAATCA	CATTCTATCT	GGGCTTTCAG	TCCACGCAAC	CCACGTGTTA	CTCCGGTA	

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## EP 0 866 129 A2

## 1557RP

	GATCAGGCGA	GACATTGCGT	AGAAATATCA	ATTGGTTCCA	GAGGAGATCT	GTCTCCTGGT	60
	CATTGTAGAG	AAGCGGCCAG	ATATAATTGT	CCAAAGTGAA	CTCGTCTTTT	TGAGAAAACA	120
5	CGCTTTCATA	CACAGCGTCC	GACTTTTGGG	CTAGACCATA	AGCAAGGTCT	ATAACTTCCG	180
	TGGCAGTATA	ATTCCAGACC	GGCGGTGGTT	GCGGCGGGAC	AAGGGACTCC	CAGTACCCAA	240
	GTAAATCCTT	CGTCATTGAG	CTTTTTTAAC	ACAGAGCCAA	CTAAGATCGA	CATGGTAAAC	300
	GACGCGATTA	MTTTTGTACC	ATTTTATAG	GAGACCAGAT	ACATTTACAG	AAGCACCAAC	360
	CGCAATCGTT	TTAATCGGTG	CAATCAGTGC	CATTCTTGCA	GCTGGGTCCA	AACTCTAGAT	420
	TTACAAACCC	CGCACGAATT	AGCTAGTGTT	GAACCAGCGA	ACATGTAAGG	AGTTTCATTT	480
10	CCCCACACTA	TTGAAAACCTA	CTGCGGTGAA	CGCAGGTGGG	GCCGCATTAA	CGCCATATAA	540
	CTGTGCGGTT	TGATAACAAT	TATCTCATAT	TGTCTTTTTT	ACGCACAAAT	ACATCCACTC	600
	ATAGAGAGCA	TTACGCCAAT	GCAGTCAAAT	ATAACGGAGA	ATTTGCATAT	CAGTACGTGG	660
	AATCGCAGCA	GTTGCTGTGA	TTTTACTATT	GATAACGGGC	GCAGCATAAG	GGCTGTGTTT	720

## 1557UP

	GATCCGCGGA	TTTGGGCACC	ACAGGGTAGT	GTGGCCGCAT	CAAATGATGG	CACACACGCG	60
	ACGTGCGTAC	TCAGCCCCCT	TATTTGATTT	GAAGAACAGA	TTGATTAGGT	CTGATCCTAT	120
20	AGCTCTGGGC	AAAGCGGGGC	GCCTTGGCGC	CTGTGTGGCC	GCGAAGTATC	GCTTAGGAAA	180
	ATGCTGGTGA	ATGTATATTA	TACGCTGACG	GGAGCATTGC	AGTCAGGTGT	CATGTATGGA	240
	CTTGCCTGCG	ATTAACATATC	GCAGCAGCCA	TCTGATGCTT	ATGCACATCA	ACTAGCACAG	300
	CAGCCATATG	ATGCTTATTC	ATACCGGCGG	CCTATCGCCA	TCTTCTTCAT	ATAAAGGCAG	360
	TGTGTACAG	ATAGGTGCAT	TGTCCTCTGA	ATTCCAAAAG	CTCATCGCGA	GTGCAGATGA	420
	AAGATCTCGC	TTCTTTGGTC	CCGCCGCAGG	CGGCACCATC	GTGGAATTTT	AGTGCACAAG	480
	ATGTTATTAG	TCTTAGCCAT	CAATTGATCA	ACCAAACCGA	GGCGGTTTAC	CACAACGTGT	540
25	TACAAGAAAA	GCCACCAACA	ATTGACAATT	ATATCATGCC	TCTAATATAC	CATGAGGAGG	600
	AAACAGACCT	GCTATGGAAC	CAGTTGGTGT	TTCTCCGCAA	TGTTTCGCCC	GATCCGGAGA	660
	TTCTGTGAAGC	GTCGAAGAAC	GCAACATCCA	TGCTGGACGA	CTGGATTATT	GGCCTTACGT	720
	CAAAGT						

## 1559RP

	GATCCAGAAT	CCAAGTTGCG	TGTTTCGTAGC	AACCGCCGCC	TGCGCAGGTT	ACGAAGCAGG	60
	CTAAGGAAAA	GGGGCCTGGA	TGCCGAGCAC	ATCTCAGAAG	TAGTACAACG	CATAAAGGAG	120
5	AAAAGCAAGC	CAAGCGCTGA	AAACAAGACC	GTGCGTGAGC	GGACTCCCTC	ATCCGCTGCG	180
	GTTGCTGATC	CTAAGAAGCG	GGTAGTTCGAT	GTCCCAAACA	ACCCGCCAAA	CAAAGTATTG	240
	CTCGTACAGG	ACCTGCCAAC	AGACATTACC	GAGCAAGAGC	TGGTGGATAT	ATTTGCAAAC	300
	GATAAGTTGC	TCCAGGTAAG	ACTAGTCCAA	GTCCGGCAAC	TGGCGTTTGT	AGACTACGCC	360
	GATGTACAGA	GCGCTACGGC	GGTCAAGAAC	AAACTGGGTA	CAAATTATGT	GATCAAAAAT	420
	CAAACAACCA	TCATAGGGTA	TGCGAAGTAC	ATAGGGCCGT	GGGGATATGG	GTTCTTACCA	480
10	GTGGGTGGGA	ACCCGACAGA	TCATTTAGGT	AACTACATAA	TGATAGTATT	TACMAGACTC	540
	CTTAAGTCGC	ACGTGCCCTCG	ATGTCATTTT	CCAAAGAGGA	CTGTTCTCAT	AGCTGTGAGC	600
	AACGACTCTT	TGCTGCGTCC	TT				

## 1559UP

	GATCCGATGA	CCGTCATGTT	CTTCTACAAG	AACAAGCACA	TGCGATGCGA	CTTCGGCWC	60
	GGGGAACAAC	AACAAGATGA	ACTTCGTCTG	TGACAACAAG	CAGGAGATGA	TAGACATCAT	120
	AGAGACGGTC	TTCCGCGGCG	CCAGGAGAAA	CAAGGGGCTG	GTGGTGTCTG	CGTATGACTA	180
	CAACTACAAG	CGGATACAAT	AGAACATTTT	TTGCAGCTAG	TGTTGTCCCA	CGATAGAAAG	240
	TTTATACGCA	ACCCGGCACA	GGCGCCGGGT	TGCTTGGCTC	CACAGCTGGC	GATGGAGCCT	300
20	TGGGTAGGGC	CCTGCTGGCC	ATTATTCCCT	TGACTCGACC	TTACGCCTAT	AGATGGTGTC	360
	TGGGCTGTTT	TGGCGGTGAT	AGTGAAAATT	TTTTGGCTTT	ACGCTCCACC	GGGTTTCAGG	420
	CTAGGCAGCA	GGATAAGTAC	WTAGGTCTTT	CTGCTTCAGG	CATTATATAA	CCTCAAGCGA	480
	GCTTTTCAGA	CCTTTTAGGC	CAATATATCT	CCAAAGTGTG	GGCATCTGGA	CTATTAAGCA	540
	GGAGGTTCTA	TTCCAGCGTC	ATCAAGAAAT	CTGTCAGAAT	AAGAACCATG	GCCTCAGAGG	600
25	ATGTGCAACT	GGCCAGGAAG	GCTGTTGAGT	TTAACAGGGA	GAA		

## 1560RP

	GATCGCGCGG	AGGTTCTGTA	AAAACCTTCC	ATGCACAAAC	CCCACACCAT	GCTCCCGCTC	60
30	GTCTCTTTCA	AACCTCTTCG	CACTAATGGT	GCCGTGCTCC	ACGACTTTAT	CATTCCCGTC	120
	AAACACTAAG	TCAGGGATC					

## 1560UP

	GATCCCTGAC	TTAGTGTTTG	ACGGGAATGA	TAAAGTCGTG	GACGACGGCA	CCATTAGTGC	60
35	GAAGGAGTTT	GAAGAGGACG	AGCGGGAGCA	TGGTGTGGGG	TTTGTGCATG	GAAGGTTTTT	120
	ACAGAACCTC	CGCGCGATC					

## 1561RP

	GATCCAAATA	AGCGTGC	CGGT	CCATACAAAT	GAACGGTTGA	GTGAAGCTAC	TTCGCTCGGT	60
	CGCGTATGAT	TACTCGCACC	AGGCTCTGGA	TGACGCCGGG	GGAGATGGCG	CTGCTGCTAC		120
5	GGCAGCCAAT	ATATACATCT	TCTATAGGTC	TAATTCATGT	CCGCTTTTTTA	AAAAATGGCT		180
	TGCGTCAATT	TGTATGTAGT	AGGCTATGTA	ACGGCTCAGT	CGGTGGACTC	GGCGAAGCGT		240
	TCCTGGATGG	AAGCAAAGAG	CTTTTCGAAC	TCTGCGTGGA	CCTCGCGCTC	GCCGCGGCTG		300
	GGCTCGAAGA	ACTTGGAGGA	CGAAACGGCG	TGTTTCACGT	CGCCGGTTGC	CTCCGACAGC		360
	ACGGCCAGT	TGGCGCCGTT	GGACACGCTC	TTTTGTGCCT	CGTCGAAGTA	GGACACAAAC		420
	GCTTTCATCA	TATCGTAGGT	CTTCCAGATG	GGGCAGAATG	CGTCGTAGGT	CGAGTAACCG		480
10	TTCTGCTGCA	AGAAGTCTTC	TTTGATTAGC	GTCGCGACAT	CCAGTACGAT	CTTGTCTTTG		540
	TCAGAGAGCG	CGGACTTACC	GACCAGCTGA	ACAACTTGCT	CCAATTCTCT	GGCGTTGGAG		600
	AGGATCTCCT	TGATACGGTC	TCTCAGGACT	GGGAACCGGG	GTAATTGCTA	TCATAGTATT		660
	TGTTTAGGAC	GTTGGTGTTT	CTTCGAGT					

## 1561UP

	GATCGCAGTC	TGTAGTTGCT	GGTACTGGAG	TCTTGACTGC	TCTATGCCTC	TTGCTTGTGC	60
	TAAAAGCGAA	GGAGACTCGG	TTACTTGTAT	GTTTTGCTGA	CCTTCTGGTG	GCAAAAGGGG	120
	TGGGGCGCGG	GGTCGGACAC	TATTTTGGAG	CGGAATCAGC	CTGAGTGTTT	TTTTTGTCTT	180
20	CACCAAGGGC	GGSTAACCTG	GCGCCAGCCG	CTGGCCGGCG	AGGTGATGGG	CCATGAGCAC	240
	AGCAGGTATC	GCGGGAATAT	GGAGTGTCCT	GGGGCGCGCT	TATGTAGACC	CAGCACGGTC	300
	CCCAGCCATC	GCGCGGAATT	GCGGCTTTTG	TAGAGTCCCG	CTAGGCGCGC	TGCCGCGGGC	360
	GTCAGCGCCT	GTGACACAGA	CAAATAAAAT	TGGGCAAGCG	CGAGACACAA	GTCCCACAAG	420
	CCGCCACTGC	ACGAAGCTAT	GCACGCATTC	AAGGAAGACT	TACCCCATAC	CGTGGGTTT	480
	GCCCTCGACA	ATGAGGAGAT	CACATTCCCC	AACTACGTGC	CCACGCATGT	GCAATCGTTG	540
25	CCCACACGCT	CCAACGGGAT	CCGACAGCTA	GTCATAGATA	AGCAGAACCA	GCGCGTCCCT	600
	CCCACATATA	ACCGCTACT	CGACCGCATG	GAGGACGCGC	TCGTGCGCTG	GCGGCCGCCC	660
	GCCAGCTCCC	ACGTCGGCTC	CTCGCTAGCA	ATCCACGGCA	CGCACCCGTA	C	

## 1562RP

	GATCATTTGA	GTGCAAAGGG	AGAAGTAGCG	CTTTTGACAG	TACGTGCGGT	GTGTGGACAT	60
	CCTAGGTACT	GTTGACATTC	ATGTGGGTCA	GTCAGATTAC	AAGTACACAA	AGTCGATATG	120
	ACAAGCCACG	TGACCATATA	TCCAAGACGC	CCCCCAGCGC	ACGCCCTGCTC	TGTGCATAGG	180
	ACTGGCTACC	TACCAGTTAC	AATGGGGTTT	GCAACTTAAC	TGCTCTAATC	CTCACACGCG	240
	GAGTTATATA	TGTGCTATAG	GGCATGCTCC	CGGGGCGCAA	TTCAGGGCCA	ACGGCTTGCC	300
35	ACCATGCCAG	AGCAGCCATA	CCAAGCGCTG	CAACAGGATG	CGATATCTCG	TTCTATATAT	360
	ATACAGATAT	ATATATATAC	TGTAACAAAA	TCCCTAGCGA	TCTCGCTGTG	AAAGGCCGGT	420
	ACTTAAATCA	TATCGTCGTC	TTCTTCAGCC	CCGATCGACA	AAGCCCGCCC	ATCGTTCCGG	480
	AAGCTTGGAA	GCTCGGGCGC	AGAAGAGCTC	AACTCGAGTG	CCGCGCATAT	AAAGCCGGTC	540
	ATGAAGAGCA	TTGTAAATGC	GCAAACCTTG	AAAAAGCCTG	CTGGCAAAAG	CATCACTGCC	600
	AGGAGGAGTT	GTAGGAGGGC	GCGACCCATG	TAACTATAGT	AGAAGGACGC	GTATTGTTGA	660
40	AGCAATGGTA	CTGGTCGGAA	TTTCAGGTAT	ACCAGCAGGA	CGGAGAGTGG	AAGGCCGAAA	720

## 1562UP

	GATCTGGCGT	GCATATATAA	CGTATCTGCG	CTCACGCGAC	CTGGTGCGGA	CTTCTTTAGC	60
	CGGCTACTAA	CTCTGTAGCT	GTGGGGGCTG	CCTGCGGGCG	CGCCGGGCGA	GCTTGGCAGA	120
	ATCCGCCGTT	GCGTCACGGC	CAGTGCCAGC	CGAACAGGAC	GCCCTTTTCT	AGCAGCAGCG	180
	CTTCCGCAGC	GGTTTCTTTT	TTTTCCCAGC	TAAGGTCGTG	TATTTTCTCG	CAGAGGGTTA	240
	GAAAAGTACA	CTTTACATCT	GAACACACCA	CAAAGTCGTT	CTGATTGGAG	AGGCACGAAA	300
	CCAAACAATT	GAAAGGTATG	TTGAGTGCTA	AGCAGACGGT	ACACTGAGCT	GGCCGTCTTT	360
50	TAGCAGCTGG	CGGCCACCCG	CACTTTCTCT	TTTTCCGCTC	TGTTGCTTCT	TGCGCGCCCC	420
	CTTGGCCTGG	ATCTCGAGAG	CCGCGGAGCT	ACCGCCCGTC	CCGCGCCAGC	CTGGGCTTCC	480
	CAGGCGGCCA	GTGGTCAGAG	CCGGTCGCCC	ACGGCAGCCG	GCTTCATGGG	CGGCTGGCGG	540
	CTCTGTTTAC	AGGGATCGGT	CACGTGCCGT	GTGAGGCTAA	GCCGGTGGCG	AG	

## 1563RP

	GATCCTCGCT	ACTTTGACAA	CATCAGGAAG	GCGCTTGCTG	CAGGCTTTTT	CATGCAGGTA	60
	GCGAAGAAAC	GCTCGGGAGG	GAAAGGCTAC	ATTACTATCA	AAGACAACCA	AGACGTGCTC	120
5	ATCCACCCTA	GCACGGTCAT	TGGCCACGAT	GCAGAGTGGG	TAATCTACAA	TGAATTCGTG	180
	CTGACTACTC	AAAACCTACAT	ACGGACGATC	ACCTCCGTCC	GTCCTGAGTG	GTTGATTGAA	240
	CTCGCACCTG	CGTACTATGA	CCTTGATAAC	TTTCAAAAAG	GTGATATCAA	GCTCAGTCTG	300
	GAACGGATTA	AACAAAAGAT	GGATCGCATC	GAAGAGCTAA	GTAAAGAGCA	ATCCAAGAAG	360
	CATAGACAGA	GCCGCGCGTA	NTTCGTGAGC	TTGTTGTAGC	TAAATATCTC	TCTGATATAG	420
	CATGTACACA	ATAATAGGAC	TTTGTAGCTG	TCCTTCGTTA	CTTCGGATTA	GCAAATTATC	480
10	GCAGAACTTA	GCAGGCACCG	CCGCCCTTGT	TGGTGCCTT	GCACGAAAGC	AGCTGGTGAT	540
	GTTCCGGCGTC	GCTAAAAACC	CTCATTTGTG	CCTATCATAT	GCCCAGCGCT	ACAGAGTCTT	600
	CGCATCATCA	TGTTTGAGAA	GGACGAGATA	CTCCCACTTG	ATGAGGCCAG	GTCCCAAAAG	660
	ATAAAGGAGT	TCCTGAGCCT	CTCCCTCGGG	CTGATCACCG	AATCCATCGA	AAAGAAAGAA	720
	TATGACTCCA	TA					

## 1563UP

	GATCGGTTGT	CTTCCGACGC	TGGTACAGGG	CTGCGATGCG	CGTCTGCGGC	TGGCGGTGCA	60
	TATCGGAGAT	ATGGCGCCGT	GCCCGTACGG	CAAAGAATCA	GCAAGACACT	AGCGTCTGGC	120
20	ATTCTTTTTT	AATGCATTAT	TTAGCTTTTT	TTTTTTTTTT	TTTTTTAGTA	TAGACACAAT	180
	ATAAAGTAGA	GTTCGTCATC	AGTAGCGCTC	GTAAGGTTAG	GGGCCGGCTT	CACGCCATAG	240
	TAGCATCTCC	GTCAGACTCC	TGGATTGGCG	CTTGCTCTAT	GCCGGCGGAT	TCCGCAACTG	300
	CGTAGGGTCT	TTCTGTTAGCG	GACTGCTTCC	CACCGGCGGC	ATGGGCAGGC	CACGAGGGAG	360
	CTCCGGTAGC	AGCCTGTGAC	TTGTCTGGCA	GCGAGCGGCC	TGGTGGGTGC	TGGAAGAAGC	420
	AGTGGGCGTT	GCGACATTCC	GCGCCGAATT	TGCAGGGCTC	GTTGATGGGG	TGGCCGAAAA	480
25	AGCAATCTAT	GCGCGTGCAC	GCAGCGCCCT	CGCGGCACAT	AATGTGTGAA	CGCGCATGGC	540
	GGTACTTTACA	CCGTTTGTTC	GTGCACTTGA	CGCCGAACTT	ACACTGCTCG	AGCGAACGCT	600
	CCGCTGGTGC	AAACGCACCG	GCTTGGAAAG	ACGTGGCGCA	GCAGCAATAG	GCTGAACATC	660
	TCGTATCTTG	GACAAGGAAG	ATGCGCCTTG	TCGCAGTCCT	CTTGTCACAG	GTTAGGT	

## 1565RP

	GATCACATGT	TTTCCCCAGA	GAGGGACCTG	GCGTTGAGAG	AGCGATGGGC	CGTTATACCA	60
	CTGAGCCCTA	TTAGTTGCTG	GATTTGTGTT	TCCAGCAGCT	GCGCATGGGG	CCGGATTCCG	120
	TCAAGTGTA	TTCCGCAGAT	GTTGGTTTTG	GCTCGATAAG	TGCATAAGGA	AGCTGCTCTG	180
35	TTAGTACATG	TCACATAGGA	GGCTTCCGCA	TTGGCGCATG	GCATCCAGTG	GCGGGCTTGT	240
	GGCGCGACGG	GTATTCCAGT	AGCCGCTCTG	GAACCGTATT	CAATCATCTT	TGGCCCAGCG	300
	GTATATAAAG	CGGCTGATGA	GCCTGGATGC	AATGGGGTGT	AGCTGCGGAG	ACTGCACCGA	360
	AGATGTCTAG	CAAAGTTTCA	TTCTATTGTA	ATTGGCAGCC	TGCGCCATAC	CACATTGCGA	420
	TTTTTCTAGC	CCAGTCCAAG	GGCTACTTTC	AGCAGGAGGG	TGTGGACATT	GCGCTGCTCG	480
	AGCCACGAA	CCCGTCCGAC	GTGACGGAGT	TGATCGGTGC	GGGCAAGGTT	GACATGGGCC	540
	TAAAGGCGAT	GATCCATACG	CTGGCCGCTA	AGGCACGTGG	TTTCCCGGTC	ACTTCTGTTG	600
40	CATCGCTGCT	GGATGAGCCG	TTCAACGGGG	TTCTGTACCT	GCGTGGCAAC	GGAGTCACAG	660
	ATACTTTTACG	CTCTCTTCAG	GGGAAGCG				

## 1565UP

45	GATCCCTTTC	ATACAGGTCA	ATATTTTATG	CAGAGACAGG	GGCTGGACGT	TGTAAAGGTC	60
	TTTCATCCAG	ATATGCTAAG	AGGCGAAATT	TCATGCACGA	GTATGATCAC	AAAAAATGAC	120
	ACAGCCAAAC	AAATTGCCAT	TATTTTATGA	GGATCTACAG	TGATACAGGA	TTGGATTATC	180
	GATGTTCTAT	CCACCCCTAT	TCCATTCAAT	CTCGCTCCTA	CCCCCTATCA	GCCCCGTCAGT	240
	GGAGCTGCAA	AGTGCCCAAG	GAACGTCTC	ACGCACACTG	GCGTCTACGA	TCAATTTAAA	300
50	AAAGCATTTA	AGGATATTTA	TGCTGTPTTT	AAGCCGCTAA	AAGACACACA	TCCGGATTAT	360
	GAGGTGATAG	TTACTGGTCT	TTCTTAAAGT	GGCGGCTATG	CTCACTTTAT	GGGTATTGAA	420
	TTGCAACTTC	TGGGCTACAA	GCCTCATGTT	TGCGCCTTTG	GATCAATTGCG	TATAGGCMAT	480
	AAGGACTTTA	ACGATTGGGT	GGATGATATA	TTTCCGTCGG	AAGACGTTTC	GAGAAGAATC	540
	CCAAATAATG	AGATGCCC					

## 1566RP

	GATCGCGAAA	CACAACGCGC	GCGGCGCGGT	AGCGCCGCGG	GCGCTGCTGC	AGGACGTGCG	60
	CGACGCGCTC	GCGGCGCACT	ACGGGGTAGG	AGTACATCAA	CCGGTACGTG	GAGGACGAGT	120
5	GGGTGTTCAA	CAACGCGGGC	GGCGCTATGG	GGCAGATGCT	GATTCTGCAC	GCGTCTGTGA	180
	GCGAGTACCT	GATTCTGTTC	GGCACGGCCG	TGGGCACGGA	GGGCCACACG	GGCGTGCACT	240
	TTGCGGATGA	CTACTTCACG	ATCCTGCACG	GGGAGCAGAG	CGCGGCACTG	CCACACGCGC	300
	TGGAGCCGGA	GGTGTACACG	CCGGGTATGA	CGCATCACCT	GCGCATGGGC	CACGCGAAGC	360
	AGTACGCGAT	GCCGTGCGGC	TCTTTTGCGC	TGGAGCTGGC	ACAGGGGTGG	ATCCCGTGCA	420
	TGCTGCCGTT	CGGTTTTCTG	GACACGTTCA	ACAGCACACT	CGACGTGTAC	ACTCTGGCGC	480
10	GCACCGTGCA	GCTGACAGCG	CGCGACATGT	TCAAGAACTT	GGTGACAAT	TTCAAGTTTT	540
	AGCCTAGATA	CATAACCACC	ACCAATGTCT	GCGCAGGCCT	CGCCCGCGAC	AGAGCTGCCA	600
	GAACCCGACG	CTCGGGCAGG	TGTACGCCAC	GCTGACGCGC	CACTC		

## 1566UP

15	GATCCTCAAG	TCTACGAACG	CCTCGAAGGT	GTTTACGACG	GCCGTTTTGG	CTGATGTCAT	60
	CACAGCTGAG	GCTAAGGGTG	ATTTTGACGC	GAAGTCTGCT	GTCCCAGGTC	ACGTGCAACA	120
	GGGCGGCCTA	CCATCGCCAA	TCGACAGAAC	CAGAGGAACT	CGTCTCGCGG	TCCGTGCGAT	180
	CGGCTTCATC	GAGGCTAAGC	AGGACGTCAT	TCGCGAAGCC	AGGGGAAAAT	GAGGAGGCCT	240
	TTGACTGCGC	CGACAAGGCC	GTCTCTCACA	CCGCCGCCGT	CCTCGGCATC	ACCGGCTCCC	300
20	AACTGAAGTT	CACCTCCATC	AGGCAACTCT	ACGACCTGGA	AACAGAGTTC	TCCAAGCGTA	360
	TGCCAAAGGT	TATCCACTGG	GAGCCTACCC	GCGCGATTGC	GGACCATTTA	GAAGGCCGCA	420
	AGAGGGTAAC	AGTTTAGTGT	CTCTGTTTCG	CCCGCTGCCC	CACTATATGT	ACCACTAGAT	480
	ACCACGATTA	TGGATAAACT	TAACATGGCA	GAGTACACTC	TCATCCACCT	GCCATGTATA	540
	TAATGTGATT	TTACTGACGA	AAACTGTTTT	AAACGCCGTT	GCAGGGTCCG	TCGCAGCTCG	600
25	TATAAATATC	TTGACGCCAC	CTCGATCTCC	ATTGGTGAGG	AAGTACCCGT	CGAGATACAA	660
	TAGTGCCAGC	TTGCTAAGGG	GTAAGCTGAC	CACTCTACAC	A		



## 1568RP

	GATCACGAAA	CGGTCGCTAT	TAGGTTCCCA	TGCAAAGCGC	ATGCAGCGGT	CCTTAATCTC	60
	CACCTTCTCA	AATGGAAACT	CTCTGGCAGT	CAAAGAGCAA	ATCTCCATGT	TGGTGAAGAT	120
5	GGTCTTCCCTA	GACTTCGTGT	GACGGTCCAC	CTGTACACAG	AGGAACTCTG	CCTGGTCTCTG	180
	CCAATGGAAG	GAGACATCAG	TAACCTGCAC	CAAGTTGATG	GTACGCAGAA	CACGGCGGTT	240
	CGGTAGCTCA	ATCAGGACAG	CTTTACACGA	CTGGTTGTTT	GACTCTGGAG	TCCAGTATAC	300
	CATGACAGTA	GATGGTGGGT	CGTTGGGTCT	GTTTGACGCC	AACCTGATGC	CCTTAGGAGC	360
	AAAGGAGAAG	TCCTGAACAT	CCTCGATCTT	CATCACCTTA	CCGCCCAACA	GCTGGAAGTT	420
	CTTCTCGGTC	TCGTACACAG	CAATTGCGCC	AGGGCCAAGA	CGAGCGCAGA	ACTTGTCTGTC	480
10	AAAGGACCAC	TTGACCATAG	GCCATTGCAG	CTGCTGCTGA	GGCGGCAGCG	CAAAGGTCTT	540
	CACGCAGACA	CCTGTTGCCA	CATCCCATAT	ACATAGCTGG	TGGCCCCGCG	ACTCGGGCCC	600
	GAATGGACAA	GCCTCGTTAG	GTTTCATCCGA	GACTTCTAGA	GGTTCGACG	AAAAGGTAAC	660
	CAGGTACTTC	TCGGTCGAGG	ACATGGAGAT	CGCCTT			

## 1568UP

	GATCATCTAC	GTGGCCCATG	AGGATAATAA	GGAGAAAGAA	TTCGAAATTG	AGCTGAGCTG	60
	GTGCTCCGCT	TCGGAGACGG	ATGGCTTGCA	GAAGGGAGGT	ACCAAAAGAG	CTATTTGATG	120
	CAGCGATTGA	GTTTGCGAAG	AAGGAGACCG	GTCAGGAGAG	TGATGATGAT	TCAAGCGATG	180
	ACAACGCATC	TGGAGGTGAA	GAGTCCTCAA	CAAAGAAGGA	TGCTGACGGT	GATGTCCAGC	240
20	TTTCATGATA	ACAGCCCGGC	ATTATGTGGA	GGTTCATTTT	ATGACAATTG	ACGGATGTTA	300
	CTAAGTGTAT	ATTAAGTTAA	TCCACCTATA	TAAATTAAATA	ACATGCAAAG	CAATTTAGAA	360
	TTTGTGCGAA	AGCAGGTTAA	AGCATGTCTA	CTCTCCTTAA	TCCTTCGCGA	AGCTGTACAT	420
	TTTCTTCTTC	AAGTGAACGA	ATTCTATCCA	CGGCTGCGTC	TGATTCCTAAT	TTCTTACGTT	480
	CGCGTTCTGT	GTACCATTTC	CGCGTCAGCT	CTTCTATCAT	TAATTTTGAA	TGCTGATCAA	540
	ATGTATCTGA	TTCATCCGAG	CCCTGCGACA	CCTGGGATAG	ACGTTTGATT	CTTCTGTCTT	600
25	TTTCCTTTAA	CAGCAGCTTT	ACATGTTTCT	CCACTATTGA	TGATGTGGCA	TTTGTGGGATG	660
	AACATATAAA	TAGAATCCCA	TTTCAGCTGG	TTTCTTC			

## 1569RP

	GATCCGATAT	ACGCTGAGTG	CTATATTACA	AACCATCAAT	TTGATGTTAT	CTTGGACGTA	60
	TTGTTGGTTA	ACCAGACGAA	AGAACTTTTG	AAAACTTGC	ATGCGCAGTT	TGCAACCCTG	120
	GGCGACCTGA	AGATTATATG	CAACCCTCCA	AGCACCAATC	TAGTTCCTCA	TGGTTTCCAC	180
	AGATTTAGCG	TTACAGTGAA	GGTTTCAAGT	GCCGATACTG	GTATAATCTT	TGGGAATATA	240
	GTTTATGACG	GTGGACACGG	CGAAGATGCA	CGCTATGTGA	TCCTTAAATGA	TGTCCATGTT	300
	GCTACAATGG	ACTACATTAA	GCCTGCAGTT	TGTGATGAAG	CTTCTTTCCG	CAAGATGTGG	360
35	AATGAGTTTG	AATGGGAGAA	CAAAATGGTT	GTCAAATCTA	AGCTACCGAC	CTGCGATGAC	420
	TACTTGAATA	AGCTGATTGA	GGTCACCCAT	ATGAATGTCC	TGACTCCTGA	AGAATCATTT	480
	GCCGACCCCG	AATGTCGTTT	CTTAAGCTGC	AACCTTACT	CGAAGTCCAC	CTTCGGCGAG	540
	GATGCTCTGG	CTAATTTGTG	TATCGAGAGA	GACCCTACTA	GTGGTTCCAT	CATCGGAGAA	600
	GTTTCGCATCC	CTTCGAAGAC	GCAGGGCCTT	GCTTTGACCC	ACGGAGACAG	TATTGCGCMC	660
	ATGGAAAGGT	CC					

## 1569UP

	GATCTGCAAT	GCTCTTCAAC	AATTTGCTGC	AAGCTATTCT	CCTGATGACC	TTGCCATCTT	60
	GAGTGAGCTT	TTTGATTCCA	ACAGCAAATC	TGAATAGGCC	TCTATCTCCT	TTAAAAGCAG	120
45	CGTCGTGCAT	GGGGCTTTGG	GTTTACATTG	GAAAAAGCCC	CAAAGAACAA	GGTAATGCAT	180
	GCCAAAAGTA	GCCTTTAATC	CACTTCACAT	TTAGATATTG	TTACGCAGTG	TATCTATACA	240
	AAAAATAACG	ACAAATAATA	TCTTTTAGAG	CTGGTTCTTT	AGACTAAAAT	AGGGCTCGGT	300
	ATGCAATACC	TCAGATGCTA	TCTTGATATC	CGTGTGGATA	TCCTCGATTG	AAGCCTCTTT	360
	CGTGGTGTAG	TTTAATTCGG	GCCGGATGTA	GCCAAGGAAG	CTGAACTTAA	TTTTGGCGCC	420
	ATAGAAGTCT	TCTTCAAAGT	CGTTTAAAT	GTGCAACTCA	ACCGTCTTCT	TACTGTTGTT	480
50	ATAGAACGGG	TTCCATCCTA	CCGATAACAC	GATTGGAAAG	ACTCCACGCT	CTGTTTCCGA	540
	CAGCTTGGAG	CCAAAGTTGT	ATATGACCTC	GCTCCCATCA	TTTCTGTGAT	GGGACCTGCG	600
	CTTCTTGGTC	CATATTAGCC	TTAACCAGGC	CCAGCCAAA	TATACTCCTG	TGGCCATTTT	660
	GTTAACTTCC	CTAGGCAATT	GTTCTATTGG	GAACATTC			

## 1570RP

	GATCCACAAC	ACACACAGCT	TGCGGACTCT	TMTTCTCAAA	GACAGTTCAC	CAGTCCAACA	60
	CTTGCAAAAC	CATCTGCTAA	CGTTTCAACG	ATTGCGCAGC	AGCAAACCCA	GCCAACCGCT	120
5	CTCTCTCAAT	CTCATCCTCA	GCAACAACAA	GGTTCACAAG	CTCAGCAGCA	GCTACTTCAA	180
	CAACAACAAG	GTTTACAAGC	TCAGCAGCAG	CTACTTCAAC	AACAACAACA	GCAACCACCA	240
	CCACCACCAC	CACAACCACA	GCAACAACAA	CAACAACCAC	AACAACCACA	ACAGCAGCAG	300
	CAGCCCCAAC	CTCAACCGCA	ACTACAACAA	CAACAACAGC	TTGGTTTACA	GCCTCATCAG	360
	CCACAACCTGG	CGCAGGCGCA	GGCGCAACAA	CCACAACCGC	AGCAGCAGAC	GCAGCAGCAG	420
	ACGCAGCAGC	AGCAGCAGCA	GCAGCAGCAG	CAGCAGCAGC	AGCAGACACA	GCAGCAGACA	480
10	CAACACCAAC	CACAACCACA	ATTGAAACCA	CAATCACAGC	AACCACAACC	GGTTCCACAG	540
	CAAGTCCAGT	CTCAACAACC	ACAGCAAGTC	CAGTCTCAAC	AACAACCACA	GCCTCAGCAA	600
	CTTTCACAGC	CTGCCCAACA	ACAATCGCAA	CAACAACAGC	AGCAGCAGCA	GCAGTCTCAG	660
	CAGCAGAAGC	TTCGCCAAGT	GCAGCTGC				

## 1570UP

	GATCTTCGGG	CCCGCGGGGC	CGCTGGGCTA	CGTGCTGACG	CTGTATGCGA	ACGCGCAGTT	60
	CTTCACAACC	ATGATCGTGA	ACTCGCACCT	GGCGACGCCG	CTGTTGGACT	ACACCATTGC	120
	GTCGCTGATG	GGTATCCATA	TTGAGTACAA	GCGCCATAAC	CCTGAATTGG	TGGAGCCGGA	180
	GGCGTTCAGC	GCATACGATG	TGCTGACGGT	GCTGCGCCTG	GTCATGAGCG	TTGCCGTGAT	240
20	GGTGGTTCTG	GTGACCATCC	CGATTCTGGG	ACCTGTTCTA	CTGATGTTTG	TGATGAATGT	300
	AAAGTTTTC	TACGACTTCT	ACGAGCGGTT	CTTAATTCTA	CGGGGACTAA	ACCAGGTGCA	360
	GCGCCGTGAC	GTGTTCTACC	AGCATATCTT	ACAGTTTGCA	TACTTCGGGG	GGTCGTACAC	420
	GGTTTTAAAT	TTGCTGCCTC	TATTCTCAGT	CTGGGGCTTT	GTGTGCTATC	CGTTGGCAAT	480
	CAAAATGTGG	GCGACTTCCA	ACATCATCCA	CTTTACAGCG	GAAGAAGTGG	AGTCCATCAC	540
	TGAATGAAAT	CATTCAATTA	ACATGTCCAT	CTATACATAA	AGATAGATAT	AGCCAGAAATC	600
25	AATACCCCTGC	CCATAGTAA	AGTACCATGC	TGTCGACACA	GCCGAATCCC	GCGCAACACC	660
	GCCCTCGTTG	GACGAAGGCA	ACTTGGAACG	CAGCAGCCAT	CCCAGCGTAG	TCGT	

## 1571RP

30	CGCAGGCCGT	AGGCAACACC	GTTGGATATC	TGCACCTGGC	AAAGGTCCTG	ACCCGGCAGC	60
	AGAAGCTCGC	GCGAACCGGT	AGTCCACGCA	TACAAGTCGC	CGCGGCGGTC	GATTGCCAAG	120
	TTGCAACCCCT	CCTCTGCCAG	CGCCACATCC	CGCAGCCGCT	CGCCCTCAAA	CCCCGGCACC	180
	CGCAACGGGA	ACCGCGTGGA	GCCAGCGTCC	TCGCCCAGCC	GCGCGCCCCA	GTAGTAGAGC	240
	CCGGGCTCTC	CTGGCTGCGG	CGCCGTCAAC	GGGATCTCGG	GGATCCCGCG	CAGCTCCTTC	300
	TTGCGCTTGA	TCTCCTTCAG	CCGCTCAAGC	GTGTTGTCTG	CCACCCGCGG	GTCGCGCGCT	360
35	AGAATCCAGC	CCTTGATCTG	CGGCCATTGA	AGATACACCG	TGCCTGCTAC	TCCGATCCCG	420
	ACGACCACCG	CCAGGCCCTG	GAACACCGCC	ATCAGCTTCT	GCATCTTCTC	CACCTTGCTC	480
	GCATACTCCT	GCTCCAGTTG	GCGCGGCGAT	TTGTCACTCC	ACTGGTAGTC	CAGCTTGCTG	540
	CGCTTGCCCT	TGTATGTGCC	ATGGTTTCAG	TGCTCTTGCC	ATCATCTCGG	GCTCATCAAA	600
	ACGCTGCCCC	TTGCGCAACG	CCCTTGCTTC	CATAGCGAGC	GCCTCGCCAC	TCGCAGCC	

## 1571UP

	GATCACGTGA	TGGGATGAAA	ACTCTGACAA	ATGCACCGGG	AATATATAAG	GCATGGAGCT	60
	GCGGACTCGG	CCAGACAGTG	CGAGCAGCGA	AACAACAACA	TCATCCAAAA	TGGCCAGAAG	120
45	ACCAGCTAGA	TGCTACCGTT	ACCAGAAGAA	CAAGCCTTAC	CCAAAGTCTA	GGTACAACAG	180
	AGCTGTGCCA	GACTCCAAGA	TCAGAATCTA	CGACTTGGGT	AAGAAGAAGG	CCACCGTTGA	240
	TGAGTTCCCT	CTATGTGTGC	ACCTAGTGTC	CAACGAGTTG	GAGCAGTTGT	CCTCCGAGGC	300
	TTTGGAAGCC	GCCCGTATCT	GTGCCAACAA	GTACATCACC	AAGATGACCG	GTAGAGACTC	360
	GTTCCACTTG	AGAGTCAGAG	TGCACCCATT	CCACGTCTTG	AGAATCAACA	AGATGTTGTC	420
	GTGTGCAGGT	GCAGACAGAC	TGCAGCAGGG	TATGAGAGGT	GCCTGGGGTA	AGCCTCACGG	480
50	TTTGGCTGCC	CGTGTGCACA	TCGGCCAGAT	CATCTTCTCC	GTCAGAACCA	AGGACAACAA	540
	CAAGGACATC	GTTGTTGAGG	CTTTGAGAAG	ACCAGATACA	AGTTCCAGG	TCAGCAGAAG	600
	ATCATCATGT	CCAAGAAGTG	GGGTTTCACC	AACTTGGACC	GTGCCGAGTA	CGTCAGA	

## 1572RP

	GATCTATTAT	TAGAGGTAAT	ACATTTAAAC	TATTATCTAA	ATTCTTCTTC	TTCTTATTTA	60
	TTCTTAACTT	TATCTTATTA	GGTAAATTAG	GTGAATGTCA	TGTTGAAGTA	CCATTTATTT	120
5	TAATAGGTCA	AAATTGTACA	TTTATTTATT	TTGCTTATTT	CTTAATCTTA	GTACCTATTA	180
	TTTCTATAAT	TGAAAAATAT	TTATTTTATT	TACTAAATAA	AAAATAATAA	TTAAATAAAAT	240
	AATAATAATA	TTCATTAAAT	ACTTTAATAT	TAATATTTAT	ATATTATACT	TCTTTATCAT	300
	TTAGGAGGGT	ACCTCATATT	GCTGACTAAC	AATAGGGGGG	TGAACCCCTAC	GCACCTAAAT	360
	GATAAGAGTT	TATCATTTAA	TTATATACTA	TATATTATAA	GTAAATTATC	AAACCATATA	420
	TAAGGTATAT	ATATTTAAGAA	AGTTTGACTG	AGTGGTTTAA	AGTGTAAATAT	TTGAGCTATT	480
10	ATAAATCTTT	ATGATTTCCCT	AGGTTTGAAT	CCTATAACTT	TCGTATTAAA	TAATTATTTA	540
	AAATAATTAA	AAATAGTTAA	TAATAATGAG	AACATGATGT	TGGTTCAGAT	TAAGCGCTAA	600
	CTAAGGGACA	TTACACATGC	CAATC				

## 1572UP

	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTCATTAAA	GAATGATTAT	TATCAAAACC	120
	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTCRC	TTAATTAAAG	ATTAGGAACT	180
	TTATCTATTA	GTCTGGGCTG	TTTCCCTTTT	GATTATTAAAC	CTTATCGCTA	ATAATCTGAA	240
	ATATTTAATT	TTAGATTAAAT	AATATATTCCT	GAGATTTTAAT	ATTTTAAATA	AAATAAAATA	300
20	TTATTCCCTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTTCGTAGAAA	ACCAGCTATT	TGCAAAATCAG	ATTTTGACTTT	CTCTACTTAC	420
	CATTATTCAT	CAGATAATAT	TGCTACATTA	ACCTGTTCAA	TCGTTTTTTAT	ATTTTATTAT	480
	ATTTTAAATA	TAATAAATAT	ATATTTTAAAT	CATTTGATAA	TAGTAAGATC	ATCTGCTTTC	540
	GGGTAAATTA	ATATTAACTA	AATTTAATTT	ATTTTAAATTA	ATTTTAAACAT	TGTTAAATAT	600
25	TTATATTATT	TTTAATATCA	TTTTTTATTT	TAATATTATG	CTAATATTAA	TTACTTGCTG	660
	ACCCATTATA	CAAAAGG					

## 1573RP

	GATCCGTATG	GAAATTATTT	TTTTATTTGA	ATTATCTTTC	TCCAGAACAT	CCAAGAAGAG	60
	TGTCAGAGTG	GTGGGCAGAT	ATGGCTTAAA	CTCTCCTTCC	AAAGATTTAG	AAATAGATTC	120
	GATAACAGAA	ATGATTGTAA	TTTGCAGTTT	AATAAATGGG	AAGAACTCTT	TAATGACTTC	180
	AAATATTTTCG	TCAACATATG	GCCTGATATG	TTGCTTCACA	ATTGATACCA	TAACACCTAA	240
	TTGTTGAAAA	TAAAACCTCA	GTATTGATGG	AGGACAGCTA	CGCATCACAT	TAATCATTTCC	300
	TGGAATAATT	TGCTTTAGGA	AGGAGACGCA	GCGGAGTCCC	AATGTTTGGG	AGATGTGTCAT	360
	CACTGCCTGT	ATGACAGCAG	TGTGATGAGA	AGATAAAGAA	GGATCCTTCA	AAATTTTCAT	420
35	TAGAGTATTG	ATCACGACGG	TTGGATAATA	TTCTTCATTG	GAGGGTGACA	TACCTTGCAT	480
	TAACAAAGCA	ACATCTATGG	ATGGGGCATT	TTGTTTCGACG	GATATAGGCG	TGCTGGATGT	540
	TCTTTCAACT	TCTCTATGTT	TATAAGGGTC	CAGAGCTCCC	AGAATCCCTA	TTAGTCTAAC	600
	TGTTTCCCTC	CTTATGCTTT	GGG				

## 1573UP

	GATCSGATAG	GACAGCGAGT	ACGACGGCCC	CTGTGCCGCT	GCCAGCGCCT	CGTTGCCAAT	60
	GTAAAAGTCG	AGGTCTCTCCG	TCCCGCGCTT	CCCAGCCAGG	TTGTTTCGACA	TCAAAGAAGA	120
	TGACGTAAAG	CCCGTGAAACG	ACGTCGCCGA	CGTCGTGTTG	CCAAAGAATG	CAGACCCGCC	180
	AGCGCCCAT	CCGCTCCCGC	TCTGGCCCAT	ACCGCTCATA	CTGCTACTCT	TGGCCGTCTT	240
45	GGAAGGCTGC	GCAGTCGCAA	TTGCCGTTGG	GAACACCCAT	GAGGGCGAGT	CGTTACCTGC	300
	AAATCCCAAT	TTGGTCAATC	CTGTACCATT	GTCCATGACA	ACAGCAGGAT	TATTGAGGTA	360
	TGACATGCTG	TATTCTCTGGT	CTCAAATGCT	TCTGGTAGAC	TTGTGTGAGC	CTTTGGCTTC	420
	GGATGGCTTG	TCACTTACTG	GCTTAAGAGT	GCTGGCAGTG	GAAAAGGGGT	CTAATGCGCC	480
	TTTCGTTTFA	GCAGTCCACC	ATCACCAACC	ACGGTACACC	TGACGAAAGG	CAACGCCGTG	540
50	GCTTGTGAAG	CCAGGAGAGC	CCTCGTAGGT	ATTCCGCGGA	GCCAATTGGT	GGCCCTCTGC	600
	GTTCCTCGAG	CGCTCCTGCT	CCATCTGCCC	TCTTGACTCG	TTTATGAACC	TTGAAACACG	660
	GCATATAGCG	ACACGGACTT	TCTGCAGGTC	TGTAGAGTAG	CCCACATCCG	GCGAA	

## 1574RP

	GATCCCGAAG	CTGGTCTGTT	TCGAATTCGG	GATATTTT	GGAAGTACGT	TTGTTCCAAC	60
	GACGTTGCTT	CCATGCATCT	TGCGGGGTTG	TTGACGCAAC	ATTTTCAGTC	TCACATTCCC	120
5	TGAACAGCTT	TGCTATCTAC	TAGGAGTTAC	TGAAGCTTTT	AATGTCTGTT	AATAAATCTT	180
	TTGAGTTAGA	TAATTCGCTG	CGCTACAGTC	TCCATGGGTT	TPCATTGGCC	AACCCATCTG	240
	TAACCTCTAAT	TGAAAGGGGAG	AAGATCCTAT	ACAGGAAATT	AACAAAGGAG	TCTGTGGCAC	300
	TAGTTTCGGG	TGGGGGGTGC	GGACATGAGC	CTGCGCACAG	CGGTATGTT	GGGGAGGGCA	360
	TGTTAACC GC	GGCTGTCCGA	GGAGACATTT	TTGCGTCCGC	GTCGACGGCT	CAGATTTTGA	420
	CTGCAATAAG	GATTGCTACA	AAGCAAGCAG	CTGGAGCATT	GCTGATCGTG	AAGAACTATA	480
10	CTGGCGACGT	TCTTCACTTT	GGCCTGGCAA	CTGAGCGTGC	TCGGTCTATG	GGCATTGATT	540
	GCCGCGTGGT	TATTGTTGGT	GATGACGTAC	TGTTGGTCTT	ACCAAGGGTG	CAGGAATTGG	600
	AC						

## 1574UP

15	GATCAAAAGC	GTGAAGCTGG	AGCGTAATGA	GGAGCAGCCA	GTTGTTTCGA	TGGACTGGGA	60
	CCAGCTGTAC	GACGTGTCTT	CGAACATAAT	GGAAGAATTT	ACAAAGGAAA	TGGACGAAAT	120
	AGTGGCAGAG	CTCAACCAGT	CGTTCAAGGT	ATGTAGCACG	ATGAACACGC	AGGGCGGGCG	180
	GGTTACTAAC	GCGATGGGTG	CAGAAGCAAT	TGCTTTGGCA	GGAGGCGGGC	TTTACCGTCG	240
	ACTCGCACAG	AGGCGCCACC	CGGTTCCGGC	CTGCGGAAAG	CTGGATGAAG	AGCAAAGAGA	300
20	CGCACCTGGA	ACAGAAGCGG	CGGGAGCTCA	ATGCATCCGG	GCGCATCATC	AAGAGCACGC	360
	TCGAAAATTT	GACGCAAGGA	TAGTCCCGGC	CGGCATCCGT	CATGCAATGC	CTTGCTCAAC	420
	ATTACATGGA	TGGGTATTTT	TGCCTATGTA	CAAACATAAT	TTACGCGAAT	TTAGCTTTCT	480
	TCCAAGGCCT	GTCCTCGGTG	TCTGCGCCAT	CGGCGGCTTC	AGTTTCACTC	TCCGAGACAC	540
	CGGCGTCTGA	GTCAAACTCC	TCCGCGACGT	CATCGTCTTC	CGACTCCGCC	TGGAAATCCT	600
	CGTCCACAGA	CTCATCGTCC	TCTGCAGCAG	AACCATGTTA	ACGTCTCAT	CTCGCTGTCA	660
25	GAACCAAGGG	CTGTTTGTAG	GCGCTGCTGA	ATCTCTTTCT	CTTCGTTTTT	GACGCGGACG	720
	TT						

## 1575RP

30	GATCCAGTAA	ACTTCAGCTC	ATCGTGAGCA	ACCGACGTCA	CCCCACCACG	CGCAGGCGAT	60
	ACTCCGGTGG	AAATCACCTG	AGTATATGCA	GTACTCTTCG	AACCATCGTG	AGCAACCGAC	120
	TCCACCTCAC	CACGCGCAGG	TGAAAGTCCG	GTGGATATCA	CCTGAGTACG	TGCAGGCGAA	180
	CTGCCGTGCG	AAATCACATC	ACTATCAGCA	GGTGAAGTCT	CAGTGGAAAT	CGCCTGAGTA	240
	CGTGCAGTAG	GCTTCGACTC	ATTGTGGGCG	ACCGATGTCA	CCTCACCCCG	CGCAGGCGAA	300
	CTGCCGTGCTG	AAATCGCATC	ACCACGCGCA	GGCGAGACTC	CAGTGGAAAT	CACCTGAGTA	360
35	CGTGCAGGCG	AAC TGCTGTC	GGAAATCGCA	TCACCACGCG	CAGGCGAGAC	TCCGGTGGAT	420
	ATCAGCTGAG	TGCGTGCAGT	AGGCCTCGAC	TCATTGTGGG	CGACCGATGT	CACCTCACCC	480
	CGCGCAGGCG	AGCTTCCAGT	GGAAATCACA	TCACCACGCG	CAGGCGAACT	GCCTGTGGAA	540
	ATCACCTGAG	TACTTGCAGT	AGGCCACGAC	CCANCGTGGG	CAACTGACT		

## 1575UP

40	GATCAAATAT	CAACTAAGGC	ACTAGTTTTT	GGTGTAGCTG	CTCAAGCATC	ACCGGATGCT	60
	CAGAAGCGTG	TAATTAACCT	ACAATCTCGG	ACTTCACCAC	CCAAATCTGA	AACACATTCTG	120
	CATATACGGC	ACAACGCTTC	TAGCGTGTAT	CAGTCGGAAA	CAACAKATAA	TATAACTAAA	180
45	GATACCGGGA	TGTTTTCTGC	AGTGAAGTCA	GGCTTTCCCC	ATATACAACA	GAAAACCATA	240
	TCAGCAGGCT	CTGAACCTGA	TGACACTGAC	TTTCAGAGAA	CACAAACTAC	CAGCACAGGC	300
	CCACTTCCAA	CTTCAAGCGA	ATATGACTCT	GCCCCGTGTA	CAGTTTCATG	AGGACTTGAT	360
	ATTTCTCCAA	GACCACCTTC	CTCTAGCTCC	ACAGATTTTC	ACGAGTATCC	AACTGGTACA	420
	ATAACAGAGT	CACACAGACG	GCCTTATAAC	GTTAGCCAAC	TTCCCGAAAA	TAATGGGAAC	480
	TCAGCTGCCA	CTCGTGTGAT	TAAGAGAAAC	AGTTCTGTTC	TCAGCTCGCC	TGGAAGCGTG	540
50	ACCACCACCC	CAATGGTTAA	TCRAGCTACA	GTACTCAGCG	CCTCGCCGGG	AGCGGTTAAA	600
	TTAACCGAGA	AACAGCATAG	TCCGGCATCA	TCTTCAGATA	TTTCCACAGC	CAATAAAACA	660
	CATTGCAATT	CTATTGATCT	AAAC				

## 1576RP

	GATCTTGTG	AGAACACTCA	ACATCGGCGT	AATTGCAGAG	CCCCGGTGA	CCATACCGAT	60
	TTTCTTGTA	GCATTTCGTCA	CATAGCTGAA	CCGTCCTACA	GGACCTTTGA	ATTCCACAGT	120
5	TTGGCCTGGC	TGTAGCCCAG	CAAACCAATT	GGATACCTTA	CCGTCGACAT	AAGATTTGAC	180
	AATGATATCG	AAATGGCCCT	CGGCAAATTT	GTTGGAGATA	GGCGTGTAGT	AACGCACTTC	240
	TTCTACACCA	TCCAGCATCA	CCTTTCGCAGC	TAAATGAAAG	CCAGTAGGTA	TATCAAGAGT	300
	TTCCACGCTT	GAACGGAGCT	TGAATCTGTA	TATCGCAGCA	TTTTTGCTTA	GAACGATCCG	360
	TTCTTCCAAT	TCTAATGGCG	TCCACTCATT	TGGAAGAATT	GAAGTCCTGC	TTCTGTATGC	420
	TAGTAGCAGG	CGTGACCTTA	CAAACATTGC	CAAAGCTAGA	ATGCCTAGAA	GGTACCATGC	480
10	GTTCCCCGCT	GACCAGGCGA	TAACAAGAAC	GCCCAATGTA	AAGATGCCGC	TGGGGATGAA	540
	GATCCCATGA	ATGGGATCAT	CCAATATCTC	CATACCTCTG	CGTTCGGTCA	TACTAATATT	600
	TTGAAAGCTC	GTCGTAGCTA	TCTGTCTAGTA	AGGATGAGAC	CGGTAAATAT	ATGCTTCCTC	660
	CTAGTTCTAT	AAGCACGGAC	TCTTTGCAAC	TGGTGAAGTA	TCTGTCTAACG	GTCATCATGC	720
	ATCTGCCGAA	AA					

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## 1576UP

	GATCAGGCCG	GACGGGTACT	TGCAGGAAGG	CCTCACGAAA	CCCAAGGGGG	GCGAGGAGGG	60
	CTTCTCGACG	TTTTTCAACG	AGACGGGCTC	GGGCAAGTTC	GTGCCGCGCG	CGGTGTACGT	120
20	GGACTTGGAG	CCGAACGTGA	TCGACGAGGT	GCGCACGGGC	GCGTACCGCG	AGTTGTTCCA	180
	CCCGGAGCAG	TTGATCAGCG	GAAAGGAGGA	CGCGCGGAAC	AACATACGCG	GTGGGCACTA	240
	CACGGTGGGG	CGCGAGCTCT	TGGACGATAT	CCTAGACCGC	ATCCGCAAGA	TCTCGGACCA	300
	GTGCGACGGG	CTCCAGGGCT	TCCTCTTCAC	GCACTCGCTT	GGCGGTGGTA	CGGGCTCCGG	360
	CTTGGGGTTC	TGCTTTTGG	AGCAGCTTTT	TATCGACTAC	GGCAAGAAAT	CGAAATTGGA	420
	GTTTGCCGTG	TATCCCGCGC	CACAGGTGTC	CACCTCGGTC	GTGGAGCCAT	ACAACACCGT	480
25	GTTGACCACC	CACACCACAT	TGGAGCATGC	CGACTGTACG	TTCATGGTTCG	ACAACGAGGC	540
	CATCTACGAG	ATGTGCAAGA	AGAACTTGGA	CATCTCGAGA	CCTAGCTTTG	CGAACTTGAA	600
	CAACTTGATC	GCCCAGGTTC	TCTCCTCGGT	GACCGCGTCA	TTGCGTTTCG	ACGGCTCCTT	660
	GAACGTGGAC	TTGAACGAGT	CCAGACCAAC	TTGGTGCCAT	ATCCAAGAAT	CCACTTCCCA	720
	TTGG						

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## 1577RP

	GATCCGTTTA	GAGAAAAACG	GTAGCCCGGT	GAAATACGCA	TTTGAGTGCG	CAGAGCGGCG	60
	CGAGCCGTCC	GAAAGGTAGA	TTTTGTCCAG	TGGGAAGTTG	ACTCGTTTGC	TTATTTTCGAC	120
	AATCGACGTC	TTCACTCTCC	CGTCTTCCAA	CGGGGTGAGC	TTGTTGAATA	AAGCTGTAAA	180
35	AACCTGGTGA	AGAGCAGTCA	GCACCAGATA	GAAAGAACAGC	ATCAGGATAG	AGACGTAGCT	240
	GACGAAGCCA	GTCGAGAACT	TTTCAATTAC	CTTCAACAGC	GCATAGGCTG	CAGGAGTGGT	300
	AATCATGGAG	GAGATCATAA	ACACTTTTAG	CTGGTCCGTT	AGCCATAGCT	TGACCGTGGA	360
	CTTGTTGAAC	CGGAATTTTT	CCTCGAGCAT	AAAGTTGTAG	TAATAGCTCC	CAAACAACCC	420
	CTGCCACCAG	TTCAGCTGTA	GGTAGACGAT	CAAAAAGTAC	AGCGACTGCG	AGATGGTCTGA	480
	TACTGGCACC	AGCATGGCGG	GCATGCGCTG	ACCTACCGCC	ACTCCTAGGT	TCCACATCCG	540
40	TGGCAGCCAG	TCGTACTTAA	TCATTACCAG	ATTTAGTCCC	AGGAACACCA	GATCTCTAAC	600
	CATACGGTAG	CGTTACTTGG	CCCCTCGTA	CGCCTGCGTC	TPTTGCATTG	TTTCTTTATC	660
	AATAACGCCC	TCCAGTTCGC	TGGGTA				

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## 1577UP

	GATCTTCGAC	ACTATGTAGG	CCGCGTAGAT	GAGCAACATT	ACCACGCAGT	CCAGGACGGA	60
	CACAGCGTTC	ATCAGGCATA	CGTAGCCGAT	AATGCAGACG	GCCAGCATCG	CAAACAGTAG	120
	GTCCACGATG	ATCGAATGGC	GCTCCGCCGC	GCTAAGATTT	ACCCACGCAG	ACCTCATCAC	180
	CATAAATATC	GCGCCCTGTA	CCACACAGAT	GATAACGCCG	CAGGCGCCCA	GCACCTCACC	240
	CACAGACAAG	CGGGCGGCAT	TGTTGGCCGC	GTTCACGAC	ATCAGACTGG	AGAACAAGTC	300
50	GGGCGACGAA	TTGCACCATG	CCAGTAGGAT	GGCTGCCAGA	ATGCCCTTGT	GCGGCCGGTT	360
	CCGTTGGCTC	GTCGAAGGTA	CCACTATGGG	ACATAAATAA	TCAGAAGCGG	AAACGCCCCAG	420
	CAACACAAAA	CACAGACTCA	GATGTAGAAC	CGTCAGCACC	ACGAACCCAG	GGATAGCTTG	480
	TTCTGTCTCGT	ATAGATACAC	TGGATGTGTG	ATCCGTGCCC	ATGTACTTGG	TGCATGGTCC	540
	ATCCTTGCAC	TCTGCCTTTC	CAGGTACTTG	GTAATAGTAG	TGGTAGCCAC	CGCAACACTG	600
	GTCAAAAAGC	ACACCTRAAA	CCTCAATATG	TAAGGCGTGC	GAATGGTAGA	TGCGTTATTT	660

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AAAATGCAGT GCTTGAGATG AACAGATAGA CTGGTGCCC

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## 1578RP

	GATCATCCTG	CTGCGAGTTG	AAGTCATCTT	GCGATTCTTT	CATGCATAGG	AGTTGGTTAG	60
5	CACCAAACAT	AGGATTTCATT	CTCAAGTCCA	CCTGCGTTAA	CCGTTCTGTC	CTATACCTTA	120
	AGTAGTCGAT	GAACGTCTTT	GTAGAGTGAG	CCAGGTTATT	AAAATTAAAC	CTGTGGGAAC	180
	TATCCCGGTC	TAGTCGGATG	AGATTATCGG	TAATCTTATT	CACGACACCC	CAGTCCTCGT	240
	TCGATAGACG	CTGGCTACCC	GCAGCCTCAT	TCCGCAACTC	CTTATCGATA	TCTATTCCAA	300
	GGATCTCGTC	CAGGAGAATG	CTACCATTTT	TATCGTTCTG	AATGAACCTG	CCTCTACATC	360
	GAGCAAAGCA	TAGGTGTTTT	ATGTGGATAT	CCGCTAGATC	GAACCCAGAC	TCATCGCCGA	420
10	CTTTCTCTGT	ATCTAGCCCA	AAACCATGCA	TTAGCAGCTT	CAAGACAATC	GCCACAAGCT	480
	GCGATTGTTT	CCATGTCTTG	CAAGGAAGCT	TTACGACATA	TGGGATTTCG	TCATCGCGGC	540
	CATGTTCAAA	GTTTTGCAGC	ATTAGCACGC	AGCTAGTGGA	TGGGGTGAAC	ACGATCCTAG	600
	TAAGGACCGC	GACGAACCTA	ACCTTCTGTG	CTACAATATC	ATCACTGGAG	AAAAACCTCA	660
	GAAGTTCCGC	GG					

## 1578UP

	GATCTTTTTT	TGGTCTTTTT	CCTTTAAACA	GAATAATAAT	TGAACAGGTA	CCGTATTATC	60
	GCCGCATGCT	AAGTGCACCT	TTGACCGAGA	CACTTTAGTG	ATATTTATTT	TGGTAGTGTC	120
20	CTCGTATACG	TGGGCCACGA	CTTTCTTGCC	ATTAATCTCG	TCCTTGGCGA	AGCCGTCCTG	180
	GTAGCATCCT	AACGCACCTA	TTAATGCCAA	TGATCGCGGG	TTGATCGCCT	CACGCCCATC	240
	CGAAACAACA	CAGACACATA	TCCGTTTCCA	GGCATCGGGG	CCCCAAATAT	CAGAACGCTT	300
	CCGTCGAGTG	AAATATTTTT	TGTTGTCCAT	GACGCCTTTT	AATGTCCGTG	CCAATAATAT	360
	GTCTGTTTCG	TTGTACATCG	TTATCACGAT	CATGATTTC	GTCTTACGCG	GTACAGCGTA	420
	TTTTAATTGT	CTCACGGTAA	AGTTCCTTTAG	CTGAAACTCA	GCTGGCTCAC	AGGTGACAGC	480
	CTGATATCGC	ATGAATTTGT	ATTCGTTTCG	GAAGTAATCT	TCTCTCATGC	CACGTGCGTA	540
25	CTGCGACACT	AGCTGTTCAC	TGACTGGACA	ATCAAAGATA	AAGTTTCCTC	GATATAGCTT	600
	GAACCTTCGT	AATACAATGC	GATTTTTAGG	CTGTTTCGAC	TGCGGTAAAC	CACTCAGAAG	660
	CCGTTCTGAG	CTGAGATCGC	TGCAGTCGCC	AGAACCTTCG	GAACCGGAGT	ATGCCGATTA	720
	GGCGCTACGC	GAGAGAT					

## 1579RP

	GATCGAAATA	CCACTGATCG	ACCGCGGTGC	CTCGCTTTGC	AGCTGCTCCG	AGAGCCGCTC	60
	TCCGAGATAC	CGCGCAGAGC	ATGCCTTTTC	CAACACCATC	TTCTCGTACC	GTTCCGGGAG	120
35	TGACCCTACT	ATACTTATGA	TAATGACCTT	CTTGTCCTTC	AGAGTGCCCT	CTGTTTCCTT	180
	CTTCAGGTAA	AGGTGCGATT	CTCGGCCAGG	CTCGTAGTAG	CCACGGACCG	CAGACGCAAT	240
	CCGCGTCGTC	CACGGCATGG	GATGGAAGTA	CTCCACCGBA	GAGTGGCCCG	GCAGAAGCAC	300
	CGAGTTGTTT	ACGCCGACCA	CGTACTCCGA	CTGGTGCTCC	AGCGGACACA	CCTCGAGCGG	360
	ATACTCCTTC	AGCGGCAACT	GGCAGTTCTG	TGACCCGGTG	TTCCGCAACGC	TCAGCTCGCC	420
	CTCGACCAGC	CCCCAGACCC	CCGCCATGTC	TCCCATGTCC	GGCAGGTACT	CCGTGTGCCA	480
	GCACCAGGAG	TCATTTCCCC	GCGCTACCGC	CTGCAGCGCC	TCCGTGCTCA	GCGTATGCAC	540
40	CTGCTTCGCA	GTCAGCTGAT	GGTACTCCGT	GCTCTGGTCG	ATCAGCAGCC	CGTCTCGGG	600
	GGTCTGCCAG	AACGGCATCC	ATCCACCAC	GCTTTGTAGA	AACGAGGTGC	TGGGGCGCCT	660
	GCA						

## 1579UP

	GATCGCACGG	ACCGCGAGAC	GAGTTCCTCT	GGTTCGTGTC	ATTGGCGATG	GTAGGCCGCC	60
	CTGTTGCACG	TGACCTGGGG	ACAGCAGACT	TCGCGTCAAA	ATCACCTTA	GCCTCAGCTG	120
	TGATGACATC	AGCCAAAACG	GCCGTCCGTA	AACACCTTCC	GAGGCGTTTC	TMGACTTGAG	180
	GATCAGTTTA	CCGTGCTTAC	CCTTCCCGTG	CGCCTTTTCG	AAGGACTCGC	GGAGCGTCTC	240
50	AATATCTTGT	GAGAGCTGTT	CCAGCGAGAT	ACCTCTTCT	GGAACGTAGG	AAACCTGTGC	300
	GCCCCACGCC	AAGGCAGCAT	GCGTTGCCAG	ATAGCCTGAG	TTACCACCTT	GGACATCGAC	360
	GACAAAGACC	CGCGCTCTTG	TGGAGGCTGC	CGACTGCTTC	ACAACATCAC	AGTACTCCAT	420
	TAGGGCATTG	AGAGCTGTGT	CTGAACCGAG	CGAATACTCA	CTGCCCCGGA	CGTTATTTCGA	480
	AAGTGTGCT	GGAATGAGTA	CCATTGGTAT	TCTGAAAGCT	GGGTAGTTCT	CACGGGCCCG	540
	CTCCAATTGA	TGCAAGGAGA	CGAAGGCTCG	AACCCACCAA	CAATAACCAA	GCCGTCAAAC	600
55	TTGTACTTTT	GGAAGTAGTA	GGCAATCATG	CCAATGTCTG	CATCTTCTGG	GACAGTTCTG	660
	TTGGTTCCCA	ACTCGGAACA	CCGCGAGATT	GCCAGCCAA	CATATCTTTC	CAGTTCAACG	720

## 1580RP

	GATCCGTGTC	GACAAGTTGG	TCACGTATAT	ATGGCGCGTG	TTCGAGCGCG	TCTGCGTGTA	60
	CCCGCCGAAC	CAGCAGCGCT	GCCATCTCGA	AGACATCATG	CTCTTGCGTG	TGTACTGCGG	120
5	CGAGGCGCGG	GGGCACCCGC	TCTTGCTCAT	GGCGATCGTT	CAGGCGGTGG	CGGCACGCTA	180
	CGGGGTGCAG	ACGCTCCTCT	GCGAGCAGGT	ATTGATCATC	ATTGACCGCA	AGTTGCGCGG	240
	CGGACAGTCA	TACTTGATGA	TCCCGCTGCG	AGGGAACGCA	AAGCCGCGCA	TCTTCACGCG	300
	GCGGCGCTTG	CTCGACACTA	TGCGGCACAC	AATACCCAAC	ATTGCCGACC	CGCGGAGCCT	360
	GGCGCTCGCC	CGGTTCTCTA	CTCCGCTCAC	GAAGCGCGCG	GGTGCTGAGA	AAATCTTCAA	420
	AGACTGGTCC	ATCTACTGCG	ACAAATCCAT	ATGGCGGACG	ATCCCTGATC	ACTCGCCCAA	480
10	TGGCATTCTG	CGCTACCTCC	CGCACTCCTG	CACGCCGATG	GACGAATCCA	TCTTTGAGTA	540
	TTTCATCGTC	TATTGGAAAA	CCGCAACAGC	AAACCACTCC	ACGAACAACA	TTTTCACAC	600
	CGTTCTTCTC	AAGCAATTCTG	AAACGATCTT	GGTCAAGAGT	ATCCCGGCGA	CGCATCCACT	660
	TTGTGCAATTG	CCGGGAGCAG	CTCATGGACT	CCATTATCGA	GATGTCTTTC	GCGAGTCC	

## 1580UP

	GATCCTTTTC	ACCAACAGCT	GTCTGGGCCA	GCTGCGGCCT	GGGATGAACT	ACAACGAGGC	60
	AGTGAAAGCG	CTGACGAACC	TGGCGCTGGA	CAGCTTTACA	CTGCCGGGGG	ACGGTGGGGT	120
	TTCCGCTGAA	CAACGTGTAC	TCTGTGCCGG	TAGAAGACGG	TGCTCAGATG	GAGCTGCTGA	180
20	AGGGGTACCT	GCAGCAGTTG	CGGCAGGAGC	CGGCCACGCG	GCTGCTGGAC	CGTGTGTATG	240
	GGGCGGAAAA	GGCACAGCCC	TCGAAGTTCT	GGCTGGCCTT	CACAAGGCGC	AAGTTTATGA	300
	ACAAGGCGCT	GTAAGGCGAA	ATAGGTACGT	AGCTGGCGGC	GCCAGGAAGT	ATTTACAAAG	360
	TTGGCTGTAT	CGCTACGAGG	TTTTGGTGCC	GTGTGCCTTG	TTGGAGCGCA	CGAGGAGTTC	420
	AACGGCGGAA	GCTCGGAGCT	GTTCCGCGTC	TTTCACGATC	GCGTTCACGT	CAATGCTGAG	480
	GTCGGTGTTT	TTGGCGCGGA	AGCCTTGGAT	CCGCGCCTGC	AGGTCTGTCA	GCGCCTGGAG	540
25	GACACGCTCA	TAGTCTGCAT	CTTCTTTTAC	GCGCTCTTTG	TATGTTTGGA	AGGACTGAAC	600
	GATGTCTTCG	ATACCGGGCT	CGACTCTGCT	GATCATCTCG	ATGCGCTGGC	GCAACAACATG	660
	ATCGCGGTCG	CTGTTGGCGT	CGCGTCCCTA	ATCATCTGCT	GGATT		

## 1581RP

	GATCTTAATT	TAAAATTTTA	ATTAACATTT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACT	TAAGATAGTA	AGAATAAAAT	TAGTAAAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAATTATTTG	TGGCATCTTA	180
	ATTTTTATTA	TTTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATATAA	240
35	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAATTTAA	TTTAAATAT	300
	AAATATACCA	TTTTTATTTA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AAATTTTCTA	TTTAATAGTC	TACCCPTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCT	TTTTTATTAT	TATTCTAAAT	600
40	TATTATTAAT	TAGTAAATTA	TATTTATTTA	TTTTATTAAAC	ATAATTTTTG	ATAATAATAT	660
	ATCAT						

## 1581UP

	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTTAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
50	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CTTAACTAAT	AAAAATAATT	420
	AATTAATAAA	ATAAATAATT	AATTAAATTT	AAAATGTTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATF	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCTTT	ATTATTATCT	TTATTAGTAG	TTTTATTACT	660
55	AATAACTTTA	TGATTTAGAG	ATATTGTAGC	TGAACCTIAC	TATTTAGGTG	ATCATACTTT	720
	AACTGTAAGA	AA					



## 1582RP

	GATCTCAACA	CGGTCGTTGG	AGAAGTGTGC	AACACACGAG	TACGTAGTAC	CCAAATCAAT	60
	ACCGACTGAT	TTAGACATGA	TCACTGATTA	GAAAACGAAA	TCTCTGGTTT	TCGGATAACC	120
5	GGGAGAAATA	CCAATGGTGA	TAACCGTACG	TAAGGCCAGA	GGTACAAAGC	TACTCCAATC	180
	TGAAGCTACA	CACGCCCAAC	CCTTTTATAC	AATTTCAATT	TTTTCTCTCC	CAAACGAACA	240
	TGGCAGATAG	TAAGAGTCTT	CGAGCCCAAT	GCCTGTTCCG	TTTTTTTTTG	TTCTGGAAAA	300
	TTCTACCATA	ACGTATGTGG	CCGTTGAAAA	CTGATCAAAC	GGGTCTCGAA	GATCTTAGAA	360
	TAGAGGCTCC	GACAGAAAGG	GGGAGGCCGA	TTCAAAAAAG	ACCGCATGAG	CCTCACTCGT	420
	GCTTCGAGGC	GGGAGAGCCC	ATAGGCTTCT	TTCCAGCGGC	CACCGACGGT	TTCTGGAAAG	480
10	GAGCGAAAAC	AGAGAATGAA	CCGAGGCGGT	TGATCTGCAT	CTTGGACTTG	GCGTAGGCC	540
	GTTTCAACTG	AGCGGGAATG	CGTGATGCG	AAACTACGCC	GTCCGCACGC	ACCTCCCACT	600
	TCCGTACCAC	CGCACGCATG	TTGGCCGATT	TTCGTAGCGC	GCCTTGATGA	AAAGCGAGTA	660
	TAGAGCCAGC	ACAATCCACG	AGCGGCGGCG	ACAA			

15

## 1582UP

	GATCTTGTTC	TCCGCATCCA	GATACTGGTC	GAAGCGCGAG	TTCATCTCGT	CTACAATCGG	60
	CTTCCACGAG	TCGGTGTAT	CTATCGCGTC	CCCGAAGCCC	GGCGTGTTCA	CCACCGTCAA	120
	CTTCAACACC	ACGCCGTTCT	CCTCGATCTC	CGTCGTGACG	GTCTCAATCT	TCACCTTGTT	180
20	CTCGCGTCC	TTGGCCCGCG	ACTCGTCGCC	GTCCCTCACCG	TCCTCAAGT	TCAACCGGTT	240
	GAACGTCTCC	GGCGTGTCTG	CCTTCGCCGT	GTATAGCTCC	TTGTTGAACA	ACGTGTTGAT	300
	CAAGTCTGAC	TTCCCCAACC	CCTTGCGCGC	CACGCAGAGC	AAATTGAGGT	TGAACCCGCG	360
	CCGGATCGAC	TTGCGATGCC	ACTGCTTGCG	AAGGTTTGCG	AACCCACAGT	ACCCGAGAT	420
	CTTGCGGTGG	ATGATCCGCA	GGTCTGGCTG	GTCTGGCAGC	ACCTGGCCCC	CCGCGAGCTC	480
	GCCACCCAGT	GCCGTCGCCA	CATTCTCCTT	GTGCTCCGGA	AGGTCCAACC	CCATCTCCTC	540
25	CTCCTTCACG	TTCAATGTCCG	AGCTTGTGTC	CTTCGCGCTC	GCCGTCCCGT	TGCTCATTAG	600
	TGCGCCCCCG	TGCTGGTTGT	CACGCCTCCC	GCCGTCTGTT	CACTGTTGGT	GTTTGCCGAA	660
	TCCTCCTGCG	AGCCTGTAGG	TAACATGCTT	GTTCTGATTT	GGTAGTC		

## 1583RP

	GATCAATTAC	CCTGGCGCCA	ACCATATTTG	GATGAATATT	TGCATTGTTG	CCGATAGGGG	60
	TTCCCTCATC	GTGTATGTTA	TAGACCTTCA	CGTCTTCATT	AAAAGGGCAT	GTGATGACTT	120
	TCTTGCTGTC	GGCAGAGAAG	GTCAAACAAA	TTACAGATTG	TTCTGTACCG	GCCAAACTT	180
	TATAAACCCCT	GAAGTTGTTT	AACACGTCAT	ATATGAATAC	CTTACGATCG	CTGGAAGGGT	240
35	CAGTGGATGC	ACTGGCCAAA	TACCGACCAT	CTGGTGAGAA	TTGGAGGTAC	CAGATTTTAT	300
	CTTTATTTTC	CGAAAGAGTC	TTACATGAC	TGAAATTGAA	CATGCACATA	GAGCCCAAGT	360
	TATCTTGAAG	CAAGTTATAA	GTGGTTTTCT	CTCCAGAACG	GTTTCTCTCG	TGGTTGTGAG	420
	GATCGTTCGCT	GAAGCTTAAC	AGGTCGCTGG	ACCGCTGGAA	CTGTATAGCC	TGTTTTAACA	480
	ACGTAATGAG	CCTGCCCCGT	GGAACCAAAT	CATTCCGGTT	GATATATTGT	GAAATCTGAT	540
	CAAGCGCCAA	TTGCCGCGAG	GCTGCCAGAG	ACCCTCCCCA	TATTTTGTGT	GCCTCTGCGG	600
40	ATTCCGCGAG	ACACGTCAAA	ATAGTCGTCA	CTGCAGAAGA	GCTGTGTCCG	GAGTCATAGC	660
	CCACTCTCCC	TCGGGCTCCT	CCACCATAGA	TATGGTCTGT	ACAGCCACAG	CGAGTCC	

## 1583UP

	GATCGACTGG	AAGTACACGT	CCAGCGACCG	GTCAAGGCC	ATGTCCTGGA	CGGACTGCTC	60
	GAAGGTCTTC	ACGAGGTTCT	TGGCGATGCG	GAGCATTTGGT	GTGCGGTCTG	GGGCGGGCGA	120
	CGCTGCGGAG	GGCTCACCGA	ATTTGCTTGT	GCGTGTGGTC	ACGTGACACT	TGGGCGGCTG	180
	GCCCCGCGCG	GCCCCGCTGG	CCCGGAATGG	CTGCCCGCGC	CTGGCACGCC	GTTCTTGCAA	240
	TCACATGATT	CATGATTCCG	CTTTTGGGGG	GGATCACTGC	GCGAGCGTTT	TTGCTGCTTT	300
	TAGCCTCCCT	GACACCCTCG	GCTGCGTCTG	GACGCAGGTC	CCCGCCGGCT	GTCCGCTGCG	360
50	TGGCTGTACG	TGTGGGGTGA	CGCCATTTTG	TGGGACAGCG	GCGACGCATG	ACGACGAGCT	420
	CGGAGGGTCC	GCCGTTGACG	ACAGCCCCCT	AAAGGAGTTT	CTTTTATTTC	ACGCGGCCCC	480
	TCAAAACACTA	TATATGAGCA	AAGGCAGGAT	GGAAGGTAGG	CTAAAGCAAG	AAAAGACCTC	540
	GACCAACGGT	ATCGAAGTCT	AAAATCTTAG	CAGGTACCAG	GATGTCTTTT	GAAGATTTGC	600
	ACAAGGCGCA	ACGCGGGAAA	GTCGAGGAGG	CAGTGACGCA	AATATGTAAG	GATTTTCGAG	660
55	TGACGGAGGA	CAAACCTCCG	GAGTTGACCG	CGTACTTCAT	CGAATGTTTG	GAACAG	

## 1584RP

	GATCCAAAA	GCCTTCCGGG	CGCGGGCACA	TTTATCACAC	CCGCTGTGCT	TGACGGCCTC	60
5	GACAATACAT	CCTATGACAT	GCGTAATCCC	TCCTATGTTG	TTCCGACGCG	GCGCAAAACGT	120
	GCCAGCGTCT	CGAAGGCTTC	GCGCGCGAGC	AAGAGTTCTT	CGCCCCCTGA	AGAGGAGGAG	180
	AAGCCATTTA	AATGCCAAGA	ATGCACCAAG	GCCTTCCGCC	GCAGCGAGCA	CTTGAAGCGC	240
	CATATACGCT	CTGTGCACTC	ATCGGATAGG	CCGTTTCCGT	GCACCTATTG	TGATAAGAAG	300
	TTCAGCCGCA	GCGACAATCT	GTCGCAGCAT	CTCAAGACAC	ATCGCAAGCA	TGGCGATATA	360
	AAAGACACGC	CACCAACCAC	CAAGAAAGGC	TGACTTTCCAC	ACATCTATGC	GAATACCCGA	420
10	TGTTGCATTA	AGAGATACAT	ACAGCGCATA	CAAGCTGACA	CAACGTCCCG	TACGCCAACA	480
	GAGGAGATGA	TAAATACTAC	ATACTCAATA	TATCAATACC	TCCTACTTPT	GGTAATCATA	540
	TATAACTGTT	TTCTTTCGCA	CTGTTCTGGT	AACGTTGTCA	TAGGTTTCCC	TGTTGCTGCT	600
	AGCTGGCCAG	GATTCCCTTA	ATGGATGAGG	TCCGGCGCGC	AACCAGACAA	AAGTTGCGCA	660
	GCTTAAGATA	GTTGGAC					

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## 1584UP

	GATCCCATTT	TGTCTTCTTC	GGCTACCGGG	ACGGCCAGTA	GAGCATCCAG	AATAGATGTT	60
	CACCAGTAGG	CTTGCCAAGT	GCTCATTAGT	TGCCGTCACA	TGGCTGCCCG	TGTACATGAC	120
20	AGTGACACAC	CATGTTGTAT	TCATATCGAA	GGTGAAGGC	CCCTCGATGC	GCCCAACGCT	180
	CAATCCAATG	GACGGAGTTG	CATCGGACTG	GGTTTTGGTG	TGGAAGCTTG	GAAAGACTAA	240
	TATTCGGAAC	CTGAATCATG	GGGACGTGGT	GATCTTCCGC	TCACCCATGA	ACCCCAAGAA	300
	AGTATACTGC	AAGCGCATCC	AGGGTAAGCA	GTATGATACG	GTGCGCACGC	GGTATCCTTA	360
	TCCGAAGAGT	ACCTGCGAAG	TGCCAAAGTC	GCACATATGG	GTGAGGGGGG	ACAATGTCAC	420
	GCAGTCGGTG	GACTCGAATC	ACTTCGGGCC	GATTTTCGACG	GGGCTTGTGG	TAAGCGAGGT	480
25	GACACGGGTC	ATATGGCCGC	CATCGAGATG	GGGCGCAGAC	CTGCACGAGG	GCATGGGTG	540
	ACGCGCAGTT	GTTGCTTCAT	GATTGCGGGA	GCCGGGGTAG	GCGAACCTAC	CGCTACGTGT	600
	ACATAGCTGA	AAGACTAGAT	ATTATATAAT	GTCGAACAAC	GTGCTGCACT	GCGGCAGAAG	660
	GATGGCTTAA	GAATCGTTGT	CCTCCTCCTT	GACGATCTCT	GGGAAA		

30

## 1585RP

	GATCCCCGTT	GTTGTGCACG	TGTGATTCAA	TATATACATA	CTGCAAGTCT	GTACATGTGC	60
	TCTATTATAT	ATGGTGCTCA	TGTTGCGCTT	ACATTCTTTC	TTTATACAGT	TCATGTCCCT	120
	CCGTGCTGGC	ATACCCAGTG	ATGCCCGTCA	TACCTGGTAA	CCACAGTTTC	TATAATCATT	180
35	CAGGCTGAAC	TGATCAATGG	AGCTGCGTTT	GCCGAATTTG	ACGCAGAGGT	TTGTATACAC	240
	ATTGATGTCC	GCCCTCGTAA	AGCCCTTGCT	AAACGTGCAG	AAGCAATTCT	TCCGTTTGGA	300
	ACACGAAGTG	CAAGGCTTGA	ATGCTATCAA	CTTATCCACA	TGCTTCAGCA	GCGTCAGTTC	360
	CTTTGTGAGC	AGCGCCTGCC	TCACCTCGTC	TGGAATCTGG	CTAAGCCACT	CGTTTGCCAG	420
	CTCAGACACA	TTTACCGGTG	CGTGAAGCAT	CTCGTTGAAC	GAGCCTGTGA	CCGAGGCGTC	480
	CTGGAACAGT	ATCGTGATCG	TGGCGTCACA	CTTAATCTTC	TTGGAGCGGC	AGATGTCGCA	540
	GCTGGGGCCC	GTCCGCTGAC	GCTTGTACTT	CGACGCCGTG	ATAACGGTTG	GCTCCTGTAG	600
40	CAGCGAGTTC	GGTGGCGAAC	AGTGCGCTGC	ACGTCCCCCG	TTGGAAGCCC	GAAGCAGATT	660
	CCGACATCAG	CGGCGACATC	GACACGCCGC	GCGCGGACTC	TGGCGAGCGC	GCGTGT	

## 1585UP

45	GATCACTCTA	CGGGGGACAG	TTGATTGAGT	CCAGTGACGT	GAATGTCAGA	GAGTCACCAT	60
	TTTTCAACCT	ATGACCCTCA	TCGGCCAGCA	TGAGTCCAAC	CTTGCAACCT	TTTAAATTTT	120
	CTACATTTTCG	CCGCAGAGTC	TCATAGGAAA	TAATCAATAC	AGGCTTGACT	ACATTACGGC	180
	CCTGGGCAAT	CGCCCACTGC	CTGACGGACT	GTGCAACCGA	GCCGTTTCGAA	AGGGAACTTT	240
	TACGTCCATC	GATAGCCAGT	GGCGAAAGGG	CATCGGGTCC	CAACCACTTC	ACAATCTCAT	300
50	TAGCCAGTTT	ATTAAGCAGG	GACGAAGGGC	AGACAATGAT	GCACTTTTCA	ATTGTAGGAC	360
	GACCTTGGA	GCCCTGCCGT	AGTAGCGTCC	ACATTAAACGC	TATACATTGC	AGCGTTTAC	420
	CTAGACCCAT	TTCATCAGCC	ATAATACACC	CATAAGCCCC	CCTATTTGAT	TCTCGAGTCA	480
	TAGCTGCATT	GGCATCCAAG	ATCTCAGGCG	AAGGCGTCCG	CGTCGGCGTA	AGAATCGGCG	540
	TCGGCGTCTC	CTCAAGCACC	TCCACAATA	TTGGCTCACT	ATCTTTACTA	CCCGGATCCT	600
	TACCACTGCC	ATCGTCTTGC	ACCTCGCCCG	CTGCCAAGAG	AGCCTGTGTA	TCCAAAAAAT	660
55	CCTTCATCGC	CAGACCACTC	ACACAGCGGT	ACAGGAATCT	TACCCCTTCC	ACTTGATGAG	720
	GGCGTTAAAT	CCGCGCCAGA					

## 1586RP

	GATCAGGCGT	AAGGGCAGGA	TATGAACTAT	GGAGACGTCT	ATTTTAAACT	CAATGGCATA	60
	TAAACACCGC	ATATTTCTTG	TGGTTATGAT	AACTTCAATT	ATCGAATCAG	TCGCAGCGTA	120
5	GAGGGTTGGT	GAGAGTTTAC	CACGATATCC	AGTTGTTGCT	GCGCCCGCAG	CACCAAATAT	180
	AACTGAGAAT	TTAAGTTTCT	CGAAGAGAGT	ATGCAACGGG	GGCTTGTCCA	CTACGATTAA	240
	AAGAGCACCA	GCTTTCTCAT	GCCTTCAACT	ATGTCAATAT	AAATATATTG	CAAAAGGCTT	300
	AAGCTCTGTA	TTGAGCCCCG	GAAATGTTTT	TAGCAATGTA	GCTCTCTCAT	CTTCACATTA	360
	GGCTGCGAAT	GTGCTGACCA	ACTGCAAAAA	CCCAGTCATA	TCGTAAATAG	TGATGATAGT	420
10	CAGCGCGATA	TTTAACCGCG	GGTGCAAAAA	ATTGATTTTCG	CCCAGGATCG	AACTGGGGAC	480
	GTTCTGCGTG	TTAAGCAGAT	GCCATAACCG	ACTAGACCAC	GAAACCAACC	TTGAAGAACG	540
	CACGCCGCGA	AACCGACCAA	CACAACCGGT	GCAAACCACG	TGCCTGACGA	CTCTTTAGGC	600
	GTGTGCTAGG	GGGGCGCCCA	CTCGTACTTA	TTTTATAAAC	CTTGGATCCA	GGTGCGTCCA	660
	TATACAGGGC	GATCCGCGCC	ATCTGCAGCA	GCCAGGAACG	CA		

## 1586UP

	GATCAACAAA	GTCAAATCCA	AAATTGTGCT	GGGAGAGAAA	AAGATTCCGC	CATCATTTGGG	60
	CCTTTTCTAT	AGCCATCAAT	TCAACAATCG	GTTAAGCGAT	TTGAAGCCTT	CAGCCCTTTA	120
20	TGAGGGTGAT	CCTGAGAAAC	AAGATGGGAC	TGCTACCGAT	GGAAGCAGCG	GTAGTGTCCA	180
	TGGGTATGCC	ACTGATGATG	ATATCATTTG	CACAGGCGAG	AACACCGTTT	ACAGCCTAAG	240
	CCAAGGGATT	GCATATCATA	TAGATGAGGA	AGGAAACTAT	TATTATGCTG	GTATCGATCC	300
	GTTTACTGAT	GCATTGGAAC	AAGAGGCAGA	TTGCTTATAT	CATGAAAGTG	AGGTAGAAAG	360
	CGTAAATGTC	AACAACTTGG	ACCATCTTTC	TTCCGATATC	AAGGAAGAAA	ACATAGACCT	420
	CGATGGTAAC	ATAGAAATGT	ACGATTCTGA	CTTTGACCAC	ACTTCCCTCG	ACCAGGTCCC	480
25	GAAGGCTACA	GAAACAATCG	AAAAATACAA	TAATAACCAA	TACTACAAGA	TGAACACGCT	540
	AATCACTGAC	TCATCAAATT	GCCAGGGCAA	CACGTGTAGCG	CTCTCATCTG	ATTATGGAAC	600
	AACTTCCGTG	CATGTTGAAA	ATGTCCTCTAA	TGAGAATTCC	TTGGGGTCAT	CAGGCTACAA	660
	GGAGATATTC	CTGAAAACCTA	TGATGACTAC	CTTTACGAAG	GGGACGAAGA	TGATTTTCGAT	720

## 1587RP

	GATCATCGAG	AAGGAGCTGG	AGGGCGTGCG	CATCCGGCTG	AACAAGTCGC	CTCCGGACAT	60
	CATTGTGAAG	AAGAAGGAGA	AGGGCGGTTT	ATCGATCACG	AACACAGTGC	CGCTGACACA	120
35	TTTGGACCAC	GACGGGATCC	GCGCGGTGAT	GAGTGAGTAC	CGCATCAACA	GCGCGGAGAT	180
	TGCGTTCCGG	TGCGACGCGA	CAGTTGACGA	CCTGATTGAC	GTCTCTGAGG	CTCCCAGCAG	240
	GCGTTACATG	CCGGCTATCT	ACGTGCTGAA	CAAGATCGAC	TCGCTGTCTAG	TGGAAGAGTT	300
	GGAGCTGCTG	TACCGGATTG	CGAATGCTGT	GCCTATATCT	AGTGGACGGG	AGTGGAACTT	360
	AGATGAGCTG	CTCGAGGTCA	TGTGGGATCG	CCTGAACCTG	GTGAGAGTTT	ACACCAAGCC	420
	CAAGGGGACC	ATGCCCCACT	TCAATGACCC	GGTTGTGTTG	CGGTCAGACC	GTTGCACAGT	480
	GCGGGATTTC	TGTAACCAAA	TCCACAAGTC	TCTGGTTGAG	GAGTTCCGGA	ATGCTTTGGT	540
40	TTACGGTAGC	AGTGTGAAAC	ACCAGCCTCA	GTACGTGGGT	CTTGACACAC	CTCTAGAGGA	600
	TGAAGACGTT	GTGACAATTC	TGAAGAAGTA	ATGTCTTGCC	ATTTATGCAT	GGTTTCAATG	660
	CACACGTTCT	CGCGCTGC					

## 1587UP

	GATCCTAATA	AAAGCTTTTC	TGCAATTGCT	CTACCTACGC	CTGGAAGGTC	GCGTAGGGCA	60
	CACGTTTCAA	ATAGATGTGC	AGGAGATACG	ACCTGCGTAT	CACCCCCCTT	AATTGATTCT	120
	TTAGTGCAAA	CCAGATAGCC	ATCAGGTTTC	GCACGTTTGA	AAGCCAACCG	GGCTAGAACT	180
	AAGGACGGTG	CGCACCCAC	GCTTACCCTG	CAGCCGCTG	TGCGCTCTGC	TACTTCTGAT	240
50	CGGATGCGTA	TACACAAGTT	TTGACAACCTA	AGTGTATCGA	GCGGCATGTC	AATAACACAG	300
	ACAGCCTCAT	CCACCGAAAT	TGGATACACT	GCGTCGAAAG	CCTTTAAACC	CTCCAATACC	360
	TCGTAGAAGG	CATTGCAAAAT	CGTTTTCGTAT	TCATCGTAGG	TATAGGGGAG	GCAAACCAGT	420
	TGGGGGCACA	AGTTCTTGCC	TTTGAGAGCC	CACATGCCAT	TTTGTATTCC	ACATTCCCAG	480
	GCAGCATAAAT	TACAGGAGGC	AACGTCCGAA	GATGAACCCC	CATGACACAC	TGCCAACGGT	540
	ACTTCGGCCT	TGCTTGAGTA	GCCCCCCTTG	ATGCCGTGAA	TAGTCGCAAA	AAAGCAATCA	600
55	AAATCCACGT	GGAAGACGTG	TGCTGGTGGG	GCCCCGAAAT	CATTTAGCGC	ACCTTCATTC	660
	ATCCGGAGAT	GCCTGTTCGAG	AAACTCTCGC	GTAGAGCCCG	CT		

## 1589RP

5	GATCATTCAA	GCATATTTAT	TAATTAGATG	ACATTAAACT	ATTAGACCTT	GGTTTGGGTT	60
	GCTGGACTTA	GGGTTGTGGT	AGTCCGTGGG	TTATATATTT	TTTGTAGACA	GTCACCAACA	120
	CACTTGATGT	ATTTCTTTGA	GCTGTGTGCG	ATAGGCTCGC	ATTGGATGCG	GCACTGCTCA	180
	TTGGCATCCT	GCCCCTCAGC	AATAACCATA	GCGGCGCCCG	CTAGAAGACC	GAAAAAGTAG	240
	GTTAGCTTCA	TCTTGTGATA	TTATTCTGTG	TTTAATTAAA	TGGAACTTTA	GTGCTCTGGT	300
	TCTCTGCCAT	AGAGATCAGG	ACCTTGGTTA	GATATCCGTG	CCCTTATATA	CACTGCTGCC	360
10	AAGGATCGAT	GGACTGTAGC	CGAGCACCTT	CCAACTCAAA	AGATCCGACA	TCAATGTATT	420
	ACTGAGAGCC	AGTATACTTA	CCGCTTATCA	CACATAAACC	CATAGCCATG	GTTACGAAGA	480
	TGCTGATCTA	TCATCCACAC	CAGCTCGCCA	CTGTAAACGG	ACTTGAGGTG	GGCGACAGAA	540
	GGCCACTACA	GGATGAGCGT	AAATCTCCAA	CAGCTAGCAA	CACATGCCAT	TATTCTATAC	600
	GAACAGTAAC	GTGCTTGATA	TTACAGAATA	CCGATTAGGT	TTTTTCCTGC	CAGACCAAAT	660
	GCTATTGGTC	AAACTCAAAT	TTAGTCAGGC	TTACATTACC	TGCGTACCTC	GAAGGTAGCA	720
15	ATGTTAGGCA	CTCTGGCAGT	A				

## 1589UP

20	GATCTTCTTG	GCCATTATTG	CAGTAGCGGT	AGGCGGGCAT	ATGAAATGAG	ATCGCGGACG	60
	TCCTGCGCTT	GAGCACCTGA	AAAATGGCAG	TAAAAAGAAA	CGATCCCCGC	AACATTTGTT	120
	CGAGTGACTT	TTGAGGCAGA	AGTACAGGCT	TCAGCCCCGC	GCTGCTTTGC	TGTGGATTCA	180
	GACCACCGGT	GGTGAAGGTG	GTGGTACACT	GGGGTCAGCT	ATGCTCTCAC	GCTGCAGTCC	240
	AGGACAGACA	TACCGCCAC	TATAGCAGGC	CGATCACATA	CATAAGTAAG	AAAATTAGCC	300
	CCAGTAGATT	ATTGTCGGGG	TCATGCAGTG	CTGCACCATT	GCGTGATGTG	GTGTTGCCGG	360
	GTAGTCTGCC	ACCATCGTGA	TACCCGGAGC	CGCCAGATCC	AACCGGAGGT	ATAAAAACTG	420
25	GTAATGGGAC	AAATCCGGGG	CCGCCCGGC	CGCCGCCTCC	GCCCCGTAA	GAAGGCAACC	480
	CCGGCCTTTG	CGCTCCTCCA	TTCGAGTCTT	TTGGGCTGTT	CGGTGGCGGC	TGTGCTCCGC	540
	CGTTTGGGCC	TTTAGGGCTG	TACGGCGGCG	GCTGTGCCCC	CCGTTCGGGT	CTTTCGGGCT	600
	GTACGGAGGC	GGTGCGCCTT	TCGGATCCTT	CGGGCTGTAC	GGAGGCGGTG	CTCCTTTCGG	660

30 ATCCTTCGGG CTGTATGCCG GAAGAACACC CTGGG

## 1590RP

	GATCATAATG	ATTTGCTCTTA	ATTCTTTTCT	TAATTATTCA	TAAATAAATT	AATTAATATT	60
	TTATTAATAA	AAAATATTKA	KAKKKATGTT	CGTTTATGAT	AAATTCCTAA	ACTTTGSARC	120
5	ACGAACTGAA	GACAACTATG	TAACGCCTGT	AATTAATTAT	AAATTATTAT	AATTAATATAT	180
	TCAAAAAATG	GTAAGATTTA	TCGAGGATTA	TCGAATTAAA	TAACATGTTC	CACTGCTTAA	240
	GTCTGTAACC	GTCTATTGTT	TTGATTTTAA	TTATTGCTAA	CGTAGTCATC	AGGCGGAATA	300
	CTTTAATTTT	CATTTAATTT	ATTCTTTAAT	TAATAAAAAA	TAAATAGGTA	TTCATTGTTT	360
	ACTGCTAAAA	CTACTCGGGT	ATCGAATCCG	ATTTGCTACT	TTAGCCTTCG	TTCCTCAATG	420
	TCAATTAATA	TATAAATTTAA	ATTTTCACCT	TATAAGTCTT	ATTCATATAA	TTATTATTTC	480
10	ACTTTTACTT	GAATAATTCT	TAAATTATTT	TTATTAATTC	TAATTATTAT	TTTAAATAAT	540
	CATTCTACGA	ACCCTTTAAG	CCATTACGAT	TAACGCTAAC	CCCCTTTGTC	TTACCGCAGC	600
	TGCTGGCACA	AATTTTGGTT	GGGATTATTT	AATTATATAT			

## 1590UP

	GATCTATTAT	TAGAGGTAAT	ACATTTAAAC	TATTATCTAA	ATTCTTCTTC	TTCTTATTTA	60
	TTCTTAACTT	TATCTTATTA	GGTAAATTAG	GTGAATGTCA	TGTTGAAGTA	CCATTTATTT	120
	TAATAGGTCA	AATTTGTACA	TTTATTTATT	TTGCTTATTT	CTTAATCTTA	GTACCTATTA	180
	TTTCTATAAT	TGAAAATATT	TTATTTTATT	TACTAAATAA	AAAATAATAA	TTAAATAAAT	240
20	AATAATAATA	TTCATTAAAT	ACTTTAATAT	TAATATTTAT	ATATTATACT	TCTTTATCAT	300
	TTATGAGGGT	ACCTCATATT	GCTGACTAGC	AATAGGGGGG	TGAACCCTAC	GCACCTAAAT	360
	GATAAGAGTT	TATCATTAAA	TTATATACTA	TATATTATAA	GTAAATTATC	AAACCATATA	420
	TAAGGTATAT	ATATTAAGAA	AGTTTGACTG	AGTGGTTTAA	AGTGTAATAT	TTGAGCTATT	480
	ATAAATCTTT	ATGATTTTCAT	AGGTTCTGAAT	CCTATAACTT	TCGTATTAAA	TAATTATTTA	540
	AAATAATTAA	AAATAGTTAA	TAATAATGAG	AACATGATGT	TGGTTCAGAT	TAAGCGCTAA	600
25	CTAAGGACAT	TACACATGCG	AATCAAACGT	TAATATTATT	AATTAATAGT	ATTAATAAGT	660
	GGTGTACTCG	TGAGTAAAAA	TTAAGAATAA	TGAACCTAAA	TTTAACTAAA	TAT	

## 1591RP

30	GATCATAAGC	ATCTTTAGCT	CCACTATCCA	TGCTCGAAAT	TTGCAGCTGA	TAATAAAGTG	60
	GTGTGTGGC	CGAGCGGTCT	AAGGCGCCTG	ATTCAAGTGT	ATGCTTACAG	CTGTTACAGT	120
	TGGACACTCA	GGTATCGTAA	GATGCAGGAG	TTGCAATCTC	CTCGCAACCA	ATTATTTTTT	180
	TTTTTTGGAG	TTCCAATGCA	ATATCAATTC	TACTGCTGCG	AAAAGGTCTC	GTCAGCAGAT	240
	AAAAGAATAT	AGAATATGTA	TATTTATATA	CAAGAAGCGT	TTACTGACTT	TTTATTGTTA	300
	TAATGCCATT	CGAAGAGATA	TCGCTTATTA	ACAGCAATAC	CCCCCTGCAG	GTCCCCGCCA	360
35	ACCGTTGTCC	AGTGATGCAA	AATATATACC	TCGCATGATA	AAGAAGGCCC	TTCATATCAA	420
	ATGGCCCAGG	CATTAATATC	ACCGTTTCGG	CGGCCTTCAA	CCAAGTAGCC	ATCTTTATAT	480
	CTGACATATT	CCACGGCATT	CTCACTATGC	TCATCACCGC	CGCAAAACCA	ATGCTTCTTC	540
	TCTTGCCGGT	TGTAAACCTT	CACTGTACCT	TCCTGGTTAG	CGACAACTAT	CTTATTCAAG	600
	TCAAACCTGCA	AACATGTAC	CGGGTGTTC	TACGAAAATG	TATCAGCCAA	TGTACCGGTA	660
40	CGTAGATCCC	AGATCTAATG	CTGTTATCCA	AGGAACCAGT	CACAAGGTTT	AGAGAATCAA	720

## 1591UP

45	GATCCCCAAT	GATCCCTCTC	CGGGCTACAA	CATCGAGCAG	CTCGCTAAAC	AGTGCAAGAA	60
	CAAGGACAGG	CTGGTGGAAC	TGCCTTATAC	TGTGAAGGGG	ATGGACCTCT	CCATGAGCGG	120
	TATTTCTGCC	CACATCGACT	CGCTCGCGAA	GGACCTATTT	CGTCGAAACA	CGAAGAAGTA	180
	CAAGCTCTTC	GACCGCGAGA	CCGGCAAGCA	GCTCGTCACC	GTAGAGGACC	TGTGCTACTC	240
	CCTACAGGAG	CACCTGTTTG	CCATGCTCGT	GGAGATTACC	GAGCGTGCCA	TGGCACATGT	300
	GAACCTCTA	CAGGTGTTGA	TGTGCGGCGG	TGTGGGCTGC	AATGTCCGAC	TGCAGCAGAT	360
50	GATGGCGAGT	ATGTGCCAGA	GCAGGGCCGA	CGGCCAAGTT	CATGCGACGG	ACGAGCGCTT	420
	CTGTATTGAC	AACGGTGTC	TGATTGCACA	GGCTGGTCTA	CTTCAATATC	GCATGGGCGA	480
	TATAGTAAAA	GACTTCTCAG	AGACCGTTGT	CACGCGAGAG	TTCCGGACTG	ATGAGGTTTA	540
	CGTATCGTGG	CGCGACTAAG	TGTGTACCAA	GTTTAAATGA	AGTTTTFACCG	CCCTAATATA	600
	GCTGTTAACC	ATCAGTGGCC	TGCGATCAGC	TGGTCCAGAA	CAGTAGTCGC	CGGTGGCTGT	660
	CACCAGCCTA	CGGGCCACG	GCCAGGTATC	CTGTTTCG			

## 1592RP

	GATCAGGAAC	TCGCAGACCT	TGGCTCTCTG	GTCGCCCTGC	AACTGGATGA	TCTCGCCCAT	60
	CTCGTCGTCC	TTGACCATGT	TGCCGTTGCA	GCCAAAGTCC	TTCCGCAAGA	CCTTCCAAGA	120
5	TGCGCTTGAG	GTCGTACTCC	TCGGGGATGC	CCTGCACGGT	GGTCAACGTT	TTTCTGCCGT	180
	TTCTCTGCTG	GATACGGATG	TGGATGTAGT	TGGAGGAGGA	GGCTTCGTCTG	TCGCCGGTGT	240
	CAGCAAAGGG	GTCGAACGAC	TTGAGGTTTT	CGATAGACAT	GGTGGCGGTG	GGGTGTGAGG	300
	TACAAGGTAA	GCAGAGAAAA	TTTTTCAGCTG	TCCTTTTAAA	AGCGCGCACC	TCGCGTCTTG	360
	GAACGCATTG	GCTTATTTGT	GAACCATATT	CTTATCTGTA	TAGGTGTTAA	CCCGCATTTC	420
	TCTGCAATTG	CCCGTCTTTT	TTTGGCGTTG	GGACAACGCT	TCCTTTTCAA	CACACTTTCC	480
10	AGGAACCTCT	TTGTTTTCCTT	GGGTAACACT	GTTCTTCTTC	GCTGTTTATC	TCCTGTTAGT	540
	AAGGCAGAGG	CTGGGATTAC	AATGAGACTC	GTCACACATA	CTTCACCTAG	CAGAACACTG	600
	CAAATCGCCT	GGATTGCTTG	AGCTGTTTCT	TCAATACYTG	ACATTTGAGT	TGTGGGGAGC	660
	GAGGAAAGA						

## 1592UP

	GATCCACTTG	TTAACGTCGG	CGCCGCCAAT	CCTCATCCCT	CCATATGTAA	CCACAAGTGG	60
	TTTGATATCCC	AACAATTGCA	GCTCAATTGG	CATCAAGTAC	GCGTATCCCC	CGCCTAGAGA	120
	ATGGCCAGTT	ATAATTACCT	CATAGTCTGG	ATGAGCATCA	TGTACTGGCT	TAAACGCGGA	180
20	ATAGATATCG	TTGTACGCCA	ACTTAAATTG	CTCATATACG	CCCGAGTGTA	CAAAGCAATC	240
	TCCCGTACAC	TTTCCAGCGC	CACTAAGTGG	CTGGTATGGA	ACCCAGGAA	AAATGAAATC	300
	CACATCCAA	TCTTGAATTG	TTACCGACCC	TCTAAATATG	ATCGAAATCT	GCTTAGCCGT	360
	GTCATTTATT	GCTATCATGC	TATAACAGGA	AAACTGCCCG	CGGGTCATGT	CCGGATCAAA	420
	AACTTTAACT	ACTTGAGTCC	CTGTTGTTCC	ATGTACCACT	TACCGTCATG	AAAAGGGTCA	480
	GTGAGTATTA	AAGTATTCAC	GCAGTAAACG	CTGTTAGTGA	GATATGACAC	ATATTTCAAT	540
25	GTATCAAACA	TCTCATCAGA	GAAAGAATGG	ACATGAAGGA	AAAAAGGC		

## 1593RP

	GATCGAAATA	GACAACTCTG	CAACGGTGTC	CAAATGGCCC	AGCAACTTCC	AGGAATAAAC	60
30	ACAAGTAGAC	CATAGCATCC	AAGTACCCTAT	GCTCCTCGCC	TTACTATGTC	TTTGGAATGC	120
	AAAGGACCAA	ACGTGCTGCA	AGACGGAGGG	AGAATTCTTC	AGAAGAATTA	CATTATACAG	180
	GCTCGAAGGT	GTGACAGCGA	ACCTATCATG	GTCTCTCTTT	GTCGGTTCTG	CCAAAAGAGA	240
	AGACCAGACC	TCTTCAAGGG	TGACTGCAAT	TCGTGTCTTA	AGGTCGCCAG	TGACACGAAC	300
	AACCGCTTTT	CTGGGCAAGT	CAGCGAGTTT	TATCGTACTA	GTAACCCGGT	TATTTCCAC	360
	TAGGAGCAAT	GCATTCAAAT	AAGCAGCCCA	CAGTTCCCAA	TCAAATTCAC	TGGCATTCCC	420
35	ATCTGGAGGA	ACATTATATT	GGATTAACAG	ACTTTTGTTAC	ATTTCCAATA	TAGTAACGCA	480
	TGTCCTCAAA	AATAGGGCAT	GTAGTGAAAT	CCACTTACGG	GAGGGCATGT	ATCCATCTTT	540
	GGTCAATATT	GTTACAGTAT	TAACGGCACT	TATAATATCT	TCCTTGGTAA	ACCGCGTAAT	600
	GTTAAATACA	GATGTTAAAA	TAGGATCATT	GGCGCAATCT	TCCACAACCT	GTATAAATGA	660
	GCTGCCATGT	CCATATATTT	CTTCTTACAA	TTTGGGCTAA	AGTTGCCAAT	ATAGTACC	

## 1593UP

	GATCGATCTG	TTGTAATTTG	GACACGGGGA	GCTGCAAGCA	GGGTAACGTA	TGAGGCGTGC	60
	TGTGGGGCCT	GGCGATGGCT	ATAGATAGGG	TCATACCACA	TCATCGGTTT	GGCGGGGTGG	120
45	TATAGCATTT	GGAGGACAGG	TTAGCCCCGA	GCCACAGCAT	AGACAGGTTT	ACGAGGCTTG	180
	CAGCAGAGGA	AAAGATGGGC	AAGCCATTTG	ACTGGCAGCC	GACGGGGAGG	CTCGTGCGCG	240
	GCCGGATTAT	CCGGGCGTTT	TTGCCCTTGA	AGCGGCACCC	GCAGCAGCTG	CTGGACAACC	300
	CGAACTACAC	GAACCTGTAC	CCGGGGGATG	AGGTGTACAG	CTTTGAGGAG	ACGGCGGACG	360
	GGCGATGGTG	TCGCGTGTAC	CAGGTGGTCC	AACCGCTGCC	GGAGGACTTT	ATCTCGACCA	420
	TGAAGCGGTT	CTCGGACAAG	CTGCCGGAGG	AGCAGCACCG	CGTGGTGGTG	TGCCCCGAAGG	480
50	CGTTTGTGCA	CTGGTATGAC	GACGGAAGTG	TGACCTTTCC	GTTCTCTGGAC	CTGCCCGACG	540
	AGCGGGAGGT	GAAGCGGGAG	GTGGCGGAGA	CGGACGTGCC	GAGCCTGCAC	GACCTGCTGC	600
	ATAGGGACGA	CTTGGGGGAC	CTGGAGCTAT	TCCGGCAGCT	GCGGCGGACG	CG	

## 1594RP

	GATCAAGACT	GCCGAACGTC	TAGTTTCCTG	CTTCATGAGG	TTTGAATCT	TGTCCACGAT	60
5	GCGGGCGTTC	ACCAGGCGGT	TACGCAACTC	AAAGTCGTCA	TTAAAGTCGC	GAGCAAACCA	120
	GTAGGAGGAT	TCTAGAAGAC	TGGTAAGCCG	GATGGCGTTT	TTGAAGGGTA	TTGCGTTTGC	180
	GAAGTTCTCA	TCCGCAAAGA	GCTCGCTAAG	CGACTCTATC	ATAAGCAGCT	GCAGGACACA	240
	TTTTACCACG	ATGGTATTCT	TAATACTTAC	ACGGTGCCCC	ATCTCCTCGC	TGCTTTTTCGT	300
	GCGCACGAGT	CGGCTCATAG	GCTTATCCTC	TTCAGTACTG	GCGTTGCCAA	CATCCTCGCC	360
	CTTCTCCTCG	CGTTGGGCAC	GCTCGACTTC	CCGATCAACA	TCACTGGCAC	ATGATTGGGT	420
10	TTCAGCAGTA	CCGTTGGTGT	TGATTGTGGC	TACTGATGGC	TTTCTTCCAC	GCTTCAATGG	480
	ATCTGACTCA	AAAAGTTCTG	TGGCAGTGGT	AAGCTCAAAAT	AACCGGGCAA	ACGAGTTGGT	540
	AACCTGCTCC	CAATGCGTTG	TCCCGAACTT	GTGGGTGTTC	TGGATAATCA	ATTGCTGCAG	600
	ACAAGACCTA	CCAATCCTGG	CAATGGTGTC	ATTTTCTCTGA	CAGATGCAAG	AGACTAACAA	660
	AACCAGGAAG	CCATCCAACA	TTTCGTTTCAG	TGAATCAAAG	TAATGCGTAA	CAGGGC	

## 1594UP

	GATCTGAATT	TAAACGTGAG	ATACCCGTTT	TTCTGACAGA	GATATATTTT	CCTATATCTC	60
	ACATGAAATC	TTCTACTCCA	CATCAGAAGA	GGTATTTT	GAGTGTATATC	CAACGACTAT	120
	GCAATGACCC	GAGAACCCTA	ATTGAATTCT	ACCTAAATTA	TGACTGCGAC	AGTAGTATGC	180
20	CTAATATTGT	CGAGACTGTT	GTGGATTATT	TGACGCGACT	GGCGCTAACA	CGTGTGATA	240
	TACACGCATC	ACAGCGTGCG	TACTATGATG	AACAAGTGAA	CAAACCCCTT	GCAACGTWTA	300
	ACCTATCGCA	GTTGCCTTTA	TTATCCATAT	CTAATGTTAG	CAGTATGTCT	GTTGCTCCAC	360
	AGCAACTCCA	ATTCCCCTGG	GAATTTGCGC	TTAAAATGAC	CTCGTTGAAA	TGTATGTTGG	420
	CCGTGCTAAG	ATCACTAAAT	TCTTGGGCGG	ACAAGGCGAC	GGCTCCAAAT	GGCAGATTAA	480
	ACCACAATAG	GGCATCTGTT	GGCTCCAGTA	CGATTGAAAG	GAAGCACTCT	TCGGCTTTTA	540
25	GCTCTTTTCA	TCACACTATG	AACACAACAC	CTGTAGGAGA	CCAGAAATAGT	GTCCAACAAT	600
	CGGAAGCGAG	TGAGGATATT	GATGATCCCA	CACAGTTTGA	AAATTTGAAG	TTAAGGAAAA	660
	CAGAACTGCA	AAAATGTATT	CGGTTATTCA	ACTTC			

## 1595RP

	GATCTTGCTG	CTATCCAGAA	ATGGGAAGTT	CTTAGACAAC	GGGGAATTAA	GCCCCTTTTC	60
	CAATATTTTG	AGCGTCGTTT	CATAGCTCGG	AAGACGCGAGC	AGAAGCCCCC	CCAGTAGTGT	120
	CTGTTTATGT	TCGCTCATGA	AAGGTGTCTC	TATCAAATCT	AGCTCCATCA	TCGCAGAGTA	180
	GTTATTATCT	TTCTTCCAAG	ACAGACGCAC	ATGCCGCAAC	TTCGTCAGGA	TTACAGTAAA	240
35	ATAATGGTAG	AACCGCGGAC	TCACAGAAGC	GACGACCGCT	CGAAATGAAG	TCGGCCCCGA	300
	GAAGATCGTG	CGGCCCTGCT	TCTCTATCAC	AAGATGGAAC	TGCGAAAGTC	TGTTTACGGG	360
	GGACACCGTG	CCCATAACGT	GCTTCTGTCAT	GAACAGCTGC	GGTACCATCT	CGCTCTTCAT	420
	CCGCGCGAGC	TCAGTCTCAA	GCTCGTTCGAT	CCGTCGCGAGC	AGCTCCACAT	TGGGCGTCGA	480
	GCTGAACAGC	TCCCGTGAGT	TCACGTCGTG	CGTAAACTCA	GACAGGTACA	CACACTCGGG	540
	CAGGCCCTTC	CAATACATGT	AGAGCACTTC	GGCCGCGCCT	TGTTGCACTT	GACGCGCCGC	600
	TTGCGGCAGA	ACACGCACGA	CTTGCTGACC	TTCCGCCCTGG	TTTTTACAAT	CTTGCCATCG	660
40	GACTCTGCCA	TCCCGCCAGC	TTCAAGCAAA	ATGAGTAGGC	TATATTATT		

## 1595UP

	GATCGCGGAC	GTGGAGCACT	GGCCGGAGAT	GCGCGCGGCC	ATCCTGGTGG	TTTCTGCGGA	60
45	CCGCAAGGGA	CACGCCATCG	ACGAGCGGTA	TGCAGCAGAC	GGTGCACACG	TCGGACCTCT	120
	TCAAGGAGCG	CGTCGCGACG	GTGGTGCCCG	GGCGGTACGG	AGAGATGGCG	GCGGCGATCC	180
	GCGCGCGCGA	CTTCGCGACG	TTTGCGCGCC	TGACGATGCA	GGACTCGAAC	TCGTTTTCAG	240
	CCACCTGCCT	GGACTCATTT	CCGCCGATCT	TCTACATGAA	CGACACTTCG	CGCCGGATTG	300
	TCAAGCTGTG	TCATCTGATC	AACGAGTTCT	ACAACGAGAC	CATCGTGGCG	TACACGTTTG	360
	ACCGGGGTCC	GAACGCGGTG	CTCTATTACT	TGGCGGAGAA	CGAGGCGCGG	CTCTGCGGCT	420
50	TCTCTCTGTC	CGTCTTTGGC	GCCAACGAGC	GCTGGGAGAC	CACGTTCTCG	ACGGAGCAGC	480
	GCGCCACCTT	CGCCGCGCAG	TTGACGAGT	GCGTGCGCGG	CAAGCTTGCG	ACGGACCTGG	540
	ACGACGAATT	GCACAGAAGA	ATTGCCCGCC	TCATCTTCAC	GAAGGTGCGG	CCAGGGCCCA	600
	GGACACTAAA	TCTCTGCTCA	TCGACCCGAG	ACGGGCTGAC	CCGCTGACG	CTATTCTCCT	660
	GCTATTTTCT	GCTCTGTATA	CCCTGCCAGA	CGCGCTATAT	ATATAGAATA	TGCATTGCGA	720
55	CGCTTACGCT	T					

## 1596RP

	GATCGACAAT	CTGAGCGAAA	TATTTAGCAC	GACATGCTAC	ATGGGCTCTA	CGGTGATAGT	60
	ATGGGAGTGG	AGCAACCGGC	TGTCCATACT	GGAGGCCAGG	CGCCAGGCGC	AGAGCATTCCT	120
5	GGGGCGGCCG	GTGTATGAGG	ACGAGGAGCA	GGGGTACAAC	TTTGCGCGAT	ATGCGCTGAA	180
	GATTCAGACC	GCAATTGACCA	GCAAGTCAGA	TGAAGGCGAC	ACCACATCAG	CGACTACCTT	240
	TGCTGCACCG	AGATCTGCGC	GCTTCGAAGG	GAAAGGCGGG	CCCCAATCCC	CAGTCTATGT	300
	TCAAGAGGGC	GAACAGCAGG	CCGTCAATGGC	ATTCAATAAG	CGAATGGGCA	CTCGAGCGTT	360
	GGCACATCAT	GTGCTGGATA	GCATCATATA	CTACACAGAC	AAGGTGGTGG	TGAAGGGGCT	420
	TGGAAATTTG	TCCGCGAGCT	TACCTTCCAA	GACCTCCTCG	GCGACAAGCG	TCAGGGGTCTG	480
10	TGTAAGGAAA	CGCATTTGGTC	TCGAAGGCGC	AAATGATGTC	TTTGTATACC	GCACAAAAGA	540
	CCTGGTATTC	GATAGTGATG	AAGATATACC	CAGAACCTAA	CTACTTGTGT	CGATATTTCT	600
	CACACCGCCT	GGTGCGGAAC	CGGGGGCATA	CATTCGTTTT	ACACAAGAGG	GGTTGATGCA	660
	TAAACGCGC	TT					

## 1596UP

	GATCTTCGTA	TCCATGTCCG	AAAGCTCCTC	CAAAATCTTT	TCGTCTCCAT	CATGAGAGGC	60
	TGCTACAGCT	TTTGAGCCGA	TAGAATTGGA	AATACCATTG	GAGATTGCTA	TTAGTAGGAA	120
	GACAATATAA	GTACCATCTG	TCGATGGGGC	AGAGGCTTTA	TCAAGAAGGT	CCATCAGCTT	180
20	GTTCTTGGAT	ACAGCAGTCT	CATTTAATAA	TAATGCCCTG	TCACCACTGG	GCAAAAATTC	240
	AGAAACATTG	AGCAGTTTCA	AGAGTGAGTT	CGACTCAAAG	TTTTCGGTCA	TTGTCTCTAA	300
	CAAGACAAAA	ACAACGTCTC	TCCTGTCTCT	ATGAACATCA	TAAGCCTTGA	AAACCTCGAG	360
	CAAAATAGTA	TTGTCTCTGA	TCACGTTCAA	AAATACCTCT	AGAATTAATG	CCTTCTCTCA	420
	CAATAAAGTG	TCAGATTTAG	GAGACAGAGT	GTGGATTAAAT	AATGATAAAA	TAACCTTCAA	480
	TTCCAATTCC	AGCAATGTCA	AATACTGAAC	CTTTATGAGA	ATGTAATACA	TCTGGCGCTA	540
25	CGAACCACAA	TTGCAAAATT	TTTGGATGAG	GAAATGTACC	TCAATAGCAG	CGGCACCGCC	600
	TTTGTTCGCA	ACAGAAATAA	CAGATCTCGG	TGTGTCAAAA	ATAATAATTC	ATAGTTCAAT	660
	AAAACCAAGT	CTAGGAGCTC	TAATCCATAC	TCCTCATTTA	TGCAATTGCT	ATCCAGCAAT	720
	GT						

## 1597RP

	GATCCATCAG	CGCGGCTACG	GAAATCCTGC	CCATAGAATG	ACTCTCCAAA	CCCCCTTGAA	60
	CTATCAGCAA	AAGCTCAACA	GCATRCACGG	GTCGCATGCC	CAGCAAAAAC	AGATCCAGCG	120
	TCAGATAAGC	GCTGCCARCG	CACCTCGATG	CGGGAATACC	ATCACCGCAA	TGGTCCAGCA	180
	TTTGATGCCC	AAGAAGAAAG	ACCAGCCACC	GCAGCAACAG	GGACCCTATG	GCCTCTCCGC	240
35	AAACTCTGGC	AACAGCTCCA	CGTACGGCGG	CAGCCCTGCT	GCCACCGCGC	CGTCTGCATC	300
	CGTAAATGCT	CCCGCCGCGG	ATGACGCGCA	AAACGCTGTG	CCACAGCCGC	ACAGCGCCCC	360
	TGCGCTATCC	GCTAACGGTA	ACACAGCCCC	TATGTGCGGA	AACTCGGTTA	GCCTTAGTAA	420
	TGGCTCATCA	GCAGGGCCCG	GTTTGTCAAC	ACAGTCAAAC	TCTCTGGACT	GGAAGCAGAC	480
	ACCGCCAAGC	AGTGGCGGAA	GCGTAACCGA	AAGAAAGCCA	AAGCTCGCTC	TATTCGCTAA	540
	GAAAAAATAA	TATCATGCGA	CCTATCATTT	ACACATATTC	TAACGTTCCA	CCTGTGTTAG	600
40	TGTACTCATT	TAATTAATTC	ATTAGTGCTG	CCACTGCTGC	AGACATGTGG	CAAGAGGCAA	660
	AAATGGTTCC	TAGCGGGATC	GAACCGCT				

## 1597UP

45	GATCGAGGCA	GCCGTACCGT	CTTTTGGTAC	GCATGCGCAG	AGTACTGCCG	GATACAGCGC	60
	AACATCTTAC	GCTGACTACA	GTTCCCTGGAC	ACACCACCTT	ACAGCTTTGG	GCCTGCGTTA	120
	TTGGTGCTCG	AAGATATGAT	GTTCCGGAAT	TTTCACTCGC	CGTCCGGCCT	GATGAAACTG	180
	GAAGACAAGA	CCTACAGTCA	TCTAGCCAAC	ATAACGCCCT	GTAGTCGGGC	TCTCGAACC	240
	AGCGTAGAGC	GTAGGAGATG	CTCCACGCGC	CCCGGTGCGT	ACAGAGAAGA	ACAAGACCGC	300
	CGGCATTCTT	TTTATTTACT	TGATTAAACT	CTTGCCAGT	CTGGTTTCCA	CTGACAAAGT	360
50	GCCCAACCAGA	TGGATCGCGG	GCGCGGTGAT	CCTGCCCCGG	CGATAGCGGG	CGACCGGAGC	420
	TTGCGTGGGT	TTCACCTGCA	TCTGCACAAG	ATGTTGTCTAC	GGCGTAGAAG	CAGCGGTGG	480
	GAGGCGCAGC	GCGCGCAAAC	AGGACGTCAG	TCTGACGCGC	TACTTCGCCC	GCGCTGCTGC	540
	ACCGGCTGAA	TTGGGCTCCC	GGCAAGTCCT	GATTGCTACG	TTGAGTCATA	GTCTCAGTAA	600
	TTATCGCATG	GTGTTACTGG	CGTTGCACGT	GACCACACTG	TGGCGTCTCT	TTGGCCCAAC	660
55	GATGAACCTG	CCATCAGCTC	TCCGCCAGGA	CGGTCACAAC	AGGCAGCAGT	AC	



## 1598RP

	GATCCTCATA	ATCATAGTAC	AATATCATTT	CCAATAAATG	GAATAGCACT	AAATAAATTA	60
	GTAATAACAG	TAGCACCTCA	ATGTGACATT	TGTCCATATA	CTAAACAATA	ACCTAAGAAA	120
5	GCTGCTGCTA	TAGTTAAAT	AAAGATAATA	ACACCAACTG	TTCATACAAT	AACTCTAGGT	180
	GATTTATAAG	AACCATAATA	TAAACCTTTA	CCAATATGAA	TATACATACA	AATAAAGAAG	240
	AATGAAGCAC	CATTAAGATG	CATATATCTA	ATTAATCAAC	CTAGTTGTAC	ATCTCTCATA	300
	ATATGTTCTA	CTGATGAGAA	AGCTAATTCA	ATATTAGATG	AATAATGCAT	AGCTAAAAAA	360
	ATACCAGTAA	GAATTTGAAT	AACTAAACAT	AAACCTAATA	AAGAACCTAA	ATTTTCATCAA	420
	TAATTAATTG	ATGATGGTTG	AGGTGAATCA	ATAACATAAC	TATTAACATA	ATTTAAATAT	480
10	AAATTTGATT	TTCTATATGC	CATATATTTT	ATTATTAAAA	TATTATTAAA	TTATTATTTA	540
	ATAAATATTA	GATTATAATA	TAATTCCTTA	TAATAAATTA	TATTATTTAA	TTAATATATT	600
	AATTTATTAT	TTATTATTTA	TTAATATTTA	TATAATCTTT	ATAGGGAATT	GAACCTAATA	660
	AACCATTAA	ATTTAATTAT	TTAATTATTT	AATTTATTTA	ATTATTTAAT	TTATAAATTA	720
	TTAATTAGAG	AGATAAGGGT					

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## 1598UP

	GATCTTATCG	TCTAATGGTT	ACGACATCAT	CTCTTCATGT	TGAAAAATATC	GGTTCAATTC	60
	CGATTAAGAT	TATTAATATA	TTTTAATAAT	TATTATAATT	AACAATATTA	ATTAGAGGGG	120
20	TACCAACATA	TTGCTAACTA	GCAATAGGGG	TGTGTACCTT	ATCTCTCTAA	TTAATAATTT	180
	ATAAATTAAA	TAATTAAATA	AATTAAATAA	TTAAATAATT	AAATCTTAAT	GGTTTATTAG	240
	GTTCAATTCC	TATAAAGATT	ATATAAATAT	TAATAAATAA	TAAATAATAA	ATTAATATAT	300
	TAATTAATA	ATATAATTTA	TTATAAAGAA	TTATATTATA	ATCTAATATT	TATTAAATAA	360
	TAATTTAATA	ATATTTTAAT	AATAAAATAT	ATGGCATATA	GAAAAATCAA	TTTATATTTA	420
	AATTTAGTTA	ATAGTTATGT	TATTGATTCA	CCTCAACCAT	CATCAATTAA	TTATTGATGA	480
25	AATTTAGGTT	CTTTATTAGG	TTTATGTTTA	GTTATTCAA	TTCTTACTGG	TATTTTTTTA	540
	GCTATGCATT	ATTCATCTAA	TATTGAATTA	GCTTTCTCAT	CAGTAGAACA	TATTATGAGA	600
	GATGTTCAAC	TAGGTTGATT	AATTAGATAT	ATGCATCTTA	ATGGTGCTTC	ATTCTTCTTT	660
	ATTTGTATGT	ATATTTCATAT	TGGGTAAA				

## 1600RP

	GATCTAAAAAG	AATCCATGTA	TGTACACATA	TTACGGAGGG	TTAAGGTGAC	GAACGGTAGC	60
	TACAGGCCTA	TAAATCTGGG	TTCTTTTGCA	AAAGTTCATG	CAACTCATCT	GGGACGTTGC	120
	GCCAGTCTTC	GGCAATCCAT	TTCTTTATCC	TATCCTCATC	GGCCTGTGCT	AGTATATCTA	180
35	CTTCAAGAGA	GCTCCTGGCA	CATGTAAAT	TGCCAGCGGG	AGAGAGGAGA	GGCGAAGATT	240
	CTTGAGTGGG	GTAAGAAACT	TGTTTTGATG	GTATGCTGCT	AGCCATCTTC	TTCCGTCTGT	300
	GTTCTTACC	GTTGTTTAAT	GATACTCCGA	TATAATGTTT	TATTAACCTC	TCTGCGTATG	360
	GGGGCAAGTT	TTTGGGCCTG	TAGTCGCCCA	CATATTTGCA	CCTCCAGTAT	ACAGACCAAT	420
	GTAGTTCAAC	ATATGCCGGG	ATGTTCTTAT	GTCTACCAAG	GTTAGGCACA	TAAACGTTTT	480
	TCCATTGGCA	ATTTTTATCT	TCAATCCTTA	TGCCGATGAA	CATCATTTCC	ACTATCCACC	540
40	AGGCAATGAA	CTGAAATATA	CTCTTTGTTC	CATGTCCATC	GTTCTTTGCT	GGCCGGATTA	600
	TACATCTCCG	GAAGGAAGGC	CTGGG				

## 1600UP

45	GATCAAGCAG	CTACTGCTCA	CCTGGAAGAA	GCAGGGCCAC	AAGGCCCTGC	TCTTCACCCA	60
	GTCCAGGCAG	ATGCTCGACA	TCCTGGAGGC	CTACATCTCG	CACAAAGATC	CCGAGCTGGC	120
	AGGCTTACAG	TACCTCCGGA	TGGACGGAAC	CACAAACATC	GCACACCGGC	AGGCCCTCGT	180
	GGACCGTTTC	AACAACGGCC	CGTACCACCT	CTTTCTTTCTG	ACCACCCGCG	TGGGGGGCCT	240
	CGGCGTCAAC	CTCACGGGCG	CGAACAGAA	CATCATCTTC	GACCCCGACT	GGAACCCCTC	300
	CACGGACCTG	CAGGCCCCGCG	AGCGCGCCTG	GGGCATAGGC	CAGAAGCGCG	ACGTGACTAT	360
50	CTACTGCTC	ATGGTTCGCG	GCTCCATCGA	GGAGAAGATA	TACCACCGCC	AGATCTTTCAA	420
	GCAGTTTCTC	ACCAACAAGG	TCCTCAGCGA	CCCCAAGCAG	AAGCGCTTCT	TCAAGATGAA	480
	CGAGCTGCAC	GACCTCTTCT	CCTTCGGCCC	GGGCGCCGCG	AGCGACTCCT	TTGCCTCTGA	540
	GATCGAGCAG	CAGACCGCCT	CCCTCCGCGC	CCAGCCGGCC	GCCCACGGCA	CCGACGACTA	600
	CGACTCCGTC	CAGCGTTTTCG	AGGGCGCTCT	CAAGCTGGAG	GGCTTCTTCA	ACGCCA	

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## 1601RP

	GATCTTTTTTC	CCCCGCAAAC	CGCACACCTC	GTTCCAGGGG	TACTTGGGCA	ACAAAAAGGC	60
	GACGGAGAGC	AAGGTTCTAC	GCGATGTTTT	CAGGAAGGGA	GATGCATGGT	ACCGGTCAGG	120
5	CGATCTCTTG	AAATCCGACA	AGTACGGGCA	ATGGTACTTC	GTGGACCGGA	TGGGTGATAC	180
	GTACCGGTGG	AAATCCGAAA	ATGCTCGAC	TACCGAGGTG	GAGAATCAGT	TGCTCTCGTT	240
	CAACAAGGAC	CTCTTTGACT	GTTTGGTTGT	AGTGGGCTTG	AAGATTCCAA	GCTACGAGGG	300
	TAGAGCCGGG	TTTGCTGTTA	TCCAACTGAA	TCCAGCGCGC	CGCGGACTGG	ACCATGCCAG	360
	TTTGTTAGAC	GACCTTGTGC	AGTATTTGAA	ACATGCTCTT	CCTCGGTACG	CCTTGCCGCT	420
	GTTTCATCAAG	TTCACAAACC	AGCTGGAAAC	AACCGATAAC	TATAAGTTTC	CCAAGAAACA	480
10	GTACAAAAAC	CAGCAGTTGC	CTCATGGTGC	GGATGGGGAC	GAGACAATTT	ACTGGTTAAA	540
	AGACTACTCC	CAGTACAAAG	TCTTGACCGA	CGAGGACTGG	GAGCAGATAT	CAACCGGAAA	600
	GGCAAAGCTT	TAGACCAGAC	AATGCCGGGA	TTGACACCGG	TAGGGAGTTC	AAAAATAAAA	660
	AAATACCTGG	GAAGCCATCC	ATAAAAGCCA	TTATCAACTA	TAGAAATAGA	AAAGT	

## 1601UP

	GATCGCCCTG	TCCCGGGACG	GAGAGCGGGC	GCTGCGCTAG	CATAAAAGCA	CGCAGGTCAC	60
	TGTGCATGAA	ACTCGAATCG	AACGCCGTAC	TCGATGGTAG	AACTAAACGG	GCTCCGCTTC	120
	GAAGTACGCA	CAGTTGAGTG	AAATGTCACT	GTCCGGCGCA	CGCGCCCAAG	AGCAGAATAG	180
20	CATGGACATC	GAACAGAGGT	CATCGCAGCC	GAGTCGAAGC	AACAGCCATG	CAGGATCGCC	240
	GGGGTACGAA	AAAGTGCAGC	CGCTGTATGC	CGCAGAGAAC	GGTTCCACGG	AGACTGCCCC	300
	GACAGCCACC	GGGCTGTTTG	ATAGCTCGCA	CGTTGTACCG	GTGTGCGAAC	GGCGCGGACT	360
	GCTGAGTAGG	CTGGCGCTTG	TGCCCGAATT	CCGGGACGCA	CGTCTCTATC	CCCCGCGGGT	420
	CAAAAAGCTG	ATCCTGGTCA	TCGTGCGCTT	TGCATGTATT	CTGGGTCCCA	TGGGGACCAA	480
	CATCATCTAT	CCTGCGATCG	GGACTATCAT	GCAGGATTTT	GGCACTTCGC	GGTTTCTGGT	540
	CAGTGTGTCT	GTAGGCACCT	ACCTCGCTGC	GCTGGGCATC	TTCCCCATCT	GGTGGTCGTC	600
25	GCTGGCGGAC	AAAAACGGCC	GCCGAACAGT	GTACGTGCTG	TCGTTTCGCG	TGCTGGTGGT	660
	GTTTCAGCGT	GGGCACGGCT	TCTCGCGCAA	CATCGAGAC			

## 1602RP

	GATCCAAGCG	CCCGCACAAAC	CAGCGATGTT	TGCAACATAT	TCGGCTAGTA	TTCTCCGTTC	60
	GACTTTACCC	CTGCGTAGCG	TTGGCGTCAG	ACTGCTGAGC	CAGGAAACTC	GGCGGGCCAT	120
	TGAGGGCGCC	ATTTCTCTCT	CCCCAGTGGT	TCTGTTTCATG	AAGGGCACCC	CAGAGTTCCC	180
	TCAATGTGGC	TTTTTCGAAGG	CCGCCATTGA	GATCCTGGGC	AGACAGGGCG	TGGATCCTGC	240
	GAAGTTTGCG	GCGTTCAACG	TGCTGGAGGA	TTCTGAGCTG	CGGAGCGGGA	TAAAGGAATA	300
	TTCCGAGTGG	CCTACAATTC	CACAGCTCTA	CGTCAACAAG	GAATTTGTTG	GGGGGTGCGA	360
35	CATCCTCACC	AACATGGCGC	AATCCGGCGA	GCTAACTACT	ATGCTCGAGG	AGGCATCCGT	420
	TCTTGTGCCG	GATACTGAGT	GATGCCGCGT	ACGGCTCCCG	ACTATATTTA	TAGGAATACA	480
	GCTTGTAATT	TACGACTTGT	ATTCTCATGC	CTTTAGACTT	GTAAATCATG	GTTGTTTAAAT	540
	TCACAAACTC	CGTTCTTTCA	GTTGAAAGAA	GTGAGAACAG	CTTGCTTTCC	GTCATGTGTG	600
	AAAGAGGCTT	CTGATGGAGG	AGGCGTGCAC	ACGCCAGCAG	AGAAAGTCTC	TCAAAAAATG	660
40	ACGTTCTAGT	GGAAGGGCGG	ACGCAATCAC	CCTTGAATGC	GCGA		

## 1602UP

	GATCGTGCCC	GGGCTTGTCG	TTGTGCCCGAG	AGTTGTGCTT	GTGCCCAGGC	TTTTGCTCGC	60
45	TGCCCTCCGTC	GCTGCCCCGCG	GGGTAGTACA	CGCCGAACCTG	CTTCAGCCGC	AGCGGGCCGC	120
	GGAAGTGCAC	CGTCAGCTCC	TGGTCCAGCG	GAGAGAGACT	GCCCGAGAAC	TCCAATTTTC	180
	TCTGCTTACA	CTTGCACTC	TTCTCGTCCA	TGCTGGTGAC	GTCCAGGTAC	GTGCCGCTGT	240
	AGCCACATT	GGCATAACCG	ATATTTTCTG	CCTTCGAGCA	GTAGTAATTC	CCTCCGATGA	300
	AATCACAATC	GCCCAGCACC	TGCTGCGCAG	CGAGCAGGCC	ACCTGCAACG	ACTGTGCGACA	360
	GCTTCATAAT	TTGTAAACGC	TTGTAAAAGA	ATGACTAGTA	GTTAGAACAG	ATAAAAGAGT	420
50	GCTTTGCTGT	GTGCGCTGTC	GCCCGTCCAC	GCCTTCCGAG	CTCACC CGCC	TTCTTA	

## 1603RP

	GATCCGGCAA	GATCGTCGTT	CAGTTGACCG	GCAGATTGAA	CAAGTGCGGT	GTCATCTCTC	60
	CAAGATTCAA	CGTCAAGATC	AACGACGTCG	AGAAGTGGAC	TGCCAACCTA	TTGCCAGCCA	120
5	GACAGTTCGG	CTACGTCATC	TTGACCACCT	CCGCCGGCAT	TATGGACCAC	GAGGAGGCC	180
	ACAGAAAGCA	CGTTGCTGGT	AAGATTTTGG	GTTTTGTCTA	CTAAGCGGCT	GCTATATAGC	240
	GTATCTAGCT	CTAATGTACG	ATACTCAGTG	TCTATTACGA	CGGCCGCGAG	CTCCACGCGC	300
	CACATACGAG	GCCAGCCGGC	GACGGCAAGC	GGGAATTGAG	ATGCGTTAAT	TAGCAGTAGA	360
	TTAGTAGTAT	ATATGTACAA	ACAGCATACA	CATGAACGGC	GTCGCCGATC	ATAATCTTCT	420
	ACCTCTTCTA	CCACCCCTTCT	TTCTGGTAGA	GTCGGATGGG	ATAGGAGTGA	CGTCCTCGAT	480
10	ACGGCCGATT	CTCAAGCCGG	ATCTGGCCAA	AGCTCTCAAA	GCAGCCTGAC	CACCTGGACC	540
	TGGGGTCTTG	GTCCTTGGTAC	CACCGGTAGC	TCTGATCTTG	ACGTGCACAG	CAGTGATGCC	600
	GACCTCCTTA	CACTTGGCAG	CGACGTCCTG	AGCAGCCAAC	ATGGCAGCGT	ATGGAGAGGA	660
	CTCGTCTCTG	TCGGCCCTTGA	ACTTCATACC	ACCGGTAAC	CTGGCAATAG	TTCTCTGCCA	720
	GACA						

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## 1603UP

	GATCTATTTG	TGCCGTCCGC	CATTAAGCAA	GCGGCAAGCA	TCGATCCAAA	TCATGAGAGT	60
	ACCCTCGGGC	TTTCACTTTC	CAAGCCTTTA	TCAACAAATC	TGGTACACGA	TACATCCATC	120
20	GCGACAGCAC	ATATACCAGA	ACGGGAAAGC	CGACAAGATG	GCACTAGACT	CTGGTAGGTA	180
	ATCTGAGTTC	GACCATATCC	ACTTCGTAA	TGGTGATAGT	TGATAAAAAG	AAACGATACT	240
	GAAAATTTTA	ATGGTTACCA	ATCTCATCTC	ATCGCCATAC	TGAAAGAATA	TTGTAGGTCT	300
	CGCAGTGGA	CAAGGATCAA	GCCCAGGCTA	AGACAATAAT	GGTTGCAGCG	GAGGCAGTAC	360
	AGGAACTACC	CCCAGATGAA	GAAGAACTGG	CCTTGGCTAA	GCTAGTGTTC	GGCGACACAG	420
	CAGACTTCCA	TGAAGCGCTG	CGAAATGCAG	ACCTTAATTA	TGTTTCTTCA	GATGAAGACG	480
25	TATATGGCCA	GGAGTCGTCC	AGTGATGACG	AAGAGGGGAC	TGAAATTGGT	CACCTGAATG	540
	ATGACCAATT	GTTTTTTTGTG	GACGAGGGTG	CAGATACCGA	GGGAGGAGCA	GATGGAGAAC	600
	GGAGGCCATG	GAGGTGGACC	AGGTTAGCGA	GGAAAGCGAC	TCCGGAGAGG	AAAGCGGTAG	660
	CAGCGCTGCA	TGGTCAGATT	CGGATGACGA	ACACTTAAAC	GTTACAATAG	GGCAAACCAA	720
	T						

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## 1604RP

	GATCCCTATT	AGAAGAGGTT	ACTGGGGCTC	CAACCTTGGT	CAGCCACACT	CTCTAGCCAC	60
	GAAGACCTCT	GGTAAGTCTG	GTTCCGTCAC	TGTGCGTTTG	ATCCCTGCCC	CACGTGGTTC	120
	CGGTATCGTC	GCCTCTCCAG	CTGTCAAGAA	GCTTCTACAG	CCTGCTGGTG	TCGAGGATGT	180
35	GTACACTTCC	TCCACCGGTT	CTACCCGTAC	CCTAGAGAAG	ACCTTGAAGG	CTGCCCTTCG	240
	TGCCATTGGT	ATCACCTACG	GTTTCTTGAC	CCCAGACTTG	TGGCCAGAGA	ACCAGTTGCC	300
	AGCTTCTCCT	CTAGACGTCT	ACGCCGACGA	GGCCGTTGCC	CAGAAGAAGA	GATTCTAAGT	360
	AGTGTGTGTA	CATACCAACA	GTTTGTCTCT	TTGCACGTGA	ACCGCCCGCC	TAAGCCTTTA	420
	GGCGCATGGC	ACACAGACTG	CCGTTGGGCA	GGAGATCGGT	TGCTTCCGA	CGCTGGTACA	480
	GGGCTGCGAT	GCGCGTCTGC	GGCTGGCGGT	GCATATCGGA	GATATGGCGC	CGTGCCCGTA	540
40	CGGCAAAGAA	TCAGCAAGAC	ACTAGCGTCT	GGCATTCTTT	TTCAATGCAT	TATTTAGCTT	600
	TTTTTTTTTT	TTTTTTTTTTA	GTATAGACAC	ATATAAGT			

## 1604UP

45	GATCAGAGCA	TCCGATGAGG	TGGCACCGGC	CGCGTCCGCT	GTGTCTTTCT	TCGCGGTATC	60
	GGCTTCCGAA	ATACTTAGCT	TCTCAATACT	TGGGACTGCC	TTATCTTCAG	AGGAAGCGGT	120
	AGCATCTTCA	CTCTTAGGAG	CGCCCTCTGC	GCTGCTCTTA	GGCTCCTCCT	TTGTTGGCTC	180
	CTCCGCCCTTA	GCCTCTTCTT	TCTTCGCGAC	AGGTTTCTTA	GCACCAACTA	GCTTGATACC	240
	GGAGCTGGAA	GCCAACTTGA	GGGTCTTCTT	TGGTTTTGGA	GCAGTCGCAT	TCGGCACAGT	300
	TCCCTTCTCA	AAGTGTGTTA	GCGTCACCGG	AGCGGTGGCT	GACTGGCCCT	GTCCGTAACC	360
50	ATAGCTCTGG	TTCCCTTAC	GGTTCCCTG	TGGCTGTGAG	TTGTACTGCT	TGTAGCTCTG	420
	ATACCCACCT	TGCGCATGTG	ATTGCTGGTA	ACCTTGGTAG	CCAGCTTGTG	CTGGGTTGTA	480
	CTGCTGGTAT	CCCTGATAAC	CCTGGTACCC	GCCGGCTTGC	TGGTTGTATT	GCGCATAGCC	540
	TTGGTACCCA	CCTGCCCTGT	GGCCATACGC	CTGGTAACCT	CCCTGAGGCA	CATACCCCTG	600
	GTAATTCCTG	AAGTTACTTG	GGTTGTAGTA	TTGGCCGAAA	TTTGCTGCC	CTGACCTTGA	660
	TTTTGACCTT	GATCCTTGGC	TTGCGACTGG	CCTTGGTCTG	TGCCTTGCGA		

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## 1605RP

	GATCTTCTCA	AAAGTAGCAT	TTACAATCTG	CGTTAGCGTT	GCTTGTGCAA	TTCCCTGGTT	60
	GGACGAGCTT	AGTGACAGGA	TGAAAAATAT	ATAGATTTGT	CTGACGGCCT	TTAATAGTGA	120
5	TGCACCGTGA	CAATTGCAAT	AAGGCTCATC	TGTCAATATA	CAGCTTGCGA	GGGCGCGGAC	180
	TACCTGCAAC	TCGACCTTCC	CATCAGTCGC	TTCTCCATCA	AAACAGTCGG	TTATGGTATC	240
	AACGGCAGCA	TCTATCAGCC	GCATTCTTGG	AGGTGGTGTA	ACACCAGAGT	CTGGCAACGT	300
	CGTGCCCTGG	TCGTTTGATG	CTGCGGAATT	TGGAGGGTTG	ACTAAAACAT	TCTCGTCTAA	360
	CGCCTTAAAG	GCAAACAAC	TTGATAGACA	ATCAAGAGCG	CTAACCTGTA	TTTCTGGAAC	420
	ATTAGTTCTA	CAGCAAGCAC	GTAGTGCCCTC	AAAGACCAAC	AGAGAATCCA	AAAACCTTGG	480
10	ATCGTTTTC	GATTGCAGGA	GTTGCTCGGT	CAAGTTTTC	ACAGTTTTCT	CAACCAGTTT	540
	TTCAATTATTA	GGATGTTTGT	GCATGGATTT	TGCTTGTA	ATACCCTCTA	ACCTTAGTTT	600
	CACAAGATGC	ACTGCGGATT	TCATCGTCCA	TGGACTACCA	GAGACATTGG	AATATGCCCT	660
	TGTGTGACGC	TTGAGATTAT	CCTGCGAC				

## 1605UP

	GATCAGAGCA	TCCGATGAGG	TGGCACCGGC	CGCGTCCGCT	GTGTCCTTCT	TCGCGGTATC	60
	GGCTTCCGAA	ATACTTAGCT	TCTCAATACT	TGGGACTGCC	TTATCTTCAG	AGGAAGCGGT	120
	AGCATCCTCA	CTCTTAGGAG	CGCCCTCTGC	GCTGCTCTTA	GGCTCCTCCT	TTGTTGGCTC	180
20	CTCCGCCMTA	GCCCTCTCTT	TCTTCGCGAC	AGGTTTCTTA	GCACCAACTA	GCTTGATACC	240
	GGAGCTGGAA	GCCAACTTGA	GGGTCTTCTT	TGGTTTTGGA	GCAGTCGCAT	TCGGCACAGT	300
	TCCCTTCTCA	AAGTTGTTCA	GCGTCAACGG	AGCGGTGGCT	GACTGGCCCT	GTCCGTAACC	360
	ATAGCTCTGG	TTCCCTTAC	GGTTCCTCTG	TGGCTGTGAG	TTGTAAGTCT	TGTAGCTCTG	420
	ATACCCACCT	TGCGCATTTG	ATTGCTGGTA	ACCTTGGTAG	CCAGCTTGTG	CTGGGTTGTA	480
	CTGCTGGTAT	CCTGTATAAC	CCTGGTACCC	GCCGGCTTGC	TGGTTGTATT	GCGCATAGCC	540
25	TTGGTACCCA	CCTGCCTGTT	GGCCATACGC	CTGGTAACCT	CCCTGAGGCA	CATACCCCTG	600
	GTAATTCTGG	AAGTTACTTG	GGTTGTAGTA	TTGGCCGAAA	TTTTGCTGCC	CCTGACCTTG	660
	ATTTTGACCT	TGATCCTTGG	CTTGCGACTG	GCCTTGGTCG	TTGCCCTGCG	ATTGAATTTG	720
	ATCTT						

## 1606RP

	GATCAAGCAT	ATCAAATTTT	CGGCAATCTG	CGGCGTCATT	TTTTTGGACA	ACAGGCGTCT	60
	CCACAGGGTC	CATCTCCATC	AGCGGAGCTA	TACGTTGCGA	CAGTGGCCTC	AGCTTGGTAC	120
	TCTGCGAGAG	AATTGAGACG	CCCTTGGAGC	TGGCTGTATG	GTAAGTGTG	TCCGTGCGGT	180
	AGGTGGTCAA	AGACAGCGAC	TCTGAATACT	CGCATTTTCG	ATCCCGGTTG	CGCCGTACGT	240
35	ATCCGTCGCC	CGTGGAGTTG	ATGGCAGTGG	TGTCCGAGCA	CGAAGACAGC	GAAGGTAGTC	300
	TCAGTGGCCG	CGTCGGCGAT	ACGTGCTACT	CGAGCACAGA	CTCGTTGTGT	CCCCCTCCCG	360
	TCATGTTCTT	CGGCTCAGTT	CGCGACAACG	CTCCCGACCA	TGCCTGCCCC	CTCCCTTCTT	420
	TTCTGTGGAA	GCGCCCAAC	ATTAAATCTA	GCTGCTTCTT	CCTGGTACTC	TGTTGCTCTT	480
	GTTTCTGCCC	GGCGAGCCCC	TCGGATTCAA	TCTCTGTATA	GCCTTTATGC	CGCACTTGCT	540
	CGTCTTAATT	GGCTGCCACA	CTCCTGCTGC	TCGAACCTAA	GGCGTCTGTA	CCGAACGCTT	600
40	TCGTTGACTT	GACCGTTGGG	GCGTAATCTA	TTATTGGAAC	CTTGTAAGG	CGGGCTTCTG	660
	TACGCTATTA	GTTAGCCC					

## 1606UP

	GATCCGCTTG	AGTACTGAGA	TATTAAGTCA	ATACCAGGAT	AAGCTTTCAA	AGCACCGTAA	60
45	TCCTACTGTG	CAATGGTGGG	GACCTACTGA	TTTCTCGCAC	TACGTCTTAG	CGCCTGAAAT	120
	TTTATCATAC	GTGTGCCGAG	ACGAAGTGGG	CCTTGCGAGT	ATCGATGAGG	CTTGGACTTA	180
	CATGGAAAGT	ACCACGGAAT	ACGGGTAAAT	TGTGGCGGAC	GAAGAGCCTC	TAGATATTTG	240
	GGAATTAGAA	TACGAAGAGA	AAAAGCTGCA	ACGGTTAGGA	TTAGGACCCA	AGTACAGCAG	300
	CATGACTTAC	AGAAAGCATC	CTGCCAGGGC	GTCGGCTGTA	TTAGATACAT	CCAAAAATGG	360
50	TTCTAAAGAG	CATAAGCGTA	AAGGAAAGCA	ACACAAATTA	AAAAAAGGAC	AGCAGTCTAC	420
	AAAGATAAGG	GTATCAAAAA	AAAGGCGACG	CGTACAACCA	CACAGCATAT	GCGATTAATA	480
	ATCTTACAAT	CGTACTAAGT	AATACATACC	GCGCTTATAG	AATCTGCTGC	TGCACGGAAA	540
	GTTGTCATATG	CGAAAACATG	CTATGCAAGT	GATGATCGCG	TACCACTTTT	TAATCCGATA	600
	AAAGTGGAAT	AGCGATAAAT	AGTAATTTCA	ATAGGGAATG	TGAATTTGAA	TTGAGAATTG	660
	GGATAATGCT	GTGGATTTCT	GTGATTATAA	TACCATAAAT	ATA		

## 1607RP

	GATCACACGA	CAGTGCCAGT	CGGGGCAGCC	GGTACCCGTT	GGCCGCATCG	TGAAGCTGAC	60
	TCCGAAGAAC	CCCTTCTACA	AAGTCCCCGA	GACGGAAGAC	CTGTCGACGG	TCATGGGCAT	120
5	CCTTGGCTCC	GGCGTGCAAC	GTGTCGCCAT	TGTGGACTCC	ACCTCTTCAT	CTATCCGTGG	180
	CATTCTGTCTG	CAGCGACGTC	TGATGAAGTA	CCTGTGGGAC	AACGCCCCGCC	AGTTTCAGCAA	240
	CCTGGAGGTG	CTGCTCAACT	CGTCGCTGCA	AAAGTTGGGC	ATCGGTGTGC	TGGATCCACA	300
	TACCCCTCCT	ACTTCGCGGC	AGTCGCGTGT	TATTTCCATT	CTCGACACAG	AGCCGCTGCT	360
	CGTTGCCCTG	CACAAGATGC	ATACAGAACG	GATATCCTCC	ATCGCAGTGA	TCGACCACCA	420
	GGGCATGCTG	CTCGGGAACA	TCTCTGTGAC	AGACGTCAAG	CAGGTTACGC	GCACCTCGCA	480
10	GTATCCGTTG	CTGCACAACA	CCTGCCGCCA	TTTCATCAGC	GTGATCCTCA	ACAACCGCGG	540
	CCTGGAGATG	GGCAAGGACT	CCTTCCCCAT	CTTCCACGTT	TACCCACCT	CGTCCCTGGC	600
	CCGCACGGTC	GCGAAGCTGG	TC				

## 1607UP

	GATCGGTGCC	CGCACCTCCG	CCCGATTCCT	CGCCAGCTCG	TTCCGAATGT	TCGGTATCGA	60
	CTTCTGCTTC	TTTATCCCCAT	CCACCTCCGT	CCC GCCGCTG	TCCAAAGCTC	GCTTGGCTGC	120
	GCCGCCACTC	GTACCTGCCT	GCCGTCTCTC	ATCTTCAATA	ACTATCACTT	GCATCCCCTT	180
	AGTAGCTGCA	CGGTGCAGAG	GGCTGTAAAC	CTCCCCCTCAG	CCCTTCAAAA	CGCCCCACCA	240
20	CATACCTTCT	CGTCCCTGGAA	TCATGATTGC	CCCTGGTAAT	CTTCACGCTA	GCACTAATTT	300
	GGTCACTAAC	TGCGCTCTTG	CGGACTGGAA	TTGGTGGTGC	AGATGGTGAA	GTCTCATGTC	360
	GTCCATTCTT	GCCGATGTTA	AAATATGGGT	TTCCGAAAAA	GCCCTGCTTG	CCCTTGACTG	420
	ATGCTCGACT	CACAGAGGAC	TCACCAGAGC	TTGAACCGCA	GCCAGGAAGC	ATTCTGTGTC	480
	TACCAGAAAG	GAGCAACGAG	GAGCAACGAG	ATCGATGTTG	CATAGTCGGG	CAGCAAGAGT	540
	GCTCCAGCGC	TCGGGGTCCG	CAAGCGCAGA	TGCAACAACCT	CCGTGCACAG	CATCACAAGC	600
25	GGTATAGCAT	GGCTTCCCCA	ACGATTTCCG	AGGTGCCGGA	CTTCAGCAAG	TATTCCCAGC	660
	CTGGCCGGTT	ACAG					

## 1608RP

	GATCAAAACC	ATCACCAAGT	TTATTCATGA	AGTGTCCGAC	GATTTCAAGG	TCATCATAAT	60
30	CGACGCAATT	CGTACTTTGT	CGCTAAAGTT	CCCAGATGAG	TGGAAGAATA	TTCTATCCTT	120
	TTTAATTGAC	ACTTTGAAAA	GTGCAGAGGG	TGGGTATACA	TTCAAAAATA	ATATCGTAGA	180
	TGCGCTGTTT	GACCTGATCC	AACATGTACC	TCAGTCAAGG	GAACAGGCTC	TGGAACACTT	240
	GTGTGACTTT	ATTGAGGACT	GCGAGTTCAA	TGAAATCTCA	GTCAGGATCA	TTTACTTATT	300
	GGGTAAGGAG	GGCCCCTCGA	CAGAAAAGCC	TTTCGCTTTAC	GTTAGACACC	ATTACAACAG	360
35	AGTTGTCTTG	GAAAATTCAA	TCATCAGATC	TGCTGCTGTT	AGCGCATTTG	CCAAGTTTTC	420
	CTCTCCGAAG	AAAGATCCGT	CGTTAGCTTA	TTCCATCGAA	AAATTGCTAA	AGGGTATCCA	480
	AACCGATGAG	GATGACGAAG	TGAGAGACAG	GGCAACCATT	CTAGTAAAGC	TCCTTGAGGA	540
	GAACAAGGAA	AAGCCTGGTG	TTGCCGATGA	ATTTATCCAG	CCAAAGCATA	GTTACGATCT	600
	ACTTGCCCTG	GAAAAGTAAA	TTAACGAACT	ATCTCCACCA	TAATGAAGAT	GGCTTTGCCA	660
40	CACCATTGTA	CGCGTCGAGC	ATTCCAAAGT	TACACAGAAG	AGGAGCTCAA	GGCTATTAAT	720
	TTGAAGCAGA	AAC					

## 1608UP

	GATCTGCGCA	AGGATAAAGG	TGTTTCATCA	GTCATTGTGA	ATGACGCCGG	CAGCCTGTGG	60
45	CGCCTTAGTG	CCATTTCTGA	TGGTCCATTC	TCTGACTTCG	TCGGGCCCGC	AGGTGAAGAA	120
	CGAGATCAGA	TCCAGCTTCT	GTCTCATGGT	GGTGATGATC	TTTGGGAAGG	CGGACTGGAC	180
	GCCGATCTTC	TGCACTCCT	CGACAGCCTC	CTCGGCGCTC	ATGTGCGACA	GTCTCTCCTC	240
	CAGGCACACC	GAGAAGGGTA	TAATTAGATC	GCCAGGGGAG	TACTTGTCGA	TCCACTCCTT	300
	GATCTTCAAG	AGGTGCTTGT	TCTTCTTTCT	AATGTAGTCC	CGCTCCGATA	GTTTGATCAG	360
	GTAGATGGAT	GGCTTGCGGG	TTAGCAGGAA	CATCGAGTTG	ATGACCTCCA	CCTCCTTGGT	420
50	GCTCCAGGAC	TGGTTTGCGA	CTCTCTGACC	CGACTTCAAA	AGCTCGATAA	TGCGCTTCAC	480
	CAGCTCGGCC	TCCTCTTCT	TCTGTTTCAC	CTCCAGGGAC	TGGCCGCTC	TCTTGGTGAT	540
	CTTCTCCACG	GCCTCCAGGT	GCTTCTCCGC	GAACTCAATG	TCCTTCAAAC	GCAATTCCGT	600
	GTTAATGATG	TCCAGGTCTC	TGACCGGGTC	GACGTCACCC	TCAATGTGGA	TGATCTCGGC	660
55	GTCGTGGAAG	CAACGCACGA	CCTGGTAGAT	CGAGTCCACA	GATCTGATGT	GCGATAAGAA	720
	GGC						

## 1609RP

	GATCAGACGG	TAATGGCGCG	CATGCTGGCG	CAGGTGGAGC	ACGTATCTAG	CGTCCATCGT	60
	CTCTTGCTGT	GGTGGCGGCG	GCGCGGCAAG	GGCTCGCTG	CGCGAGAAAT	ACAGTAGGGA	120
5	TCTGTGCGCG	CCGCGCACCA	GGGCACGCG	GGCCGCGAAC	AGCGCCGTTT	GCCCCCTAAT	180
	CGGGACAAAC	GCATATAAGT	AGAGGCTTAG	GCGCTGCTCG	AGGGACGGCA	GAACACACAC	240
	AAGGACCAAT	GAACACGATT	ATCAACTTCC	AGGAAGGCAG	CGCGCAGGCT	CTCAGCGAGC	300
	ACAGCATCTT	CCCAGATGTG	CTGGTGTCCA	CTGCTGAAAA	CGGTCCATCA	GGACACCTTG	360
	TAGTGGAGTA	CCCAGGCGAG	TCTACAGCGG	TGACGCTGGG	GAACGTTATG	CCTGTGGAGG	420
	CTACGCAGAC	GGTGCCCAAC	CTGATGTTAA	TCACGACCGA	GCCGGAATC	GTCAGGGAGG	480
10	GGGACCTATT	CACGCTGGCG	ATGACAGACC	CAGATGCTCC	CTCGCGGTG	GACCACAAGT	540
	GGTCGGAATA	CTGCCACTTT	CTGGAAACGA	ACATAACGCT	GGGCTCGGAT	GACGGGGTGT	600
	CGCACGTGGT	GCTAAAGGGC	ACCCCGCAGG	TGGAGCACAT	GGGCCCTGCG	CCGCCGGGCC	660
	GGCACAGGGG	CTCACCGGTA	CGTGTGGTTG	TT			

## 1609UP

	GATCGAGAAG	ATTTGGAGAA	GGAAAGCGTC	TTGGTGCTAG	CCTCGTGACC	CCCTCCCGGG	60
	CTGGAACTGC	GCGATATACT	ACATAAAATA	CGTTATCCCT	GGAATTTGTA	GCATTAAAGG	120
	ACTTATGGAC	TATTCTGTAT	ACCTGCGCTT	CCCGCTGCCA	CCCGTAGCAA	TGCCAAACTC	180
	ACTCCGAGGC	CTCGCTGCTG	GCCCAACAAT	CGGACTCACG	CGGACCCGAG	CCCCGAGTC	240
20	ACGTGCCCCC	CGCATTCGCG	CCACATCAC	TCCGCTTGCC	TCGCTTCCGC	ACCCCGCCAC	300
	GCGACTCCGG	GCCCCGCGAG	CCCACGTGAT	TCTAGTTGCA	TAGGAAACTA	GGCTAAATC	360
	ACGTGACTGA	ATCGCGCGGC	CACATCATAC	CATGGGACAC	GACCCCGACT	ACCCCCCCCC	420
	CCCCGCGCCG	CGCGCTGCAC	AGCAGCCGTA	TACGGCGCAG	GCGCAGTCCG	GTGCGCGCGC	480
	TCTGAGAGGG	CGCATGGCCG	CCGATGCTGC	ATGGCTGCCT	CGGTGTTGCC	GAAGATGTGG	540
	AGGCACGTAC	GCGGGCAGCT	CAGTTACCCG	AAGTTACCCC	TTCTTCTGAT	TAAATTTGGA	600
25	CTGAAACTTA	AAAGCCGTCA	GCAGTGGCAA	ATCCACGGTG	AGAATAATTA	CAGGAAACAG	660
	CGGTGGACCA	GCTGCGGAAC	TAGACGACGG	GTTGGTGTTG	CACGCATAGA	AGGTATGTTT	720

## 1610RP

	GATCAATTTT	CTTTCGTATA	GTTGGCGTCC	CAGGCTCCGA	GATAGCCCCA	CATGATAAAT	60
	TGCTATCGCA	CATGATGTCC	TGGTTGTGAT	TGTTGTCCAA	ATTGCTCAAA	TCAAAAATGA	120
	AACTACCATC	ATCTGGTTTC	ACTTTTCAGTA	AACTATCGTT	TTTCTCTGTT	GCAGGGTCTGA	180
	AATCCATATC	ATCCCGTAGA	TATTCTATGT	ACAGCAGAAA	CGGAACCTTC	TCTGCTGAGT	240
	TCAACACCTG	AGCTTCGTTA	GCAGCAATAT	TTACAATTCC	ATGCAGCTTG	CCCTTCTTAT	300
35	TAGGCGGCAA	CAGTGTAGGG	ATATCTACCT	CAGCTGGCAA	GTCCTTATTC	ATGATAGAAA	360
	GCTCAGCTCT	CAATGAAGTT	AGGCGAGCTT	CAGTGGGAAC	TTGCGCCAAC	TTCTTGATA	420
	TCGTTTCTAG	AGCAATCACA	AACTGCATCT	CGCAGCGGAA	GTAATTTGCC	TTCAAGATTT	480
	TGATTTTATG	TGTGGCTGAT	AAACTGGAGG	GCTCCAGGTT	ATAGATGTTT	GCTCCATGCC	540
	GAGATGTCTT	CCGTTTGTGG	CTCTTCTTTA	AATCATTTGA	CGGAGACTGC	GTGATGCTAC	600
	CACTTCCATG	CTGCTCCAAT	GATTGCTGAT	CCTTATACGA	GTGGAGTGAC	GTGCTGGATC	660
40	GAGAAATCAG	ATGCAAAATTA	GGCATAGAGT	TTGTGTATTTC	CTCTAGCTTA	GCACCATCGT	720
	TATCTTTGGG	C					

## 1610UP

	GATCGATCTG	TACAGAGCCG	TTACAACAGG	CACTTGTAATA	AAGCAATATC	GTTACTTTTT	60
	TGCATGTCTG	TTTTTTCCCTC	GAGCCTCGTC	AGCGCGAGGA	ATGAGTAATG	GATACTTTGA	120
	CGACAGAAAA	AGTGAAAACCT	TTGAGCGGAC	ATCGCAACCT	GCTCGTTAGT	AGCACCTAAG	180
	CGCAGGTTAG	CACAAATGGCG	CCAAAGGATA	CGGCGGTGTC	GGAGACCTCT	ACGCGGTCTC	240
	GCTATATCAA	AAAGGGCAAG	ACTTTAGAGA	ATGACATTGA	GCTACAGTCG	GTGACGCCAG	300
	CCACCGGGGA	GTTCCCCGAG	GACCACACGG	AAGAGGGCGA	CTACCAGGAG	ACGGAGGTCA	360
50	AGAGGGCGCT	GAAGGCGCGG	CACATCTCGA	TGATCGCGCT	GGGCGGGACG	ATAGGCACAG	420
	GCCTGTTTCT	TGTGATTGCA	TCCCGCTGTC	GGACAGCGGG	GCCAGTGGGG	TCGCTGTTGG	480
	CGTACATCTT	CATCGGTACG	GTGGTGTACT	CGATCACGCA	GTCGCTGGGG	GAGATGGCGA	540
	CGTTTATTCC	TGTGACTCCT	CGGTGACGGT	ATTTTCAAAG	CGGTTTCTGT	CGCCTGCGTT	600
	TGGCGTGGCA	AACGGGTATA	TGTACTGGTT	CAACTGGGCG	ATCACGTTTG	CTGTCGAGCT	660

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TTCTGTGGTT GGCCAGATCA TACAGTACTG GACGGACCGC GTGCCAATCG CGGCGTGGAT  
TGTGATTTT

720

## 1611RP

	GATCCATCGT	GGTGTCTGTC	ATTACCTGTA	ATTCCATTGA	TATCCTGGCT	ATGCAGTGCT	60
	GGAAACGCTC	CTCCAGCGCC	TCTATTTTGT	TATTTCAGCTC	CAAGTACTCC	GCGAGCTTAA	120
5	AGGTCAACGA	GAGCGACCTT	GGATTGCACC	TGACGGCGAT	CTCAAGGACC	TTCTCGTGCT	180
	CGTTCTCGTC	CACAAACATG	GCGTAGTTGT	ACCATATCTC	CGGCGCAAAG	CACATGTGCT	240
	GCACAGCCTG	GCGGTGCACG	TATTCCACGC	GCTGGCGCAG	CACGACTTCG	GGCAGGTGCA	300
	GCTTGTTGTC	CAGCTCCAC	TGGATCCACT	TCGTCCAGAT	CTGCAGCTGG	TACTCATCGT	360
	ACTGACCGGG	CGCAGGCAGG	TTCTGCTGTG	TCGCCTGGTT	TAGCTTCGTG	GGCAGCGAGC	420
	GCCGCAGGCC	CTTCGTCAGG	TTCGACCACT	CCTGGTACAG	CGAGCGCGCA	TTCATGTAGC	480
10	TCGCCCAGAG	CTCTCCGATG	AACTTCCGCG	CCGTCAACTG	GTTGACCTCC	TGCTCCCACT	540
	GCGTGATTTT	CTCCAGTAC	CGCTCCAGCG	ACTCCAATGG	CAGGCACAGC	AGGCGCTTGT	600
	ACAGCTTGCG	CAGAATCTCG	ACCCGGCTCT	GCTCCTCCCA	CTTGCTCACC	GGCTTCCACT	660
	GCTCCA						

## 1611UP

	GATCTAAGGG	ATGGGTGACT	GCTGCCGGTG	CTCACAGCAG	TGGCACGTAG	CTAGTAATGG	60
	TGCGAAATCG	ATCAAAGAGG	GTGCGTCTGG	CGGTACAGGC	AGAAAGCACG	CCCGCCGATA	120
	CAAGTTCCAG	TTCTACAAGC	ACCTGCAGTT	CCAGGGTACG	AGGTACCAGG	TGGTGACTTC	180
20	GCGGCCGTAT	CTGATAGAGC	GGTACGGGGA	GCGCAAGGCG	GCGACGATCA	GGTCGTTTGT	240
	CAAGTGACATC	CATCGGAAAA	TCAACGACGA	TGTGACACGG	ATCAGCGACG	AGCGGGTGAC	300
	GCACGGGGTG	TCGAAAGTGG	AGAAGTCGAA	CTGTPTCTTG	CTGCTGGTGA	CGCTGTGCGA	360
	GCGGGGCGGG	CCGGAGTACT	GGCTGGACAA	GACGAACGGG	TGCCAGAGCC	GCGCGGGCGG	420
	AGACGGCGCG	CGGAAGAGCG	ACCAGGTGGA	GGAGGGCGGG	AGCCGGCGGG	GCCAGAGGCT	480
	CGTCTGCACA	CTGGTGGAGC	AGATCATGCG	CGAGAACATC	ACGGAGGACT	ACGACGAGAG	540
25	CGTGACGAC	GAGAACTACG	TGTTCTCGTC	GATATGGGCG	AACTTCATGG	AGGGGTTGAT	600
	AAACCACTAC	CTAGAGAAGG	TCT				

## 1612RP

30	GATCCATGCG	ATAAATCTCC	TAGTGGTGTG	GTTTCACACG	AAGCAGCTTC	CGTCGTTCTC	60
	GTGGTTTTTC	CTGCAGCTCT	GTTTCGAGCTT	GATTTTGGTG	TTTTTTGGGA	CGTGGACCAC	120
	GAGGTGGCGC	GAGCTTCGCG	ACACGTTTTT	TGAGGGTCTC	ATAGATCAGG	AACCTATTAC	180
	GGGTGGGGCT	GAGTCTCCCT	ATCATGGCAG	TTCTCAGAAC	AGACAGCAGT	TTGAGATGAA	240
	GGACTTGGAG	GCACAGAAAT	AGCCTACATT	ATAAATACGC	TTGAGATCAT	TCTAGCGCCA	300
	CGGTGAGACT	GATCATTCGT	AAATAGCATT	TTAATAACGT	AATATATCAT	ACGCTGGTTA	360
35	TTTCCGGATGC	AGGACTCCGA	AATAGTCTGA	CAATTATGTA	CTGTTAAGTT	ATTTATTTTC	420
	AGACGGCGTA	TCTCGCTTGA	AACCTGTTCC	AGTGCACAGC	AGATCCAGCA	GCTCGAATAC	480
	TGATTTTTTC	GTATTGTTAC	CTGGTCGACA	GATCTCCAAG	CCACCCCTCA	ATCGCTGCCG	540
	CAGCTGCAGC	ATTGCTACCG	TAGACTCCAG	CCTAGTGACA	AGATGATCCA	ACAAGGATAT	600
	CCAATCGTAT	TCCGTGTTCT	GGCTCAGCGC	TTTATCAACC	TTTTTATCAC	GAGTCATATG	660
	TGTGGGTAGT	TGTAGGACAC	TATTGTGAT	TTGATCAGA	CCGCCGTT		

## 1613UP

	GATCAAATAG	ATGTGCGCTG	CCACATAGGA	CGGAGTCGCG	GCTAAGCTGT	GTGTTTTACC	60
	TGGAGGCAAC	TGTTGGACTC	CTGTGTCAGC	AATCGCGCCC	CGACCTGCCG	AACAAGCGAC	120
5	TATATAACAA	GCGAGGAAAC	CACCTTGTGA	TACGCACGGG	GACCAACGAC	ACAGCAACGA	180
	CACAGCAACG	ATGGCGGACC	TCGGGGCTCT	TATTGACTTG	ACGCGGATAT	CGGAGACGCG	240
	GTATGAATCG	ACGAACCATC	ATAGGATGAT	ACACGGCGGC	AAGGCGCTCT	ACGGGGGTCT	300
	GCTAGTGGCA	CAGGCGATAC	TGGCGTCGTT	CTACTTTGTC	CCCAGGGACT	TTATTCCGCT	360
	CTCGGTGCAC	TGCCTGTTCA	TGGTCGGCGG	AGACAATGCT	ATCAAGACGC	AGTACGAGGT	420
	TGAACGGCTG	CGGAAGGGGA	GCAACTTCGC	GCACCTGTTG	GTGCGCGCGT	ACCAGAAGGA	480
10	CAAGGAGCTG	TTCAACAATGC	AGATCATCTA	CCGGCGCGAC	CTCGGCAAGC	AGCCGGACAC	540
	GCTGCACCGC	AAGGACAACC	TGGGCCCTGT	GGACCGGTCC	CACCTGGAGG	ACGCTGGCAC	600
	GCTATGCAGG	CGGGATCTAC	TGTCCAACCG	TGAGAACCTG	CAGGCGGTGA	GCGCGTCTTC	660
	GAGACGGATA	AGGGCCTTAA	TAACATTCTG	GAGGGGTTCG	ACAACACGTC	GTCCGAGTAC	720
	AGGCTGCCTG	GC					

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## 1614RP

	GATCGCGGCG	ATGGACCCGT	GCTTCGACCG	CCTTCTGGCG	CACCGCGCGG	CGTTCCTCGC	60
	CGCGGTGCAG	GAGCAGGTGC	AGCGGGACTA	CGGGGCGATG	GAACAGTTCC	ACAAGTTCCC	120
20	CGACACGATC	CGTGTGACA	AGTTGGTCAC	GTATATATGG	CGCGTGTTCC	AGCGCGTCTG	180
	CGTGTAACCCG	CCGAACCAGC	AGCGCTGCCA	TCTCGAAGAC	ATCATGCTCT	TGCGTGTGTA	240
	CTGCGGCGAG	GCGCGGGGGC	ACCGCTCTTT	GCTCATGGCG	ATCGTTCAGG	CGGTGGCGGC	300
	ACGCTACGGG	GTGCAGACGC	TCCTCTGCGA	GCAGGTATTG	ATCATCATTG	ACCGCAAGTT	360
	GCGCGGCGGA	CAGTCATACT	TGATGATCCC	GCTGCGAGGG	AACGCAAAGC	CGCGCATCTT	420
	CACGCGGCGG	CGCTTGCTCG	ACACTATGCG	GCACACAATA	CCCAACATTG	CCGACCCGCG	480
25	GAGCCTGGCG	CTCGCCCGGT	TCCTCACTCC	GCTCACGAAG	CGCGCGGGTG	CTGAGAAAAT	540
	CTTCAAAGAC	TGGTCCATCT	ACTGCGACAA	ATCCATATGG	CGGACGATCC	CTGATCACTC	600
	GCCCAATGGC	ATTCTGCGCT	ACCTCCC CGA	CTCCTGCACG	CCGATGGACG	AATCCATCTT	660
	TGAGTATTTT	ATCGTCTATT	GGAAAACCGC	AACAGCAAAC	CACTCCACGA	ACAACATTTT	720
	CCACACC						

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## 1614UP

	GATCCTTTTC	ACCAACAGCT	GTCTGGGCCA	GCTGCGGCCT	GGGATGAGCT	ACAACGAGGC	60
	AGTGAAAGCG	CTGACGAACC	TGGCGCTGGA	CAGCTTTACA	CTGCCGGGGA	CGGTGGGGTT	120
35	TCCGCTGAAC	AACGTGTACT	CTGTGCCGGT	AGAGGACGGT	GCTCAGATGG	AGCTGCTGAA	180
	GGGGTACCTG	CAGCAGTTGC	GGCAGGAGCT	GGCCACGCGG	CTGCTGGACC	GTGTGTATGG	240
	GGCGGAGAAG	GCACAGCCCT	CGAAGTTCTG	GCTGGCCTTC	ACAAGGCGCA	AGTTTATGAA	300
	CAAGGCGCTG	TAAGGCGAAA	TAGGTACGTA	GCTGGCGGCG	CCAGGAAGTA	TTTACAAAGT	360
	TGGCTGTATC	GCTACGAGGT	TTTGGTGGCG	TGTGCCTTGT	TGGAGCGCAC	GAGGAGTTCA	420
	ACGGCGGAAG	CTCGGAGCTG	TTCCGCGTCT	TTACAGATCG	CGTTTACGTC	AATGCTGAGG	480
	TCGGTGTTTT	TGGCGCGGAA	GCCTTGGATC	CGCGCCTGCA	GGTCTGTTCAG	CGCCTGGAGG	540
40	ACACGCTCAT	AGTCTGCATC	TTCTTTTACG	CGCTCTTTGT	ATGTTTGGAA	GGACTGAGCG	600
	ATGTCTTCGA	TACCGGGCTC	GACTCTGCTG	ATCATCTCGA	TGCGCTGGCG	CAACAGCTGA	660
	TCGCGGTGCG	TGTTGGCGTT	CSCGTCGCTA	ATCATCTGCT	GGATTTCTGT	ATCGGTCAAG	720

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## CCCGAT

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## 1615RP

	GATCATTTCAG	CTGGACGTCA	GCCGACTACT	GTTGGACCCC	ATATTTCACGG	TCCCCGAGGT	60
	GCAGAACGAC	ATGGTGGAGA	TTCTGCGCCA	GTATATGCTG	GAGTCGGGGC	GGCCGTACAA	120
5	GCAGGGTTTC	CATGAGCTAT	GCGGCATGTT	CTACATGCAG	CTTTACCGCA	ACGGCTACCG	180
	GGACGGCATC	CAGCACACCA	CGCTACATAT	GTTCAGGAG	TTCATCGCAG	AGGTAGCTGT	240
	GACCTTCTAC	GACGAGGGAA	ACCTCATCGA	GTGGACGAAG	AACACGTTTG	AACCGATACT	300
	TCGACACGCG	TTGCCAGGCT	TGTACGAGCA	GCTTCTAATG	CACCATGAGC	TGGACAACCTC	360
	GATATGGCTC	ATCCGCTGGA	GCAGGCTGCT	CTTTCTCCGA	GAGTTCGAGC	TGGAGTACAC	420
	GCTTTGCTTG	TGGGATCACC	TGCTGACATT	TAGATACCCA	GTATCCCAGC	TCGTAGCAGC	480
10	CATTATCGTT	GTCTGTCTGA	CACTCATTTGT	ACAAGAACTG	CATTCTCTGTG	AAGACCACGG	540
	CGACCTGATG	TCTATTCTAC	TGCACCTACCC	TCCTCGAAGC	TGCTGAGCGC	CCCCAGATGA	600
	TCCGCTCCGC	CCGGACGCTT	CCTGATCTGT	GGCTCGCCGA	ACAATATGAA	GACATGCAAC	660
	TCATCTGCGA	TTCACTAATT	AAGTCGCACA	ACGGCGCCTG	GTTC		

## 1615UP

	GATCTCGTTA	TTCTGGACAA	CATTGCGTAT	AGGGACTGCT	CCTGCTTTGT	GTGAGGAGAC	60
	GTGTGCTGAC	TTTAAATAAG	TACGATGAAA	CGGTCAGCCT	ACGGTGGGGC	CCCGTTTTTC	120
	AGTTTCGCAC	GGAGAGGGTA	TCAAAGGAGG	TCGAACACAG	CTACGTTATT	GGTTCGTATA	180
20	GCATGCTTTT	GAAGCCCCTA	GCTTCACGAG	CGCTCCGACC	ATCCCAGCCA	CCGCGCCCCT	240
	ACGCCCAAGG	CCAGCTCCCG	CAATACGGCA	GCGCCGTGGG	CCCCTTTTCG	TAAGTATATA	300
	TGGCGTGGCC	GCGCCGCGCG	GCCGAGGTCTG	CGCGGTTCGAC	AATGGCTTCT	CGACTTGACA	360
	AGCTCCCGGA	GGCGGTCACT	CGCCTGCAGA	GCCTCAGCCA	TAGACAGCTG	CTCCGTCTGG	420
	CGCAGGGCGT	GTGCATCCCT	GCCCTGTCCC	CGTCCCTGCA	CAAGGGCCAG	AGTGGACGCG	480
	TGTGCGTCTG	GGGGGGGTCTG	CTGGAGTACA	CCGGCGCGCC	GTACTTCAGC	GCGCATGCCG	540
25	CGGCGCTCAT	GGGCTCGGAC	CTGGTGCACG	TGCTGTGCGA	GTGGAACGCT	GCAACGCCGA	600
	TCAAGGCCCTA	CTCGCCGGAC	CTGATGGTGC	ACCCGCACCT	GCGCGACAGT	AGCTCCCTGG	660
	CGCGCGGGCT	GGAGCCCGCC	ACAGAAGCCG	TGCGCGCGCT	CGTGGA		

## 1616RP

30	GATCTGCTTC	AAGAGCTCCT	TCTGGTAGGA	CGAGCCCAGG	ATGAAAATCT	TGGAGACGGT	60
	GACAGGGTCC	AGGAACGGCT	TGAACAGGCG	GAATGCGGCG	GAGAAGCCGA	ATGGCGCGTT	120
	GATCATGTAG	AACTTGCCCA	TGCGCTCGGG	GTAGTAGTTC	TGGCCGATGT	TCGAGGCCTC	180
	GCGCACGTAG	CTGAGCACCT	GCGCGGCTGC	GGAGATGGAG	ATGCCCTTGA	GGTCTAGGAT	240
	GGTGCAGGAC	GTCTCGACGA	GGCAGTCCGC	CTGTCTGGAG	CTGGCCGGCA	AGCGGTACCG	300
35	CGAGAAGGAC	TCGTACTCCC	ATATCAAGTT	CTTCAGCATG	CGCTCCTGCG	TCGTGATCTT	360
	GTACATCTCC	GTCAGTTTCA	CCGCGCCCAG	CTCCTCGATG	TACACCGGCC	TCCCGTCTCT	420
	GTCCGTCTTG	TGGTAGTACT	GCGGGTAGAA	CTTGGCCACC	AACGGCTTTT	CCTCGTAGTG	480
	GAAGTCTCTG	AAGATCGTGT	CCACGCCGTT	TTCTTTACGC	CACCTTCTCGC	AGTTCTCAAA	540
	CATTGCCCGC	CGAGCCGCC	ACGTTGGAAC	TTGCGCGCCC	GCAGAAACCG	CAAAAGCGTC	600
40	GAGTCGTCCA	GACGCTTGGT	GAATCCGGCC	TGCTTCAGCA	CCTTGCGCAG	CTCCTCCAGC	660
	GCCGCTCCG	TGCTCCGCTC	CGTCAGG				

## 1616UP

45	GATCACCTTT	TGGCAGGAAC	GCCACAGAAA	ATCCATTACG	CGATTCTGCC	CGTTCAATTC	60
	TGTACGAATG	GGGAAATGAC	TCGTCGCCAT	GGCACAGGTG	ACTATCGCAT	TTCTGTTTCGG	120
	GGGCGTGATG	CCCAGATTTT	CTTGCAGAAA	GCCGCCACCC	TGCGGGATAG	GGCTTTACCT	180
	CACATGAGGC	GCAAAGCGAC	AATAATCGCA	GAGCTGCTTC	TTACTTCATT	CTCTACCCCA	240
	CTAACGTAAAT	CGATCGGACA	GGCACAGTCC	TACGGTAATC	CTCTGAGATA	CCAGATTCGG	300
	TTGCATAATG	ATCTCGCCTA	CAGGGCCGTG	TTTGTTTCGAG	CCCATATCTC	ATGCAAGATC	360
	GCGATGCCCC	TGACGATCCA	CCTTCACCAT	TTACTCGTTT	CTTTTTCATG	TTTTCAAAAA	420
50	GAAACGAAAA	GGTGAGATAA	AAAGCAAACA	TTACTACCGA	CATTTAAAAT	AGGTGATGTC	480
	CAGGACTGTA	CCTCATTGTG	GGCGCTAACA	GCACCAGCAA	TGTCTGTGTC	ACCCCTTGTG	540
	CTGTTTGACT	TTTCAACAGA	CAATCCGAAC	ACACTGCCCC	GGGAATACGA	CCTTGCAGTG	600
	GCCCGAATCT	GTGTGCTGGG	CCACGGGGGC	AGTGGCAAGT	CATCACTCGT	TGCTCCGATG	660
	GCTACACGGA	CTGGAGAGTG	GCCTG				

## 1617RP

	GATCTTGACA	CCAATCGACT	TCCGGAACGC	CTGAGTCAAG	GCCTCGGTCT	TGGATAGCTC	60
	CAACGAGAAT	ATCTCTGACC	CTGCCATCGC	TGTGAAGGGC	ACATCTGCGC	CCAGTGACTG	120
5	CGACAAGCCC	ATCGCCAGCG	CCGTTTTGCC	GGTCGACGGC	GGACCAGCAA	CCAACACGGC	180
	CCGCCCGGCA	ATCGTACCGT	TCTGCACCAT	TTTGAGAATC	ACGCCGTGCGG	CCCTCCGCGC	240
	CTGTAACGGG	CCCACCATTC	CCTGCGAGCT	CGGCTTAGGC	TGTAGGTTCT	CGTCCAGTCC	300
	CAGGCCAACA	ATGTGCGAAT	GTGTGCGCAAT	TAGCGACAAG	GACTTCAGAG	ACATGTCAATG	360
	CGCCTCCTGT	GTTTGAATCG	ACATATTATA	GATCTTTGAA	ACTTTGAAAC	CGTCAAGAGA	420
	GTCCAATGGC	CTTTGTCGAT	GACCGTCTAA	CTGTTCAAAC	GGTTGTGCAA	CATACCAAAT	480
10	TTTGCCGGAG	CCTGAGGACT	AAAACGCATG	TTATACGAAG	TCAAGAAGAA	GCATCGTTTG	540
	AGCTGCTAGC	AGTTCCCTGA	CTCTCAACTT	GGTGCGAGCG	TGCGGTGTGA	TGCTTCGCAT	600
	GGGAGAGTAC	ATATGTGGTT	GCAAGCCACT	TTGGAACCTG	TGGGCTAACG	ATGTACGCAT	660
	CACCGTGAAT	GGGAAGCGGT	ACTTGGTGAC	TGGGCTCCTC	AGT		

## 15 1617UP

	GATCAGTTTCG	TCGAAGAATT	CATGTCATGC	AGAGAAATGG	GAAGCAATTT	ATGCTCAGCT	60
	CCCTCCCCCT	GTTCTCTTTC	TACCGCCAGG	CCATGCAGGC	ATGTCAGGCG	CTCAACACAC	120
	CTAGTGACAA	ACTCGCCGTT	GTCCGTGACAG	CCTATGCGTT	CGTAAATGTT	AAGGCCATCC	180
	GATGTTTCGAA	GAGGTGACAG	AAATTCCCGC	TGTAAATTCT	CAAAGAAACT	GTCCAAGGGC	240
20	GTATCCTTTCA	CAAAGTCGGG	GCGCCGCTGC	AGCACATCTT	CCAGCTTCCT	CTGTTCCCCC	300
	GAGGCGTTTC	TCATGCTCGT	GGCGATTGCA	CTTGCTCAGC	TCGGCCTCTG	CAAGTACGTA	360
	ATTTTAGCTA	TCGAAAATTT	TCCCTCCTGG	CGATGAGCTC	ACGAAGTCTA	CATACCGATT	420
	GACTAAGACA	CTTGCCACCC	GTTTGCGCCT	CATGCCACTA	CACCAAGGAC	CTCTGGACAT	480
	CGAGGATCAA	CTTGCCATCA	TTGCCGACGC	CCGCATAGGC	GATCTTGACA	GCCTCAAGCA	540
	AATCTTTTTC	GAGCTCATCG	ATCCAAAGCT	CCTGCCATCG	TGCAGCGACC	CAGACACGCT	600
25	CTGCACGCCG	CTGCACATGG	CTGCCGCCAA	CGGACACGCC	GACGTCGCCC	GCTAACTGCT	660
	CTCGCTGCTC	GAGCCCGCCG	CGGGACGCCA	CTGGGG			

## 1618RP

30	GATCCGGCGT	CCGGAAGAGC	AGCTTATGCT	GAAGGGCTAC	CTAAGGGACA	CAATCCCCCC	60
	CCCCCCCCAA	AAAAAAAGCA	TGAGACTCTG	TATCAGTAGG	AAGTCTATCG	CATCTTCTTA	120
	TTTAGCCTGT	ATATGTCCCT	TCCGCGTGTA	GACAKTGCGT	TGGACGAGTA	TGCTCGATGC	180
	GGAAATATAAC	GTACTTTTTT	GAAGAGTAAT	ATGGACTTTC	GACCTGCAAA	GTACCGTCTG	240
	CCGTTGCGGT	GTCAGACACT	CATCGGAACG	CAATTGTTGC	GGGATCACGG	TATGCTTCTG	300
35	TTGTATGCTA	TGGTAGCTAT	AGGGTCTGGA	CGGCTATCCA	GAGAGATATT	ATCCCATTAA	360

## 1619RP

40	GATCAACAAT	GTGCCGCGGC	TGCTCCTGTT	CCGCCCGGGC	GGTGATCTGG	ATAGCTACGA	60
	GCCTCTCGGG	ATTCCGTGCG	ATACAGGCGG	CGCACGGGTG	CGGGCGATCA	TCGACACCCT	120
	CAAGAGTTAC	ACCGGCATCG	AAGACTTCGA	GTACCACGAA	CCAGTGAAC	GGGGCCAGTA	180
	TGCCGCTATC	CTCATGATGG	CCGTCCCCGT	AGTAATCATG	CTGCGCAACT	ACTGGTCCGT	240
	TGTGGTGTCC	ATCGCCCTTT	TCCGGCCTCT	GTGGGGGTTT	TCCTGCGTGT	CGATCGTCAT	300
	CGCACTTGTG	AGCGGCGCGA	TGTTTCAMCAA	GATTAAGGAC	ACTCCCTACG	TGGGCTCGTC	360
45	CGGTGATGGC	AATTACGTCC	AGTACTTCGC	AATCAGGCAG	CAACAGGTTT	AGTTCCGGGT	420
	GGAAACTCAA	ATCATCTCCG	TCAATATATG	CACCTTCAGC	GCAGGAGTCG	TACTACTTGC	480
	CATTGGCACC	AAAAGCATCA	GAGCTTACTA	CATCAAGTAC	AACTATAGCA	TGCACGCGGT	540
	GGTGCACTTG	TTGTTGTCCC	TCGCCGCAAT	ACTGCTTATC	TATATCTCCT	TCGCCGCCCT	600
	GCTCGCAGTC	TTCAAACCTGA	AGAACTTTGA	GTATTCA			

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## 1619UP

	GATCGCTTGC	TGGAGACCAC	AGATTTTCTA	GCGTTGTCCG	TAAGGGCGAG	ATGGCGTCGA	60
	CAACCACGGA	GGAAAAGCTC	ATGAAGCTGA	ATCCAACAGC	TACAGATGCG	AACAATTACA	120
5	TTAATACTGA	TACCACTGCG	AGCAAGCCGG	CTCCACCTTC	GTCAACAGAG	GCTGGACAGG	180
	CAATTGAACG	AGAAAAAATA	CTAGACCGGA	GGCAGACTGA	GAAGGACAGT	GTAGAGAGCA	240
	GCAAGGTTGA	GCGCCCGGTA	GTAGATGCAT	CGTACGTAGG	GTGGAAGCAA	ATCGGCGGGT	300
	GGGAAGAGCG	CGACCGACTC	ACCGAAGATG	ACCTGCACTG	GGAGCTTGAC	AGAGAAAACCT	360
	TTTTAAGCCA	TGTGCTGCCT	GCTGCTGCGT	ATGGCGACTG	GTATCACTCC	GTGGGGATAT	420
	TCTTCCTCGG	CGGATTTTTA	TCGTTTGCCT	TGGGCTACTT	CAAGTTCAGT	TTATCACCTG	480
10	TATTCTTCGT	AATGGTTTTG	ACGGCTTTGC	TATACCGTAC	ATCGATTTGG	AAGTACAGAG	540
	GGTCGATAAG	GGAAGCTGGT	CAGAAGGAGC	TCACAGTGCA	GAAAGTAGAG	GATGACTACG	600
	AGAGCATGGA	CTGGCTCAAT	AACCTCTTGG	ATAAATTCTG	GACCAGAATA	GAGCCCAACA	660
	TTTCCGTGAT	GGTTGTGGAT	CAGGTGAACC	ATGAATTGGC	TAAGAACCGT	CTGTGCCGGG	720

## 1620RP

	GATCAAACCTA	TTTCTTGTGT	TGTTGGTGGA	AGCATACTTT	CGTCAGTACT	AACTTCTTCG	60
	CTCCACTCCA	TAAATTCGTA	TTCCCTATTG	GGATTAAATT	CCGGACCCAA	GGTAACGACC	120
20	AAAAACATTA	GAGCAATAGA	TCCCCACACA	AAATAGGCCA	TAAGTCTACC	ATAATCATAC	180
	AATTCCTTAT	TGCCATTATC	GAGTGGAAAA	TTTCTTGCAA	GGCTGCTTTC	AAGCAACGAT	240
	GAGGGGCTAG	ATGCCAAGTT	TCCCAATTGA	TATGCCACGC	CCACGAAAAA	GGTTTTCGTG	300
	TCTGAGTTTG	GAGCTAAGCA	GTGTAAATGA	TGTGGGACAA	GGCCCCATGC	TCCTTGAACA	360
	AAAAACTGTA	GGAAGAACAC	GGACACTATA	ATACTTCTAT	CATGTACAAA	TCCCCACGGA	420
	TAAACAAGAC	AGGCAGCCAA	CAAAATACAC	ACGAGGATAA	CAACTCTTCT	AGAGCTTATG	480
	CTGGAAAAAC	GTGAAATGAA	AAGTCCACCT	ATTATAGCAC	CAACGTTGGC	TGCACAATTT	540
25	GTGACGGCTG	ACTGATTGGG	AGAATAACCA	AGTTGTTTAA	TGAGCATGGT	TGGAAAGAGA	600
	TCCTGAGACG	CATGAGAAAA	GTAATTATAA	CCCGTCATAA	GCAATATCAT	GTAGATGACA	660
	ATGT						

## 1620UP

	GATCAAATAA	AAATAGAAAT	TAGCTTAATG	GTAGAGCATT	CGTTTTACAC	ACGAATAAAT	60
	TGAGTTCGAT	TCTCAAATTT	CTAAATAATA	ATTAACAATA	ATTTAAATTT	GGGTAAAAAT	120
	TAATAAATAT	TAACGTATAT	AATAATTATA	TACTTTATAA	AATTACTCAA	TGTTATTAAT	180
	AAATTTATTT	CTTATCATT	ATAATGATGT	ACCTACTCCA	TATAATATAT	ATTTTCAAGA	240
	TTCACTACTA	CCTCATCAAG	AAGGTATTTT	AGAATTACAT	GATAATATTA	TATTCATAT	300
35	GTTACTTGT	TTAGGTTTAG	TTTCTTGAAT	AATAATTATT	ATTATTAAAG	ATTATAAAAA	360
	TAATCCTATT	CTTTATAAAT	ATATTAAACA	TGGTCAAATA	ATTGAAATTA	TTTGAACAT	420
	TTTACCAGCT	ATTATTTTAT	TAATAATTGC	ATTTCCATCA	TTTATTTTAT	TATATTTATG	480
	TGATGAAGTT	ATTTACCACG	CTATAACTAT	TAAAGTTATT	GGTTTACAAT	GATATTGAAA	540
	ATATGAATAC	TCGATTTTAA	TTAATGATAA	TGGTGAAACT	ATTGAATATG	AATCTTATAT	600
	AATTCCTGAA	GAATTATTAG	AAGAAGGGTC	AATTAAGAAT	GTTAGATACT	GATACTAGTA	660
40	TTGTTATTCC	TGTTGATACT	CATGTAAGAT	TTATTGTTAC	AGCTCCTAGA	TGTTATTTCAT	720
	GAATTTT						

## 1622RP

	GATCCGTGTA	TTTTTTATTT	ACATTATTTA	ATTAAAAATA	ATGATTTAAA	TAAATATTTT	60
	TTATAAAAAA	TAATTAGTGC	ATTGTTACAT	GTTCAATTAA	GAATGATTAT	TATCAAAACC	120
5	ATCAACTAAT	TGTTATATAT	TTATTAAATA	TTAATTTTAC	TTAATTAAGA	ATTAGGAACT	180
	TTATCTATTA	GTCTGGGCTG	TTTCCCCTTT	GATTATTTAA	CTTATCGCTA	ATAATCTGAA	240
	ATATTTAAAT	TTAGATTAAT	AATATATTCT	GAGATTTAAT	ATTTTAAATA	AAATAAATAA	300
	TTATTCCTTA	AATAATATTA	ATAACTATAC	CATATATATC	TAATATTTAA	ATAATCATAC	360
	TAACATATGT	TTTCGTAGAAA	ACCAGCTATT	TGCAAAATCAG	ATTTGACTTT	CTCTACTTAC	420
	CATTATTCAT	CAGATAATAT	TGCTACATTA	ACCTGTTCAA	TCGTTTTTAT	ATTTTATTAT	480
10	ATTTTAAATA	TAATAAATAT	ATATTTTAAAT	CATTTGATAA	TAGTAAGATC	ATCTGCTTTC	540
	GGGTAAATTA	ATATTAACATA	AATTTAATTT	ATTTTAAATTA	ATTTTAAACAT	TGTTAAATAT	600
	TTATATTATT	TTTAATATCA	TTTTTTATTT	TAATATTATG	CTAATATTAA	TTACTTGCTG	660
	ACCCATTATA	CAAAAG					

## 1622UP

	GATCCAGTTA	CTTAGTAGAA	TGATAAAATT	AATAAATATT	ATTTATTAAT	ATTTGGTTAA	60
	CAATAAAAATT	CAATAATTTA	TTTAAATAAT	GATTAAATAA	TCTCAATATA	AAATTATTAA	120
	TATAATGAGA	TATATATTTT	TAAAAAGAAT	ATATAATTAA	ATAATCCCAA	CCAAAATTTG	180
	TGCCAGCAGC	TGCGGTAAGA	CAAAGGGGGT	TAGCGTTAAT	CGTAATGGCT	TAAAGGGTTC	240
20	GTAGAATGAT	TATTTAAAAT	AATAATTAGA	ATTAATAAAA	ATAATTTAAG	AATTATTCAA	300
	GTAAAGATGA	AATAATAATT	ATATGAATAA	GACTTATAAA	GTGAAAATTT	AAATTATATA	360
	TTAATTGACA	TTGAGGAACG	AAGGCTAAAG	TAGCAAATCG	GATTCGATAC	CCGAGTAGTT	420
	TTAGCAGTAA	ACAATGAATA	CCTATTTTAT	TTTTATTAAAT	TAAAGAATAA	ATTAAATGAA	480
	AATTAAAGTA	TTCCGCCTGA	TGACTACGTT	AGCAATAATA	AAAATCAAAA	CAATAGACGG	540
	TTACAGACTT	AAGCAGTGGA	ACATGTTATT	TAATTCGATA	ATCCTCGATA	AATCTTACCA	600
25	TTTTTTGAAT	ATTTAATTAT	AATAATTTAT	AATTAATTAC	AGGCGTTACA	TAGTTGTCTT	660
	CAGTTCGTGC	TGCAAAGTTT	TAGAATTTAT	CATAAACGAA	CATAACTCTA	AATATTTT	

## 1623RP

30	GATCACAAATC	GCATGGTATG	ATCGTTTTAG	AATCAACGAA	ATATGACAAA	ATGAAGGAAC	60
	ATATTGCCAT	AAGGACTTCA	GGTATTACAG	TCGCAGATAT	TCTATCGAAG	TCCACTGAGT	120
	ATGGTTTAGT	ACCTATACCA	AAAGAACAAT	TTGAACAGAT	TAAAATGGAA	TTAGAGCATC	180
	CAAAGTTTAC	TAGAGAGATG	ATTGTTGACC	ACGCTGGTGA	CTTCGACTTA	ATTGCAGTGG	240
	AATTAAAGGA	ATACAATCGC	CTCAAAAAGC	AATCGCAGTT	CTCCTTTGGT	GACATTTTCG	300
	ATAGCATTAA	CACTGACGAG	GAAAGTGAAG	CATCTGATTT	TGAATATCAT	GATGACGAGA	360
35	TAAAGCAGCT	TAACAAGACA	GCCAAACGCT	TTGGGTTATT	ATGTATTCCA	GAAGCTGCGT	420
	TTATCGCTAC	TTCCGTCGCT	AGCACGCCTG	ATGTCGATAA	TGTCGTCGTG	CTACCAATAA	480
	GCTACTATAA	TAAGTTGATT	GCGAATGAAG	CAAAGAGCCT	CGAAAAGCTG	ACTGACTGGG	540
	ATCTTCAGTC	AGAAGCTAAA	AAACGTGGCT	ATCATATAAA	TTTCAGCTTC	CAGAAGGAGG	600
	ACGCCCCACC	GCCGCCCTCA	ACCCATATGC	CTCCACGGAT	GCCGAAGTTT	TCCCCAAAAC	660
	CGTTCGACTT	TGTCACATGA	CTCAAAAAC	ACTAGAAGGG	CGTTTAAATGA	GGCTGCTACT	720
40	GTGCGCGCAC	AGAGCGAATT	TGAACAG				

## 1623UP

	GATCAGCGCA	AAACACATCT	GTATTCCAG	CAGCATGTCC	TCCTCCACCT	GCCGCATGGC	60
	CTGGCTTGCA	AAGCCGTCCA	CCTCGCCGTC	AAATGAAATG	CTGTCCGGAA	TATTCTCCAG	120
5	TTTCGCAACC	ACAGGGTTCC	CGTGCTCGTC	GTACTCCTGT	TCCTCATCCT	CCTCACCTGC	180
	CTCGTCTCCG	CCGCGCACGT	CCCACGGCCT	AATGCTCAGC	TGCGGAGCCT	CCTCGGGATA	240
	CCGCTCCGGC	AGCGTAATGT	CCACCACCAA	GTGCTGCTCC	TTGCTGATCG	CAGCCGCCGT	300
	GAATGAAGAG	CTTGCCAGCG	GGATCAGATC	CAGTTTTAGG	TCCACTTCAA	ACTGGATTTT	360
	CGGGTACTCC	CCGCACACCA	CCGTCAAGTC	ATCGGCATAG	ATGGACTCAA	GCACTTCCAG	420
	CTCCTGCTTT	TGCTCCTCCT	GATAGTCCAT	ACCTATCCGC	TCGACCAACT	ATGAGCCAC	480
10	GCGCAGCTTA	GGGCTAGACC	GTTACAGCTG	CAGGTGACCG	TCCGGGGGAC	GATGCGCTAT	540
	CGCTGGCGAA	ATTTTTCGCC	TATACCACCA	CTTATGTTAC	CCGGTCTATA	GTGCTGCTCT	600
	CCGACCTCAC	TGATGGTCT	GTCCCGCGGG	GACTGCTGCC	TCGTGCGGGC	AAATCCCCAC	660
	CGCTCTGAAC	GCTCGTTCCA	TCTGCGTCAC	GGGTTGACCG	AACGGGAATT	GCGCGCGCCG	720
	AGAAATCTTG	GCGAACCATG	CTGCACTTAG	CCTTACTG			

## 1624RP

	GATCGCACGT	CATTTTACCT	ACAGGCTGGG	CTTTTGAAGA	AGACGCCTGC	ATGGTACAAT	60
	GTCGTAGCCA	GGATCCCAAC	TGTGACCAAG	TTCCGCCAGAG	AACCGAAGCT	GCATGACCCA	120
	GTTAGCGGCA	AGTACAAGGG	CGAGCTGGAT	ATAATGACGG	ATAGATTAAA	CAGAAACACA	180
20	GAGACGTACA	AGACACGCGC	TGGGAGTTCC	GACCGGCAGA	CGGCCGCGGT	GCACAAGCCT	240
	TCTAAGCTGC	GGTTTATCGA	GGACAAGCTG	CGGTGCGTGT	TTTTCCAGCA	GCATCCTGG	300
	GAGCTGTGCG	GGCCGAAGGT	GCTGGTGGAG	AACATGGGAA	ATGAGCAGTA	CGACTGGTGC	360
	CGGATGTTGC	AGCTAGGCAA	GCCGCTTGAC	GGTGAGTCTG	TGGTGCAGCG	GACGCTGTAT	420
	CTGCTGAAGT	CGGGCGCGCA	CCGGGAGATG	CTGGCGGCAT	ACGACCAGGC	GCGGTTTGAG	480
	TTCTATCGTC	TGAGGATGCA	GCAGGAGCTG	GAGGAGCAAA	TAGCGTACGA	GGAGGCCACG	540
25	ATGGTTGGCG	CTGTGTTCAA	GACAACCGCT	GTGGAGCACG	GTCTGCAGCA	AGAGCAGAAG	600
	GTCTCGACA	AGTGAAGGA	GGACGTGGTT	GCGGGGTTGC	AGCTGATGTC	TGCGAAGAAG	660
	AACCTTACAA	AGCAGTCGTG	GGCCGAAGCC				

## 1624UP

	GATCATATAT	CTTCCTGTGG	TAAGGTCTGT	GGGAAGCAGC	TCTCCTGCGG	GAATCACACT	60
	TGTCCCATGA	CTTGCCACGA	TGGTAACTGC	ATGGATCCAT	GCCTCGTTAT	AACTGAGCAG	120
	AAGTGTGCAT	GCGAACAGAG	GCGTTTCCTT	GTTCTTTGCC	AGTTCCCCCA	TTCCCCAAGT	180
	TGCACGTCAA	AATGTGAATC	ATTGATGTCT	TGTCGTGCGC	ATCGGTGCGC	TGAAAGATGC	240
	TGTTCCGGTA	GACCGCATTC	TGTCAAGCGG	AACTCTAGGC	GGCGCCGTGA	GAGTCCAGAT	300
35	GATGAATCTG	AAGTTGAGGC	CCAGCACGTG	TGCTTAAAAG	ATTGTAATCG	GGTGCTGCTT	360
	TGTGGTATCC	ACATGTGCAA	TTACAAATGC	CATGCAGGCA	AATGTCCTCC	CTGCTTAGAA	420
	TCAGATTCCA	ATGACCTTAT	CTGTCCCTGT	GGTAAGACAA	TCGTACCAGC	CCCTGTCCGT	480
	TGTGGAACAA	AGCTCCCTCG	CTGCACATCAT	CCATGTGCGA	ACTCGCTGCT	GGATACTTGG	540
	CCCTGCGGAC	ACAGTCCACC	TTGCGATAAT	TGTCATCCCT	TAGATGAACC	TTGCCCCCCA	600
	TGTACCATCA	CAGTCAAGAA	AACCTGTGCG	TGCGGTAAAA	ACGAGATCAG	GACATTCTGC	660
40	TACAATGATG	ATGTGTCGTG	TTCGAGACCG	TGTTAGAAGC	CATTGTCTTA	TTGCAATCAC	720
	TTCTGCCAAG	TTCCCTGTCA	TT				

## 1625RP

	GATCAACTAC	GAGGACTTGA	CGACCGCACG	ACGGGAGCTC	GCGGCCGCGC	TGGCCACTTT	60
	GGAGAATATG	TAGCGCACAA	CATCAGCAAT	GTTACAGTAC	AGACGTCTAT	CCGTGGGGTA	120
	CGGCTATGAT	GAATAGAAAT	ATATACACAG	CTGCCTGCAG	GCAGCTTAGA	AGCGCAGAGG	180
	CTTGGGCTTC	TCCCACGAGT	ACTCCTGGTT	AGTGAAGTGC	CCGTACGAGG	CGGTAGGTAG	240
	GTAGATGGGC	TTGGCGAGGT	CGAGCTCTTT	GACAAGAACA	CCTGGTCTGA	GGTCGAAGTT	300
	GTTGCGGATG	ATCTCGATCA	GCTCGTCGTC	GGACTTGGTG	CTGGTACCGT	AAGTCTCGAC	360
50	GTGGATGGAC	AGCGGCTCGG	CAATACCAAT	GCGGTAGGCA	AACTCAACCT	GCACACGCTT	420
	GCACAGGCCG	GCGGCCAACA	GCGACTTGGC	GACCCAGCGC	GCAGCGTACG	CAGCCGACG	480
	GTCGACCTTC	GAATAGTCCT	TTCCGGAGAA	CGCACCGCCA	CCGACCGCGG	CGGCACCGCC	540
	GTACGCGTCA	ACAATGATCT	TTCTACCGGT	CAGACCTGCG	TCACCTTGTG	GCCACCGATC	600
	ACGCTGCGGC	GCTGCGCTGC	AAGTAAATCT	TGCTGTTTTC	GTCTAGCATG	TGCGCAGGCA	660

55	TGACCTTGCC	TACGATGCGA	TGCGCAACG	CGGAACGCAG	GTCTCGGTG	GAGATGTCGT	720
	CCGCG						

## 1625UP

	GATCTGGCTC	TGCGCCATCC	CAAACAACCT	GGGTGTTGAC	AAGAAGTACT	ATGATGAGCA	60
	CAAGAAGGAA	TGGGCCATGT	ACCAGGAGAT	GATGAAGCAC	TATGCCAACG	AGGACCTTGT	120
5	CGACACCAAC	ATGCAGGGCG	GGTTTATCGT	CGCGCCGCCA	CTCCACGAAA	TAGAGCTGGA	180
	CAACTTCCAG	CTCGGCGTCT	ACAAGGAGCT	CGTAACTAGC	ATGTTCCCTT	GACTTCATGG	240
	AGTCCAGCAT	CGCCCATGTT	TTATGCCCAA	TACTTTTGAG	ACTATACTTA	TATTATATAC	300
	TGATAAACAA	TTTCCCGCGC	TCTCTCACGC	CCACTACTTG	TTCTCCGCGT	AGAAGAAGTT	360
	CACGGCCATC	AACTCGAGGT	TCTTCTCGCC	CGCAAACCTG	CCCACACCCA	CAGGGGGCCG	420
	CTTCTCGGTG	TAGCCCCAGT	TCACGCGACT	CTGCAGGCGG	GTGACCTCCT	CCTCGCTCAG	480
10	TTCTAGCCGC	CCGGGCTGCC	GAAACAACAA	CCACACGTAC	CGGTGAGCCC	CTGTGCCGGC	540
	CGGCGGCGCA	GGGCCCATGT	GCTCCACCTG	CGGGGTGCCC	TTTAGCACCA	CGTGCGACAC	600
	CCCGTCATCC	GAGCCCAGCG	TTATGTTTCGT	TTCCAGAAAG	TGGCAGTATT	CCGACCACTT	660
	GTGGTCCGAC	CGCGAGGGAG	CATCTGGGTC	TGTCATCCCC	AGCGTGAATA	GGTCCCCCTC	720
	CTGACG						

## 1626RP

	GATCCGTGGG	GACCATGCGC	AGATGGCGCC	CTTAATATAA	GCCCCCTCCTC	GCAGGCATGA	60
	CGTCTGCCAA	CTCCGACCAT	TCTAAATGGC	CAGCTGCTGC	TTTGATGGTA	GCGTCCGCGG	120
20	CTGGCGCAGA	AGTAAATATA	GCCATTAAAT	CCCCTTCTAA	ATATACATTA	CATACCAGCG	180
	CTCCAGAGGC	GCTCCCGAGG	CGCTCCCGAG	GCGCCCCACG	TCTCGCCGCA	GCGACGCCGC	240
	TGCGAGCTGG	CCCTCTGGCC	ACGCAACAT	GCGCGCCGAC	GCGCCCCAGT	TATATACAGC	300
	CTGGCCTGTC	TCATATGCAG	ATGGGTCTGA	GCGAAAGAAG	TTCTCTGCTC	TCCGAGAAGC	360
	AGTCGTCTGT	ACCCTCGCGC	TCCGCGCCCA	ACCGCGCAGC	AGAGAATCTT	CCAGCGCTTC	420
	CCGCCGACCC	GCACTCGGCG	TACCCGTGCA	GCTAAGGATA	CTTCGCGGCC	GCCGCGGCAC	480
25	CACCGCCCTC	AGCCTGACTT	GCGCAACGCG	CATACGCAGA	GGACCCGCCT	GCTTCCGCGC	540
	TTTCGTGCCT	GTGCACGTGA	TCTCACCGCC	TGCCCTCAGCC	GCCCTCGTCA	ACGATGCGCA	600
	CCAGACCCTC	CAGAGCGTGC	CTTCGTGCCC	AAGTCGGAGC	CCA		

## 1626UP

	GATCCATGCA	TATTTGCGAA	CTTACGAAAA	AAGGCGTGAA	GAGGCGGAAC	GTAATCTAGG	60
	TTTGGAAGAA	TTAATGAATG	ACAACATAGA	CCTTGTTACA	GGAGAAAATA	ATGAAGAACG	120
	CCAGCTGAAA	CAAAAGAAGT	TGTTAGAGGA	GCAGTTGGCA	AAGTTGGAGA	AATCAAAGGA	180
	AAGACGACAA	GCACGCAAGG	CCGCGAAGGA	GAAGAGCAAA	GATGGCAAAG	TCGTGAAAGT	240
	AAAAAACACC	ATCGCAGCCT	GCGCAACATG	CGGTGCGATC	GGGCATATCA	GAACATAATA	300
35	ATCCTGCCCC	ATGTACAATG	GTGGCGTTTG	AGCAAACGCA	AACGCAAACG	CGAATGCGTC	360
	GAGTGCAGCA	GCTGCAGGTT	CTTCAGGGAT	GGCCTCAAAT	AATAGCGCTA	CCAGCAAGTC	420
	TATAACTCCT	AATGCCAGTA	TTCCGCCGAC	TTCATTGCGA	TAGCTCGCAG	TATAATATAT	480
	ATCTAATATG	TACCAATTGT	ACTTCTTTTC	ACTGCTATAG	AACTTTCTCC	TCTTCTTGCA	540
	TCACATGTGC	AGCACTGCAG	CACCGTGCGC	CTCGCAATAC	TTATGGACCG	CGGCACGGTC	600
40	GGCCTCGTAT	CCAGCGTACG	CTATGTATCC	TGCGGGACCC	TTATTCTGTG	GCGACACGGG	660
	ATAGTGCACA	GACTCCACAG	AAGTGTCTCT	TACAATGCAG	AAGA		

## 1627RP

	GATCTTCCTT	GAATTTACTT	AGCAGCTCGT	TAATTTCTCTG	CTTCTTCTGC	TCTCTAAGCT	60
45	GGAATCTGTA	AAAGTCCTGC	TTGGCCTTCT	TGTCCACCAT	GCTGGGAGGC	TTCTCCTTCC	120
	GTGTATGCTT	AAGAAGTGGA	TTGCGGTTCA	GAATCCTACG	CCTTATGGAG	TTTAACGATT	180
	TTGTGTTCTT	CCCTACTACA	AGTGTGAACC	CGTCCCTCGT	CACAATACTC	GATTGAACCT	240
	CATCCTGCGC	AAGTTGTTCC	CGTTGCTCAA	ATAACAACAT	ATGCTCGTGA	ATGTCGCTGC	300
	GCAAGTACTC	AAGGTCGAGT	GGCTTATAGA	AGCTCTGGAA	GGTCGCTATC	GAAGGAGACT	360
50	GGAACGCCCA	CTCCACCAAT	TCCTTTTGT	TGTGCGCGTA	TTTGCGCAGA	GCAGCCCAGC	420
	AGTTCTCCAG	AGATGCCTGG	TCCACAAACT	TCAACAGAGC	ACTGTTTCTC	GGTGTATACC	480
	TTCTGTCTTC	CGCATCCCCG	GTGTCTCTGA	AATCGGACGT	CAGCGCACCC	AAATCCACCT	540
	CGTGCAATCC	GAATCGTCCG	TGATGTAGCA	GCTCTGCCAC	ATGCGCCACA	GTCTCGTACT	600
	GCGCGCAAAT	CCTGCCAAAG	CTCTCCTTGA	TAGAGTCGAC	CTGTGTCAAC	AGAGGTAAAT	660
55	TGACAATAAA	CAGGCAATTA	GCCTCCGATT	CCACCTTCGT	CTGATGCTTC	CTC	

## 1627UP

	GATCTTTGAG	ACGCGGCCTG	GAGAGTTTAG	AGCAGATTGT	TGACCAACGC	ATAGCAGATG	60
	CTAGACCCTGA	GTCATACACC	CTCCGTCTTG	TTGGAGACAC	GGAATTGCTA	AATTCAAAAA	120
5	TAAAGGAGGA	GGCAGATGAA	GTGATTGAGG	CTATAACGCC	AGCTGAACTA	CAATGGGAAG	180
	TTGCGGACTT	GCTGTATTTC	CTCATGGTTA	AAATGAGGAG	CAATAATGTG	ACTTTAAAGG	240
	AGGTGGAAGC	CAACCTAAAC	ATGAAGCACA	TGAAGATTAC	GAGACGGCCT	GGAAACGCGA	300
	AACCAAGTA	CCTACCCGCG	CAGGAGTGGC	AGAAGAACAA	GGAAACTCCT	GTAGATATTG	360
	CACCATCTGC	CATTTACTTG	AACGTCGTAT	CCTCAGATGA	TGAGGCCGCA	TTGAAAACAG	420
	CAATTACAAG	GCCAATTTCAG	AAAACACTG	ATATATTAGG	TCTTGTGAG	CCTATAATAA	480
10	AAAAAGTGAT	AGAGGAGGGC	GACAATGCGT	TGACTGAAT	AACAGCGAGG	TTTGATGGAG	540
	TAAAGATAGA	AACACCAGTA	CTAGAGGCTC	CTTTTGCGCA	CGAGTATTTA	AAAGGATTAA	600
	CGGAAGACGT	CCGTACGGCC	ATAGATATTT	CGATGGAGAA	TGTCCGTAAA	TTTCATGCCG	660
	CACAGCTGAG	AGACGATATT	CTCAAGGTCG	AAACGCAACC	GGGGGTGGTA	TGTACGAGAT	720
	CCCAGGCCA	TAGAGA					

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## 1628RP

	GATCTGCCCC	TTTAAGCAAC	CACATATTA	GCCGCTGACA	CACAGACTGT	CAGCGCTTAG	60
	AAATACTTCG	GTGAGTGTTT	AGAAGCCCC	GCGCTCGGAG	TTATTCATGA	TCACGTGATG	120
20	GGTATTGACC	TTGCGATCCA	CAGACAGGCG	GAAATATGCA	TATATGTAAG	CCAAGATGCC	180
	GGCAACCAAT	TGGTCTAACT	GTAATGCATA	ACACTGTATT	CCGCGAAGCG	GCTCTGAGCA	240
	TGTATGGTAT	TCGGCGCTAG	ATTGTCAGCC	CACGTATATT	TCCACGTGAC	GCCCTGATGC	300
	TATTTACAAC	ATAATCACTA	TTGACGAGCA	AGGATAGTGG	TCGCACGTTA	CGAAAAAGAA	360
	ACGTTGAAAA	ATTTGGATGG	TGGTGATGAG	GATAGAGATAT	TAACGTAAAT	GGCGGAGCAC	420
	GAATTTGGTC	GAAGTTCTAT	ACTGCCAACG	ACGTTTCGAG	ATTGCTGAGT	TGATGGGTTC	480
25	CAAAAGTATT	AAAAAGGCGG	TAGTCCCTAA	ATTATCGGAA	AAAGCCAAGG	AGGAAGAGTT	540
	GAGCACTTCG	GGCTCCTCTG	ATTCTACTTT	AGAATCAAGT	TCATCTTCCT	CGTCGGAGGG	600
	CAGCTCCAGC	AGCAGCTCTA	GTTCTCCGG	ACAGTGAATC	GAGCTCGTCG	GACAGCGGCT	660
	CCAGCTCTTC	TAGCAGCAGC	TCGAGCTCCT	CCGGCGAATC	GGGCTCC		

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## 1629RP

	GATCTCCAC	ACTAGGCTGG	GTCTTACTGT	CCATGAATAG	CATTGGAAGA	ATGGAGGAAT	60
	CGGTCTTCAA	GTCAGCGGGG	AAATTTTCAG	GGCAATATAA	TGGTTCCCAA	GTATTTAGAA	120
	CTTCTCGACT	GTCGTACAGTA	CTTGGCCCTT	TTAAATCGGC	TGTTCCCTTT	GAAGATATAC	180
35	ACCATTCATT	CCAGTGATAT	GTACCCGAAA	AATTAGCAGT	AATGGCACTT	GGAACATCAT	240
	CCGGAATCGT	GTAAGCACTT	GCAATAACTG	AAAGCTTTGT	AAGAGAGGTA	AAAATCGGTG	300
	CCGCGGTTCC	AAAATTGTCC	AATTGTGAGA	TTTGTGTGATC	TTCATTAGGC	CTACTGGCCA	360
	GTTCCACTAG	TGATCTAACG	GGGCTTATTT	CAGTGGTTAG	AAATTTATCC	TTCTCAGTTT	420
	TCGACTTACA	AGCAAACTCA	GTGAACAAAG	GGGGGTATCG	ACGAGCAGCT	CTTGTGTAA	480
	CTGCTGAGGT	TTTCCCCTGT	GAAATAACAT	GTTCTTTAGT	TTTATGTAGG	GCTCCAAATC	540
40	ATGCCGTTAA	CTCTTTTATA	CTGGTTGCTT	GGAAATTTAA	AGTACCAGAG	TTATTAGAAT	600
	ATTCTTCCTG	AGGTGAAGAA	GTTAATGGAG	AAGAGATAGT	CATTGGAAG	CAGTATTTAC	660
	GTGCTCTTTC	TGGATGGTGC	ATGGCACTGA	GTAATAATAC	TCCAAATCTG	TCCGTTTCTT	720
	CGACTGCAGT	TTT					

## 1629UP

	GATCTCGGCT	CGCTGCTCGC	GCTCGAGCCC	TACTGGGCAG	AGCGCTACCC	AATAACAAC	60
	GCCCTAATCG	GCGGTGCAGA	TAAATTGCAC	AAGCTCTACT	CAACCGATT	TGCGCCCATC	120
	GTCGCCGCCA	GGACTTTCGG	CTTGAACCTC	GTCGACAAGC	TTGGACCGCT	GAAAGACCTC	180
50	ATAATGGCAA	AGGTGAGCGG	CCCAAATTAA	TAGTCACGTG	TACATAAAGG	TTTTCTTAAT	240
	AGCTATACAG	CTTGCCCGCG	TCCTCAGCTT	GCAGCGCGCA	ACCGGCGTGC	AGCCATGAGC	300
	GTCCTACTGG	AAACTACCAT	TGGCGACCTT	GTAGTAGACC	TGGACTACAA	GACATGCAGC	360
	GCCGAGAGCT	CAAACTCTGC	CTCAGCACGC	CTCGGCGATC	CACAGGTGGG	CTTTGCATT	420
	TACGACCTCC	ATCCTGAAGG	CAATACCTCG	ATCGAAGGCC	TGCGCGACAC	ACGGGCGGTC	480
	CGCACGGATT	TGCTGTACAA	CTCCGTGCCC	GCTCAACCCG	CAGAGCGCTT	CGGACAGGTC	540
55	ACCCCGAAGC	TCATTGAAGC	CTCCGTGCCC	CTCCGATGCA	AGCTATGCTG	CGGCGCTTAAT	600
	AGCTATGCTG	TCATTGAAGC	CTCCGTGCCC	CTCCGATGCA	AGCTATGCTG	CGGCGCTTAAT	660

EP 0 866 129 A2

CCCGAACTCG GCCCCACATC AACACAGTGC GCTTCGCGCA GGTCATCGAC GAGTCGCTGG  
CAGTTCTGCA GCAGCTCAGC GA

720

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## 1630RP

	GATCGACTTT	CAAACATTAT	TATACAGATG	GAGGGCATCT	CACATCTTGC	ACAGCAAGAC	60
5	GGCAATCCAA	CAGGTTCTGT	AATGCAGCCT	AAGAGGCGAA	GGGTTGAAGA	TGGAGCGTCT	120
	AGTGATGGAG	AAGTACGAGG	AGAGATAAAG	CGCAAGTATG	GTATTGGCGC	GCAGTTGATG	180
	GCCAAGATGG	GATATAAGGA	GGGCAGCGGT	CTAGGGAAAG	AAGGTACGGG	ACGCACGACG	240
	CCGATATTGG	TATAGCAGCG	GCCGCAGGGC	ATGGGGCTTG	GAGCCAACGT	CTCCATTTCC	300
	TCTGACTCAG	AGCAGAGTGA	GGTGGAGCTT	GTGACTCGCG	AGGCAGTGAA	GTTTGAATCG	360
	AAAGGTGTGG	AGACTGACAC	AAGCAGAATA	GCAGACAAGA	TAGCAAAGCT	GGAGATCGCA	420
10	GGAGTGCAAG	TCCCCGCAGA	AGTGATGAGT	TTGCGTTCTG	GGACAAAGAC	GCTGGGTTAC	480
	CAACGGGCTG	CAGCGATGGA	AAGGGTGCTC	TCCGAACTGC	TGCAGGTGGG	TGAGCAACTT	540
	CGGACCCTAC	AACTACGCGA	AGATCAGCTG	CAGCAAGGGC	TAGATGCGGC	CATTCAAGAT	600
	AGTGACCTGT	TGAACAAGTT	CTCAACGCGC	TGCAACAGCC	GACTGCGCTG	CCGGAGCGGG	660
	TAGCGGCATA	TTGGCCTTGG	AGGACCCAGA	AA			

## 1630UP

	GATCGTCGCC	TCATCGGTGA	GCTGCGCCCC	ACGGGCGAAC	CTGGCAGCCT	GCCCCGCGAC	60
	CCGCGCGCGG	TGGGCGACCC	GCGTCCAGTC	GGCGAGCCCC	GTGGTCCCCG	GACCATGGTT	120
20	ACCGTATCGT	CCCCGACAAA	TGGCGAGGGG	TAGATGATGC	CCTCCTCCGC	CTCCGGCGTA	180
	CCGCGCGCGT	CCGGCGTGTG	CGCCTCCTCT	GTCCGGCCTG	GCCGCGTCCC	GTCCCCAGAC	240
	AAACGGTGGC	CGGCGCGGAC	CCCAACGCGC	AGGCCCTTCG	CGGGCGGTGG	CGGCGGCGCG	300
	CGGCTCCGCG	CTCCGCCAAG	GCCCTTGCCC	TGACCCAGTC	CTGTAGGTCT	CTCGTGGTCA	360
	TCGAAGGGCG	TCCAAGCAAT	TCGTGTACGA	TGATCTATGC	CAGCCGCAGC	CTTCGTCACC	420
	AGCGGCGGCA	GCTGCGGCAG	CTTGGGTTTG	GTCTCGTCCA	TATCGTGGTC	TGGTCTCTG	480
	TAGGCATCAT	ACATCTCCCG	CTATCTTTCT	CTTGCGCCTG	CACCGGTACC	GTGCATTGGA	540
25	AACGCTGCTC	CTGCCCAGAG	GCAGTTCTAT	AACGTTGCCA	GTGAAATCG	TGCAGTACGG	600
	AACAGTAGCT	CATCGCGCAC	CAGGCGAACA	CATAGGCAAC	AGCTTCGGTG	TAGCGGGCTG	660
	CGGGCCCCGAC	CACGATACTC	ATGTTACATA	GACTCACATG	ATCAGGCAGC	AC	

## 1631RP

	GATCTAATTT	ATTTACATTA	ATTAATAATT	AATAATATTT	AATAATATTC	AATAATTTAT	60
	ATATTTTATT	ATATTTAATA	ATTATATAAA	TACTTTTAAT	ACATAAATAC	TTTAATTAGA	120
	GAGTTAGGGT	TCACCCCCCT	AATGCTTATC	AGCATTATGA	GGTACCACCT	TAATTAAAGG	180
	TAAATATATA	TATTTAATAA	TAAAAGGATA	TAGTTTAATT	GGTAAACTA	TTGACTTCAA	240
35	ATCAATCATT	AAGAGTTCAA	ATCTTTTTAT	CCTTGTTATA	TTTTAATAAT	ATAAATTAAT	300
	AAATAATAAA	TATGATAAAT	CATAATATTA	AAGATATTGA	TTAATATTTT	TAATTAAATTA	360
	AATAATATGC	AATTAGTATT	AGCAGCTAAA	TATATTGGTG	CAGGTATTTT	AACAATTGGT	420
	TTATTAGGAG	CAGGTATTGG	TATTGCTATT	GTATTTGCAG	CTTTAATTCA	AGGTGTATCA	480
	AGAAATCCAT	CAATGAAAGA	TACTTTATTCT	CAATTTTGCTA	TTTTAGGTTT	GCTATTAGTG	540
	AAGCTACAGG	TTTATTCTGT	TTAATGATTT	CTTTCTTATT	ATTATATGGT	GTTTAATTTT	600
40	ATTAAATTAT	ATAATAATTA	ATATTCAAAA	TAAGTTATAT	TAGCTTAATT	GGTAGAGCAT	660
	CCGTTTTGTA	ATCGAAAAGG	TTAGGAGTTC	AAATCTCTTA	TGTAACAATT	TAATTAAATT	720
	AAATAAAGA						

## 1631UP

	GATCTTAAAA	TAAGATAGAA	TGGTAATAAA	TATCATTTCAG	GTACAATAGA	TGCTGGTGTT	60
45	ACTAAAGGAT	TACCTGGAAT	ATAATTATCA	GGATGTCCTA	AAGTATTAGG	TGAAAAGAAT	120
	ACAAAATAATG	AAAAGAAAAT	TATAAATACA	AATACTGTTA	CTAAATCTTT	AAAAATAAAA	180
	TAACCATGCA	TTGGTAATCT	ATCTAAATTA	CCTGTAATAC	CTAATGGATT	TGATGAACCA	240
	TGTACATGTA	ATAGCATTAA	ATGCATAATT	ACTATTGCTG	CAATAATAAA	TGGTACTAAA	300
50	TAATGAAATA	GAAAGAATCT	TATAATAGTA	GGATTACTAA	CACTAAATGA	TCCTCATAAT	360
	CATAGTACAA	TATCATTTC	AATAAATGGA	ATAGCACTAA	ATAAATTAGT	AATAACAGTA	420
	GCACCTCAAT	GTGACATTTG	TCCATATACT	AAACAATAAC	CTAAGAAAGC	TGCTGCTATA	480
	GTTAAAATAA	AGATAATAAC	ACCAACTGTT	CATACAATAA	CTCTAGGTGA	TTTATAAGAA	540
	CCATAATATA	AACCTTTACC	AATATGAATA	TACATACAAA	TAAAGAAGAA	TGAAGCACCA	600
55	TTAAGATGCA	TATATCTAAT	TAATCAACCT	AGTTGTACAT	CTCTCATAAT	ATGTTCTACT	660
	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	CTAATCTAAT	

## 1632RP

	GATCTTCGCG	CCGTTGCGGC	CCAAAACCCG	CAGCTCCCAT	ATACCCGTGT	TCAGGTTGAA	60
	GCTGATGCTA	GCGTGCTGCC	GCGACACCAC	TTTCGCAGGC	CCCAGGTGCA	TGTGTACTGA	120
5	CCGGTCCCTGC	GGAGACGTGT	TCCGCCCGAT	ACTCGTCATC	ATGTCCTTCA	CGTAGTACGT	180
	CCAGTCTCGT	CCCAGATATCT	TGGCGTACGC	CTGTACTTCC	GTTGCCGTGT	TCTTGTCTGT	240
	CGAATATACT	TGCGACACTG	TCGTGCGCTC	CTTCGGCGCA	TCCAGCACCG	AAATCACCCG	300
	ATTGATCACG	TCCTGTCTCC	GTTAGTACTC	GGTCTCGTGC	CGCCCGTCTC	GCTCCTACAT	360
	ACCTGCTGGT	GCTGCTGAGA	CGCAAAATGGG	TAATTCATCT	CGTCGCCTCA	ATTTCTGCTCC	420
	TCCACTGGCT	GCCCCAGGGT	AACGTCGGAC	TTCCGTTGCT	GTGGAAGGGG	TGGTCGCTCA	480
10	GCGTAGCTCG	GTACAGCTGA	TCTCGGTCCT	AGTATCAACA	AAGCAAAAAT	AAAAATAATA	540
	ACAATAAGCT	TTTCACTGTG	TGTGAACGTC	CCAGAACTG	ATTCCAACGC	TCCAACACCG	600
	CACTTCTTGA	AGCAACCTCA	CGCACCCCTC	TGAATGACAG	ATCACCCCTCA	CTAAACGG	

## 1632UP

	GATCGAGACT	GTGATATAGC	TGTATAAGAA	GGTTTGAAA	CCTTAGTAAA	TACCCAACTT	60
	TTTTAATTCG	AACCTTGTTAC	AGGTTTTTATA	CTCAATTGTA	GCTTTGAGTT	GCAAATACCC	120
	GAGGCATAAA	ATCAAAGCGT	ACTTAAAAAC	AATCACTACA	TACAGTCCTC	CACACCCCTGC	180
	CAGAGTGGAA	TAACATGAAG	AATAAATATT	AAGGACAGTA	ATGCTATAAA	TACATGTGCT	240
20	TCAAATAAAT	ATATGCTTGC	TAAGGGTTTT	CAAATTCGGT	TTGCGGCAAA	GAGTACGCCA	300
	TAAGTGGATC	TTGGGAAAGT	GATGGGGGCA	GATAACGACC	AAACAAGTGA	GTTTCCACGT	360
	TACCTATATC	TTCTCTTGGG	ACAAAACCTGC	CACGTGTTGAC	CATTGTTGTG	CTAGGTGTTT	420
	GATGTATGGA	TGGAGTATCA	GCACGTCCGG	TAGAGGAAGT	GGGAATTAGT	GAACTAACG	480
	TCCCGGAGAA	ACTGGATGCC	ACACGATTGT	TTGGTAGTGT	GGGGGGCGTG	TTAGGATTTT	540
	TAATGTTGGT	TACTGGGGTG	CCTGATGGCA	ACGATGGGCC	AGAAAAGTAT	ACTTGCTCCT	600
25	GTGCTTTCAA	AGATGGGTCA	ACAGCCCAAT	TGTGAAAGAA	ACTGGCATT	CTAGTCTCAG	660
	GGATGCTAAT	AAGCTCTTGG	ACAGAGTTGT				

## 1633RP

30	GATCAATTAA	TAAATGGTTT	AACTAATAAA	GTAAATAATA	AATCTATTAA	TTATATAAAA	60
	CTACCTGATT	TTATTGAATC	AAATAATATT	TTCTTAATGA	ATACTACTAA	ATCATCATCT	120
	ATTGAGTTTA	TATTAAATTC	ACCACCTCTT	ATTCATTCAT	TTAATACTCC	TCTAATTCAA	180
	TCTTAAATA	TTCTTAATTA	TTAAATTATA	TAATAAAAGT	TAGTGGATAT	AGTTTAATTG	240
	GTAAACATA	TGTTTTAGGG	ACATATATCT	TCAGTTCAAA	ACTGAATATC	TACATATTAT	300
	ATCATTAATA	TAATAACTCT	TTAATTAGAG	TGGTACCACA	AGAATGCTGA	AAGCATTAGG	360
35	GGTGTGTACC	TTAGCTCTCT	AATTAAAGTT	ATAAAATTAT	CCTAACTAAT	AAAAATAATT	420
	AATTAAATA	ATAAATAATT	AATTAAATTT	AAAAATGTTA	AAAAAAGAAA	TAAATAATAT	480
	GTTATATTTA	AATAGATCAA	AATTTCAACA	ATTTCCATTT	CATTTAGTAC	TACCATCACC	540
	ATGACCAATT	GTTACATCAT	TTAGTTTATT	AGGTTTACTA	TTAACTTTAG	CTTTTACTAT	600
	ACATGGTATT	ATTGGTAATA	TTTATCCTTT	ATTATTATCT	TTATTAGTAG	TTTTATTACT	660
40	AATAACTTTA	TGATTTAGAG	ATATGGTAGC	TGAACCTACT	TATTTAGGTG	ATCATACTTT	720
	AGCTGTAAGA	AAAGGTATAA	CTTAAGGTT				

## 1633UP

45	GATCTTAATT	TAAATTTTTA	ATTAACATT	TATAATTTAG	AAATATATAA	TCTAGAGATA	60
	TATAATCTTA	AAATCATAGG	TAAAAATACA	TAAGATAGTA	AGAATAAAAT	TAGTAAAAATA	120
	AATAGAAAAC	CATAAGTTAA	TTGATTCATA	AAGAAAAATG	GAAATTATTTG	TGGCATCTTA	180
	ATTTTATTTA	TTAATTGAT	TATTATCTAT	TTAACATAAA	ACATTTTAAA	ATGTTATATAA	240
	ATAAATAAGA	AATTACTTAT	AGAATATTTA	TTAAATAGTA	TTTAAATTTAA	TTTTAATATT	300
	AAATATACCA	TTTTTATTAA	TAAATAGATT	ATTAAGTTTA	TTAATATTAA	GTGATATATA	360
50	ATTTAATTTA	TATAAATTAT	TTAATTTACT	TCATTGATAT	ATATAATTAT	TAAATGTACC	420
	TTTCATAATA	TTTATTTTTA	TTAGTCTAGT	AATATTTCTA	TTTAATAGTC	TACCCTTTAA	480
	TTGGATATTA	CTACCTACTA	AATATTTACC	TAATAATATA	TTATTAAGAA	TACTTAAATC	540
	TAATAATTTA	TTATCTAAAG	TATATAAATT	AATTAAATCT	TTTTTATTAT	TATTTAAATT	600
	ATTATTAATT	AGTAAATTAT	ATTTATTTAT	TTTATTAACA	TAATTTTTTG	ATAATAATAT	660
	ATCATTATTA	AATGGTTAAT	TTATTAATAA	TTATCTTTAA	TGATTTTAAAT	GATAAACCAT	720
55							

## 1634RP

	GATCCATCTG	CGGTTTGTGC	GACGTCTCTG	GAAACTCTAC	CAGGCGAATA	GAACCTCTGAT	60
	AGACGACTGG	CAGGTGTCTG	TTGAGTGGCA	ATAACGGGAT	TTGCATCATC	TATATGGGCA	120
5	TTCTTGGTAG	TATCTATCCT	TAGACTCGAT	AGGGACCCAT	GCTTTACAAG	TTCAGGTTTC	180
	GCTTGGCGGAG	CCACGACATC	CTTTTCTCGA	TTTAGGAATG	ACAAAATTGA	GGAGTTCCCTC	240
	CTATGCTTGT	GTTCAAACCTC	ACCAGCAATG	CTGGCTCGTT	TATTGGTACT	CGCAGATACA	300
	TTCTTTGAAT	GTCCATAGAT	ACTCGAAGAC	GGCCTTCCAG	TGGGAGCTGG	AACGGCCAGA	360
	CTGTCTTGTG	CACCTAGCCC	TTCTGAATCG	TTTGGAGAGG	AAAGCATGGA	AATTCGATTG	420
10	AACAACCTCCA	CAAACGAGCC	ACCCGATTTT	GTCTTCTTAT	GTCTCGCTCT	TATACTCTCT	480
	TCCGGAATGG	CCCTTTCAAA	AGTACGCTGC	ATCGGAGATA	TGCCAGGATT	ACTGTAAGGA	540
	TTTCCAAGGT	CTGGGCCATC	AGGCTGTTTC	TCCACAGCAG	GCTGCATAAA	TACTGTGGGA	600
	TAGATTGCTT	TCTCGAGGAA	GTGTAAGAAG	CTGGTGAGTT	TAGGGTTTGT	GGGCCGTGTT	660
	CGTAAATGGT	AATGTGCTGA	TTCTTGGCTT	GATTCTGCAA	AA		

## 1634UP

	GATCACAGCG	TGGCCAAGCC	CAGCATTTGTG	TCTAAGTTAC	ATGTAGAGGT	CGAACAGCAC	60
	GAGGGAATGC	TTTTTCGCTAC	GGCGGAATTC	GAGACCTTCA	GACTGACACC	GCAGATTTTC	120
	TGTGCGGCTC	ACCGACCCCT	AAATAGCTAC	AGCAACACAG	CTGCGCCGGT	GTACACTGAT	180
20	AGCAAAGATG	AACCGGTCTA	TCCATTCTGT	GGTGACTCGG	ATGGCCTCGG	ACGACGCCAG	240
	CAGTCTTCGG	CATGAGCCGT	CGACGTACTC	GGCGGAGTCA	GAGGAAACGC	TCGTCAACTC	300
	GTATGGGCCC	TACAGCACCA	CGGGAATCGT	GATGACATCT	GTGATGATGA	ACAAGGCCCA	360
	GGCAAGGGC	GAAGTGTCCG	AGCAGTGGAT	GCGGCTCTTC	CTGGACAGCA	CGCCTGTCTGA	420
	GGACGTGGCG	GTGCTGCAGC	GCGGGATGTC	GGTGACGGGG	CGCTGCCTGG	ACACGTTGCA	480
	GGCATCTCTG	CAAAGCATGC	ACGGATACCG	CCAGATCGTC	CCGGGCTTGG	CGATGTTCAA	540
25	AGAGGCATGG	AACCTGCAGT	GCTACCACGG	CAACGAGGCG	GACTTTCCGC	TGCTCGACGT	600
	GCCGATCAAG	GTCAACAGCC	TGACCACACT	GGCCAGCCTG	CTGGTCGAGC	ACCGCGTGTC	660
	CGGTTACAGC	ACGCCGATCG	AGCAACTCAC	CACGGTGCTT	CAGTACCTCA	ACAAGCTGCT	720
	GCAGGCGTCG	CGCGTC					

## 1635RP

	GATCCTAGGG	TGGTTTCATGG	CACCTGAGCGG	GACCGTGTTT	TTGGACCGGT	CGAACCGCAG	60
	CAAGAGTCTG	AAGTCGCTGA	ACGCGTCGCT	GGAGCGGCTG	AAGCGCAATC	GGCAGGCGGC	120
	GTGGATTTTC	CCAGAGGGCA	CGCGGTCTGT	CACAACGGAG	ATGCAGCTGC	TGCCATTCAA	180
	GAAGGGGGCG	TTCCACCTGG	CGAACACGGC	GCAGATTCCG	GTGATTCCGG	TTGTGATGTG	240
35	CAACACGAGC	ACGGTGTTCA	ACCCGCGGCT	GGGCATCTTT	AACCGCGGCA	CGATCACGGC	300
	GAAAGTGCTG	GAGCCGATCG	ACACGGCTAA	CATGACCAAG	GATGACGTGG	ACAAGCTTGT	360
	GAGCGACGTG	CAGGCCAAAA	TGCAGGCGGA	GTTCGAGGCG	CTTGGCTACG	CGCCTGCGAT	420
	CGTGGACACG	AGCCTACCCG	AGGAGGCGCT	GCGGCCGGAG	TTTGTGGACT	GCAAGGAAGA	480
	CATCACGGAG	GTAACGCGCC	TCTTGAAGTA	ACCCTGGTTG	GTATCATATA	AACGTTGCGA	540
	CGAGTTATGT	ACATATAGCG	CTGCTAAGTA	GGCATTCACT	CCCACGAAC	CATACCTGCG	600
40	TGAGCTCTAC	GCCCCGCCGA	TGTGGGCCAG	ATACTTGTCG	ACCTCGCCAG	CGGACCCGAG	660
	CCAGATCGAG	GACTTGTCGT	GGATGTGCTC	GGGAGTAAGG	TCCAGAAATG	CGCTCGCCCG	720
	GGTCGTTTAC	GGCCTTG					

## 1635UP

	GATCGGACTG	ACGGTGAATA	GGCCACCGTA	GCATGCGCCG	CTGAGCGCGC	TGGCGAGCGA	60
	TAGCAGCGGT	CCGTCCGAGG	CTCTGGTGGC	CAGGACAACG	ATCCACTGGC	CCACCACGCC	120
	CAGTAGGAGG	ACTGCCCACT	GGACTGACAT	CGTCGACACA	CCGTTGTGGA	TGCAGAGGTC	180
	AATTATCAAG	CCCACAGGGA	AGCGCGAGCA	CGTCGAGGCA	ATCGCAAATT	CTGGCAGCAC	240
50	CGACGCCTGG	CCCAACAGGC	TGCACAGCGA	GCCCCATGTT	GTGAGGAACA	TCTCCATCGG	300
	GCCCAGCGAC	AATAGCAACA	CAAGGGCCAT	GAAAGTACGC	GCTGGGTCTG	GGAAGAAGTT	360
	GCGCAGCCGG	CGGCGGATGT	CCTGCGGCAG	CAGCGGCTCG	GTGGGGCTCT	GCATGCCCGC	420
	GAAGGTCAGT	GTTGCGGCC	TGACCTTGAG	CATAGTGACG	ATGCTCGTCG	CAAACCATAT	480
	GCAGAGCTG	ATCAGCGTAT	ATGCCACAGC	AAGAGTCTCT	AATACACGAG	AAAGGTCAAG	540
	GTACGGCAGG	CCATTTTCGAA	ACCATTGGTAT	CTTCAGCAGC	TGCGACCCTA	GCACAGACGC	600
55	CTTTCGCGCT	CTTTCGCGCG	CGGAGCTTAT	CGAGCACACG	TTGCTCGCCG	GGTACAGTTT	660

EP 0 866 129 A2

TGATGCGGTG AACAGCGCAC TGAAGT

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## 1636RP

	GATCTTCTTC	TGCTCGATGG	ACGAGCCAGT	TGTATCTTGG	ACTCTACGGA	TAACCCACAC	60
	CTTTTCCTTC	AGCGACAGGA	ACTTGGCATC	GGTTGGGTTA	TTCGGGTATA	GATATAGCGC	120
5	TACGANCGCT	ACCACAAACG	TTAGGCTGCC	GATTATAATT	GACAGAATTT	TCCAATGTGA	180
	GATAGCTGGG	TTCTTTATCA	GCAGGATCAA	GTAGGAAAGG	ACGCCCATTG	GTATGGATAC	240
	ACTGACCGTC	GCGATAACAA	AAATCGGGGC	GGTCGCTGCC	TTTTTCATTCT	CTGTTAAGAA	300
	CATCAGCATT	GTGTTGTTCA	ATGCAGGAAT	GATAATAGCC	TCCGTGAAAC	CTAAGCAGAG	360
	ACGAAGAACA	TATACACCTT	TGTAATCCGT	CATTGCACAT	TGTACCATCA	TAATGATGCA	420
	CCATATCGTC	AGGAGGACGA	TAACAACGTT	CTTCAAAGGA	AACTTCTGGA	TAAACAGCAA	480
10	GTTGATCTGT	CCGGTAATAT	AGCCAACGTA	GAATAAGGTA	TTACCATTGT	TGTAACGATT	540
	CAAGGACATG	TTTACATCTT	CAAAAAATCC	TAACAGAGTG	CTGTAGGACA	ATTGCGCCTT	600
	GTCTATGTAG	GTGATGAAAT	TAATGCTCGC	CGTCAGTCCC	ACGATGTACC	ACATAACCTT	660
	TCGTGCAAGC	TTCTTTTCCT	CGGCTTCTGT	GATAGGAGGG	ACATCCTTGT	CTTGCTTCAA	720

## 1636UP

	GATCCGCAAG	ATGACCGAGG	GTAAGGGCCA	CCTGCTTTTCG	CACCACCGCT	TAGTTTCCTT	60
	TGGAGGTGCA	GGTGGTCAAC	ATGCAGTTGC	AGTGGCACAC	TCATTGGGGCA	TAGAAACCGT	120
20	CCTCATGCA	AGGTACTCAG	CAATTTTATC	TGCGTATGGA	ATGCTTTTGG	CGGATGCGGT	180
	AAAAGAGGAG	CAAGTGCCAT	GCTCCATTTT	CTTGCAAGAT	ACATCTTCTA	AAGACCAGCT	240
	AAATGAAATA	TTCCACCAAT	TGATTACCAG	TACCTCAATT	AGCCTTCTTA	AGCAGGGATT	300
	GGCCGACGAT	CGGCTTGAAT	TCGAGAGATA	CCTGAACTTA	CGTTATGAGG	GTACTGAAAC	360
	AAGTCTTATG	GTTCTACAAG	AAGGAGACTC	GTGGGATTTT	GTAGAAAAGT	TCACAAAAC	420
	CCACAAGCGT	GAGTTTGGCT	TTGTTTTTCG	CGAGAAGAGG	ATTTTAGTGG	ATGATGTCCG	480
25	TGTGCGTGCT	CTAAGTAAGT	CTATGGTGCG	GAACAGGAGC	CTGTTGATCA	GCAGTTATCC	540
	CAGGTCACCT	GTTCTACAGC	TGACCCCTTC	AAGGATGCAA	AGTTCTTTAA	GGACGTGTAT	600
	TTCGTTCGAT	GGTTTATTAA	GACCACCTAT	TTACAGGTTA	GATAGTTTAC	CGGTAGGTAC	660
	CTGTATTGAA	GGACCTG					

## 1637RP

	GATCTGCTCA	TACTGAGCGG	CCAACTGGTC	GTACTCCGTA	TGCAAAACAT	CTGTGGTTTC	60
	CTGGAAGTGC	GCCACCTTGA	GCGATATCTC	ATTAAACTTG	GTAACCAGCT	CTCCCAACTG	120
	ATGATTGACT	GCACTGGTTT	CCGTCAGCAG	GTCCCTCCAGT	TCGCCAGTTC	TGGTGTCCAC	180
35	TTCCGCCACG	TATCCGCTGT	ACAAATGATA	CTCGTCGTTT	GCAAGCCCCA	GAGCAGAAGC	240
	TCGCCGCCAC	TGTGGCGCCA	GCAGCTCAAT	TCAATCTCTG	TTTCAACCGT	TTTCAACCGT	300
	TGCCAACAGA	CTGTCTACTT	TTTGGCGTAA	CGAACTATCC	CCAAAAGCG	GAGGCAGCTC	360
	ATCGTGAGAG	GAGGCACCGG	GATTTGCCGC	TACATCCTGT	ATGACTGAGT	TCTTCCGGCT	420
	CCTAGGCATG	GTGCAGTTGC	TGCCTCAACG	GCTTTCCTTC	TGGTGCAGGT	CTGCAGTGGT	480
	TCGTGCTTAT	GCGCAAGCAG	AATACCATGT	TGAGCCGGCG	AAATCTCATC	ACGTGATCAT	540
40	CATCTTGCAA	CGGCTCGGAG	GACGCTGATG	CACTGTTCCA	TAGGCTTAGG	GCGCAATTAT	600
	ACGCTAGCTA	GTTATATTGA	TAATATGTAC	ATGATGCCCT	CGGCACGACA	GCGCACTCAG	660
	TGCTCGGCCG	CCGCGCCGCG	CTCCGGCAAG	CTCTTGCTCT	AACCTGGGCC	TTCTCGGCCT	720
	CCACGT						

## 1637UP

	GATCTTGCCG	TCCTTCTTGT	CCAGCTGTAG	GTCCGGATGA	GGGTACGCCT	CGCTCAGGTA	60
	CTCCAGCCGC	AGCTCGCCGC	TCTCCATGGA	CGCCTCCAGG	ATCGAAGGCG	CCGGCACAGC	120
	CTCGGAGGGG	AGGGGCGGCT	GCAGGAGGGG	CATCTCCCTG	CGCTCCTGGT	GCATCTGCAG	180
50	CGCCGCAGCG	CTCGGCTCCA	GCGCCGGGTC	GAAGTACTTC	ACATTTCGTCA	GGCCCGACTT	240
	GTACAGATTG	AGGATGCAGC	CCTTGAGCTG	CGCACGGTGC	AACCGGTACG	CAGTCGCGAC	300
	ATACTGGTAC	CCGCTCGTCC	CCCCTCCCGT	GAAGTGCGGC	CGCTCCGATC	CGATCGAAGA	360
	CAGTGACGCT	GTTGGCTGGT	GGCTGTATCG	CCCCTCGCGC	GCCGGCGCTG	CGCCCTCGCG	420
	CTTGTTTACC	CACCCGAGCC	GAAACACAGT	CCCGTCGTAC	GTCTCCCGCT	TCAGCCCGCC	480
	TCCACGTCGC	ATCCGGCGAG	CCGCCGGCTG	CGAGCAGGGC	GACACCTGCT	CCTCGCAGCG	540
55	CGCACCCGCC	TTCATGTCTT	CACATGTCAG	CGTCCGCTTG	TGCGCTTGCC	CCGTCCGGC	600
	CTGTAAGCTG	ATCCGGCGCT	GTGGCTGCTG	CTGCTGCTGC	TGCGTGTGCT	GTTGCGGTTT	660

GCCTGTTGGC CTTGTTGTGT GTA

## 1638RP

5	GATCCTGTGCG	CTGGAAATGT	CGCGGACGAG	AACAGACAAC	CGTCGGGGGC	GGGCGGATCT	60
	GCCGGAAGCT	GTCCGAAGGA	GACCAAGAAG	GAAATTGTAA	AGCTGCAGCC	AGCGCCGATT	120
	CCACAGAACT	CTCCGTGGAA	ACCGGTGCAG	ATGGGGACGG	GGGCCGGACG	GGCCACCGAG	180
	GACGGCCGCT	GGCCTTCTGC	GCACGAGGTT	GCGACAAAGC	TTGCTGACGA	CGGCAGCGGG	240
	CGGGGGCGCT	CGCAACCGAT	GGTGACGACC	GGGAAGGAGA	AGTGGGTGCC	AATGAAGCCG	300
10	GCCATGCTTG	TGCCCGGGCA	GGGCTTGCGC	AAGATGCAAC	GCAAGAAGAA	AAACGGGCAG	360
	GCGGTCAACG	GCGGTGCCGC	GAAGCGCAAG	ACCGGAAACA	AGGCACCCCC	CAGCCAGCAA	420
	AAGAGAGCTC	CAGACTCCCA	CAGGAAGGCG	CATGACGAGG	CGAGCGCCGC	GAGCGCCACG	480
	CCATCTGCAC	CGGAGGAGCA	CGTGGAAACAG	CGCGAGCTCG	GCGAGCAGCA	GCAGGTCCCC	540
	GAGGCCGCGAG	AACAGGGTGC	GGAACACCCG	ACACAGCATA	TGGCGCAGAT	GCAGCCCCAG	600
15	CCCAGAAGAC	GCTTCTACGG	CGGCAGGCAG	CAGCACTCCG	CTGACGGACA	CAAGCCAGTT	660
	TGTGT						

## 1638UP

20	GATCTGAGAA	CTACTGTGTG	TCGGCTAGCG	CAAACCTTATC	AGAATTCCAT	CAACTCACCG	60
	AACCATAGCA	CATCTACGTC	ACCTCCCCCT	ACCGCTACAG	ATACCGGGAA	TGATCAATTT	120
	TTGCGTGTTT	ATGCTGTAAC	CATATCGCAT	GATGACAAGT	ACCTAATATG	CATGAGCAAT	180
	GACACGTACA	TTGATGTCTA	CGACATGTCA	GAATTATCGC	CTGATTGTGA	ACGCTCGCAC	240
	GAAATTAGGA	CTCCTAGACT	ATCTAGACTT	AATATTGGGA	AGCAGATGAT	GTCCATGAGC	300
	GGGCCAGTTG	GACCCGATGA	TTCGCTTTTA	CTAATCAGTG	TACAGCCACA	CGAGCTTCAG	360
25	CTATGGGATT	TCAAAAGGCA	GATTATGGTC	CAAAGATATG	TAGGACAGCG	GCAGGTGGCA	420
	TACATCATCC	GTTTCGTGCTT	TGGGTATGGG	GACAACTTAG	TTGCTGGAGG	TTCCGAAGAC	480
	GGGAAGATAT	ACATTTGGGA	TAGATATTAT	GGTAATATTA	TTGGCGTTCT	ATCTGGGCAT	540
	AACATGGAGA	GACCGGACGA	CTCCAGAAAT	AAAAACTTCC	CAATGACCAA	AGTTTGCAAT	600
	ACTGTAGCAT	GGAATCCCGT	CAATTCAAGA	CTATTTGCCT	CTGGAGGAGA	TGACGGTCTG	660
	GTGAAGATAT	GGAAGGTTGA	CCCTAATTGA	TGAATCCTAT	AGCATGACGT	TATTTGTCTA	720
30	TAGAACTTCG	AGAAATCCTG	CCGATCTGTT	GTTTCCTAAA	TTGTA		

## 1639RP

35	GATCCATCTG	ACTATTGTTT	CACGCGATTC	GGGGACCAAC	TGTGCAGTCA	GGCCCAGGAA	60
	CCGGGAGAAA	TAAGCCTTGA	ACGAGCGCTG	GTCGATATTA	CAGTTGTGCG	CACCTTGACA	120
	TCCTGCCTCG	TACAGGGTGT	CGTTGCTGAG	GAAGATTCTG	GCGCTGTCCA	AGAAACGCAG	180
	TGTTCCGTGG	TGCCACAGCT	CGTCTGGGT	ATGGTTGTAG	ATGAAGGCAC	AGCCTGCCAT	240
	GATCAGCCCA	TGGTTGTAAG	TCCACTGCAG	CTTATTTAAG	TTGGTACAGT	TGTCGTTGAT	300
	GTCTGTACCG	TCGTAGACGA	CGTGCCAGTT	TGGCTGCACA	ATCGAGATCA	GCCCAACGCC	360
40	ATACATCCAG	TCGTAAACCC	GTPCCGCCCA	CTCTAAGTAT	GTGGCATTCC	CGGTGTAACG	420
	CGTTAATCGT	GCCGCCATGT	GGAACAGCGC	ACCGTTGGAA	ACGGAGTTT	TGTAGTGGTA	480
	CCCGTCGTTT	CAGCGGAAAA	TCTGCCATCT	GAGCCCGCCG	TTGCACGTCT	CCATATCCCA	540
	GCGCAGGGCC	ATGGTATTAA	ACACCGCCTG	CGCCAGCGCC	AGCCATTGCG	GCTGCTCCGC	600
	GGGCGGGTTC	GGAAGTTG	GCTCCGCGGC	AGCCATCACC	GCCATCCCCC	AGAAAAAA	

## 1639UP

45	GATCGAGCGG	GTGAGGGACA	CGGTGCACAT	AACGACTGCG	GACGGTGCTT	GCTATGTTTC	60
	CAAGTGCGCG	ATTGTGACCG	TGCCGCAAAG	CGTGCTGGAG	CTGTCTCTGA	AACCAGAGCG	120
	GGTGCCCGGG	CGCATTTAGT	TTCCGCCCCC	CCTCAACGAC	AACATCACGT	CTGCGTTTGA	180
50	GCGAGCTCAC	TACGCCCTCG	TGGGCAAGAT	CTTCTTTGAG	TTTGACAAGT	GCACCTGGGA	240
	CACGCAAGCG	CCGCGGGTTG	CTATCGCAGC	CAAAGTTCCC	GACGACTTTA	GTGCGCAGGT	300
	CCGTAAGGCC	CAAGATTTGC	AGGAGCTGCT	GCGATCCGCC	AGTGCTCAGA	CTGAGGTGAA	360
	GCTGGGACAA	GACTGCTTTG	ACTTTCCACA	AGAGTTTCAG	AACATGGTTG	CGCTGGCAGG	420
	GATACCGACA	CTTATTGCGT	TCACGCAGAC	ACCTCTTACT	GAGCACGTCT	AGCGCTTATC	480
	AAAGCAAGAG	ATTGTGGACT	ACTTCAAACC	CGCAATTGTT	GTTGCACTAC	GTGCACTGGG	540
55	GTCCAAGGAG	GAGTGCCTCT	TCGACCTCGG	AAACACGCAA	CCGCAAGACG	ATAGTCATCC	600
	AGGCCCAATC	CTAAAGAACG	TGATCTTCAA	TCCGTGGTCA	CAGGATACGT	ATTCTCGTGG	660
	CTCATACACC	GGTAGTCACG	TGGACGACGA	CCAGCTGCCC	TTGAACGTGG	CCCTCAACAA	720

## 1640RP

	GATCAAGCCG	AGCACGCTGA	CCTTGGCTCC	CCGACGCAAC	ATCGGGTTGA	CGGGCTCCCC	60
	CGCCGTGCGC	TCCTCGACGC	CATCGCCCAG	CTTGGCACTG	GCGGCGTCGC	GCGCCGCGGC	120
5	GAGGCGCGCC	ATGTCCATGA	AGACCGGGAT	GTACGAGCCC	TCCGTGATGG	TGTATATAGT	180
	GTTACAGCAG	AGCATCAAGC	AGTACAGCAC	CGACATCAAA	ATGAGCGCGC	CGTAGGTCTT	240
	GCTACCCTGG	CTGACAAACG	GCGTGGCAAG	TGCGCCGTAC	ATTACAATCG	ACAGCGTCAT	300
	GAGCCACTTG	CGGTAGTTTG	AAAAGTCCGC	CAAACCCATG	AGCACAAATCG	CAATGAGGCC	360
	CTCGATGGAC	GTGTACAACG	CCCGCATATA	AAGCACATAT	GCCGTGAACT	GCACGTCCCT	420
	TCCGCCCCACG	TAGATGTAGC	AGTCATCGCC	GCGCGGGCGG	CAGTGC GCGG	CGGGGTGCCC	480
10	CTTGGGGTGC	CCGAGCTCGT	GTGCGATGGT	CTGTAACGAC	GCAGGCACAA	AAGAACGCAT	540
	CATCACGTAG	GTGCGCCCCG	TCGAAAAGCA	CACAAGGAGC	CATGCAGGAA	ATACCCACCG	600
	GCCCCGCCAC	CGCGCCAGCA	CTCCTCGTCG	GCGCGCTGCC	CGCCCACTAG	CGGCTGCTGC	660
	TCGTCCAGCG	TCACTGACAC	CTGCATGTCA	GCGCCCTTGC	TT		

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## 1640UP

	GATCAACGAG	CTGGCGCAGC	TGCAGCTGGA	CGATGCGGAG	GAAGGCCTGG	AAGAGGCCGG	60
	TGGTGCGCAG	GAGGGCGCGG	CGCTGTGGGC	GCAATTGGAC	GGTGACGACG	ACCTGAAGGA	120
	GTACGACTTG	GAGCACTACG	ACGAGGAGGA	TGCGGGCGCG	GGTGACGAGG	TGACGATGTT	180
20	CCCCGGGCTC	TCCGGCGAGG	CGCGCTTCCA	CGAGGGTGAG	GAGGGGCAGG	ACGCGTACCT	240
	GAGCTTGCCA	ACCGTAGAGG	AGGAGCAGGA	GGAGCGGGCG	GAGCTGCAGG	TGTACCCGAC	300
	AGACAACCTG	GTGCTGGCAA	CGCGGACGGA	AGACGACATT	TCGTACCTGG	ACGTGTACGT	360
	GTACGACGAC	GGCGCGGGGT	TCCACGACGA	GGCGGTGCCG	CAGGAGGCCG	GGGACGCGCA	420
	GGACCCCGAC	GTGGCGCGCG	GGCTGATACG	GGACGCGTCG	TTGTACGTGC	ACCACGACCT	480
	GATGTTGCCG	GCATTCCCGC	TGTGCGTGGA	GTGGGTGAAC	TACCGGCCCCG	GGTCCGAATC	540
25	TGACGCGCCG	GCAAACTTTG	CGGCGGTCCG	CACCTTTCGAC	CCCACGATCG	AGCTGTGGAA	600
	CCTGGACTGT	GTGGACCGCG	CGTCCCCGAC	ATGATCCTCG	GCGAGCCCCG	GGACTCTGCG	660
	ACCGCGTCCA	AGAAGTCGAA	GAAGAAGAAG	AAGGGC			

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## 1642RP

	GATCGCGGTT	TCGGAACGGC	TTGCTTCGCA	CAAAACACAG	GGTTCGAAGT	TACATACTCT	60
	TCAAGAAATT	GACGAGGCCT	TGAAAGCGCT	GGAGCTACGC	GGGTCAGGGA	NTGATGGTAA	120
5	TGCCTCATAT	AAGTGCAACT	GCCAGGCCAC	TATGCATCCT	CTTTTTGAGC	TAGCCCCAAA	180
	TTGCCTGAAC	TGTGGCAAAA	TTATATGTTG	CCGAGAAGGT	CTTCATATGG	ATTCTTCGAG	240
	TTATTGTGGG	ACGCTGTCTG	TACCGAAGCA	GCAGCAGCGG	GATATAGAGA	AGGTGTTGCA	300
	GCGCGAACGC	GAATTGGTAA	AAGCCAAGAG	ACAAGAGACC	GGCTCGACTG	GCAAGAAGAA	360
	GGAAAAGGTC	TTTAAGATTT	CGAACGCAAA	GGGGAGAAAT	ATGTTTCAGTG	AGCAAGAGAG	420
	GCTATTTCGAC	AAACTTGACA	GGCAGCGGGA	CGTGAAATGA	AACGCAACCA	GGTACTTGGG	480
10	GCAGAGGACT	GTCTCAGGAG	GAGGACTCGA	TTCTGAAGGC	TGAGGAAGTC	GATCCGGAAC	540
	TAAGGGCGGC	CAGGCGCGCT	TGGAGAATCT	ATTGCACTTT	CAAGACACTA	GCGAAGAGAG	600
	GACTAAAATA	ATAGATACTG	CCAGTGACTA	CAGTATGTCA	AACGACGCAG	GAATTTGGGG	660
	GTCCGCATAT	GAGAAGGC					

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## 1642UP

	GATCTCGTAC	CCGGTACGGT	GCGCGAGCTT	GCCGCCGGCA	GCCGCGCGCT	GCCCTGCTTC	60
	TCCGCCGACA	GCCCCGCAAA	TACCGTGTTC	TACAAGCTGC	ATGGATCGCT	GCCACAGGCC	120
	GTGCGTGTG	CGACGCTGCG	GCACTTCTCC	TCAGACGCTG	CGGCAACCCG	GGGGAAGCAC	180
20	CTGGTCTCTGT	TTTGTACCGA	CGTCGCGCTCG	CGTGGCTTGG	ACCTGCCGCG	TGTCAGCACT	240
	GTCATCGAGA	TGGACCGGCC	CTTCGCGGCT	GAGGACCATC	TGCATCGTAT	CGGGCGGACC	300
	GCGCGTGCCG	GTGTGGCTGG	CGAGTCGTTG	CTCTTCCTGC	TGCCCGGCGA	GGAAGAGGGC	360
	TACATGGAAC	ACATCCGTGC	CCACCACCCT	CGTGGCTGGG	AGCTGCTTCG	CTACGATCGA	420
	GACCTACTGG	CGCCGGCCTT	CGCGGCCCTT	GTCCGCCGCT	CCGACCGTCC	GACCAACGCA	480
	ACGGACGCCG	CCTGGGACAG	CAACGCGACA	ACTTGGCACC	TCAACGTCCA	GCGCCGTGTT	540
25	GCTCGAAGAC	CCTCCGCGAA	GGATCTTGCC	ATCAAGGGCT	ACACCAGCCA	TATCCGCGCA	600
	TACGCAACCC	ACATCTCTCA	GGAAAAAGCG	CTTCTTCAAC	GTTCGCTGTC	TGCATCTTGG	660
	CCACCTGGCG	AAAGCCTTTG	GACTTCGCGA	GCGCCCCAAA	GCA		

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## 1643RP

	GATCGGAACA	AGGAGCAGCA	GTCCATCCAG	CTGTGCGAGC	AGCAGCAGGG	CACACTGCAG	60
	GACAGGAAGC	CGACATACCA	AGTCATGTCT	CTCCAGAGCG	ACACGACGGT	GACCAAGTTC	120
	AAGGTCGACG	ACTCCATCAG	CAAGCGTTTC	GAGTTCATGA	ACAAGCCGAA	GGCCAAGCGC	180
	GCGACCGCGC	CGCGGCAGGC	GGCGACCAGC	AGCCCTGCAA	TGGCCTCGGG	CGCCGGCAAG	240
35	CGCGTGCA	AGCCCAAGGT	GCAGCAGGGC	CGCGGCAGGC	CCGCGCAGGC	CGATTCCGGCG	300
	AAGCAGAGTA	ATACGCCCCAG	GGGACTTCGG	TGCGCTCGGA	GAAGACCAAT	CGCTGCAGGA	360
	ATTCTCTGTCG	CAGTCCGAGA	TTAAGAGCGA	TCTGTTTCGAA	CTGGAGGAGC	AGAACGACGA	420
	GAGCGCAAGC	TCCAACAAGG	AGAACGTACC	CCCGAGCTCC	TCGTCCGTGT	TCCAGCAGCA	480
	GCTTCTGCCC	ACAGATATGG	ACGACTTTT	CAACCTCGAC	CTCGACCATA	TGAAGAACAC	540
	CGATGATGAG	TGGTTCCAGG	GCCTGTTCCG	CACTCTCTCG	GACGCGACCA	CCTGCAACAC	600
40	CATGCCCATC	GAGGAC					

## 1643UP

	GATCGTTGCA	AAGAAGCTAT	TACGGTGTCT	ACACGTTTCGA	GAACAGCGCC	CGATGCCATA	60
45	TCCCACACCG	CCGCTGTCAA	ACGCGTCTCT	GGGCACGAGC	GCTGACGGCG	GGAGCGCCGC	120
	AGGGCTGGCG	CAGCAGGCGC	CCGCAAAATC	GTACTACCCG	CTGGTGCCCG	ACGGCGCACA	180
	GCTCACGCCG	CCACTGTCTG	CCGTGTCCAC	GGCCGGCGAT	GACGCCGGCC	TCTACCGCTA	240
	CCACAAGCAG	ATCAGCAAGT	CGTTCCAGGA	CGACCTGATC	TACTGCCCGC	GCGCGCTGCT	300
	GAGCAAAGTC	GAGCTGACGC	AGTGCTACCA	GCTGGACATG	CTGCTGCTGA	TGGAGCAGCA	360
	GCAGCAGGCC	CAGCCGAGTG	TCAAGTTCAA	CCCATATACG	TCGCAGAGCT	TCAACCCCGC	420
50	GGGCCCCGCA	TCGCCCCGCT	CCTAGGGCCG	GCGGGCCGCC	CGGGACCATT	TAGTTCGACN	480
	GAATCNCTAT	GTCAAGACTG	ACGCTTGCTC	GCATCCGGGT	TTATGTTTTA	TTCCAGTT	

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5	GATCCTTTGC	AAATTCGTCC	ATAGGAATGT	AAACGGACCT	GCCCTCCCAC	CTCTTGGTAT	60
	TGCAAACAGG	CATCTTGAGT	TCGTTTGGCC	ATTCCATCTT	TATATGCTGT	TCTTCATCGC	120
	AAGGCACATT	TTCGTCTTCT	TCGGGCTTCT	CAAAAACAAC	CTTATGCACT	CTCTCAGTAA	180
	TATACACAGG	GTACGGGGTC	GCCGTCCCCTG	AACATTAGGA	AGAAGCAGCC	AAATGGGCCCT	240
	GTGCTCGGCG	ACTCTGGCGGA	CTTCTGCACK	AAATCCCACC	TCAAGTATAT	GACCATCAAG	300
10	TCCCTGAACC	GCGTGCTAAA	CTGCTGGTAT	GTTGTGTCTGA	TATCTAGCGG	ACCGGGAGCT	360
	AGCGAATCGG	TATGCGGCAC	TTCCAATAGG	TAATCGCCCG	GCGTTTGGAA	CGGATGGTAT	420
	ACCCTAGTAA	CTTTGCCCTGC	AAACTCAATA	TGGGGCTTGG	GCTTTTTCCA	GTGGGCCTGG	480
	TTTGTAATTG	GTATCAATGT	CTGCGGAGAT	GAGATGGAGC	TGTCGCTCGA	AGATATGTCC	540
	TTTAGCAGGT	TATCGTCTTC					

**1645RP**

15	GATCTTGGA	GAGGAGGACT	ATTCAAGTAA	AATGGCACGG	CGGGAAGATA	AGATGGAAGA	60
	GGAGTGGATA	CGAAAGTACG	AGCGTGAGAA	GAAGAAGAGA	AAGAGAGGCG	CATAATCCCC	120
	AGTGTAAATA	ATCAAAATCCG	CGGTTTCGCT	CGCGTGTAGC	ATAATAATAGT	CTACGATAGT	180
	GGTCAGATAA	GGTATTTCAA	AAGTTAGGCA	ACCCATGAAA	CATCAAACCT	TTCAATGCAA	240
	TGATATGTAA	GTTGCATATA	TTACGAGCTG	TGAAATAGAG	AAACTCAAAT	GAATACTTTT	300
20	ACCACACCAT	AACAAACGCA	CAATGTTACG	AGAATGAAGA	CGATAATGCA	GCTTGAATAG	360
	TGCCACCATG	CGCCATATG	TGACCTACTG	AACAGCAGAA	CGAAGCTAAA	CGAGCTCAGC	420
	ATGAGGGACA	CCACTAGAGA	TACCAGGATC	AACGCTGTGA	TATAATTACT	ACCTTCAAAC	480
	TCAGTCTGGT	CATTTCCAAG	AGCGCTGAAC	AATGAAAACA	TGATTCCCAC	AGTGGTACCT	540
	GTGGTTATGC	AAGATACGAG	CAGGGTCGTC	AGGTAAAACA	ATGAGACCAC	CTCATCGTGC	600
	TTGTATCCAT	ATAGGACATC	AAGTTCATCG	TAAACATACTA	CGCGAGCCTC	GTCATCCCAG	660
25	TTTGGAACTT	GCAGTTGGCT	ACCATCCCCG	GCAACGTGCT	TTGCAC		

1645UP

30	GATCAGCGGC	GGCTGCGCGC	GCTGTTGCCG	TAGCGCTGCA	GCAAGCTCGC	GCGCGCGCC	60
	GCGCTCTGCG	CCTGGCCCTC	CGGCTGCGCG	GCACCGCGCT	CGGGCGTCTG	CCGCCCAAGC	120
	TCCAGCCGCG	TCGGGTTTCG	ACTGATCACG	TGATCCACCG	TGCTGCCGTC	CCGGCCGGCC	180
	CTGTCCGGCG	CCGCCGGCGC	CTCGCCCGCC	CGGCCATCGC	CGCGCTACAC	ACGGCTCTTC	240
	GGATCGTACC	GCGTCTCCTC	GCCGCGCACG	TCGTGAGGTT	ACCGCGCGCG	GTCATGCCGC	300
35	GGCCGGATCG	CAGGCGCCCC	CACGCCCGCC	CGCGCCGCCC	GCGCGTCCAG	TCCCAACTTG	360
	TACCGTTCCA	CTGCTGCCGC	CGCGTCTCTT	GCCGCTGCCG	CGGGCTCCGC	CGCCCGGGCC	420
	GCCACTGCCG	GCGCCACCGG	CCCCTCGAAC	CCGTACCATC	GGTCCCGCTT	GGCCTCAAAG	480
	CTCAGCGCAT	TCTCGTCCCG	GACCTGAAAC	GCGCGCTCGC	CACCATCGCC	CCGCGCCTGT	540
	TTGCGCGGCC	GGAGCAGGCA	GTCGCGCCGG	TCATGATTGG	CGCCGAGTTT	TCGTGCACCG	600
	CCCCGCTCCG	CGCCCCCGCC	CGCGCGCGCG	TGCCCGCCAC	AAAACGGTCA	CTTATTACCG	660
	AAACTGTGTA	GCCACCGAGA	AGTCCTGAGC	GCCCTCGCCG	GGCTC		

1646RP

45	GATCGAGAAC	CGCATGGACG	ACAAGCCCAA	CGTGGTGATC	CTGGGGTCCG	GCTGGGGTGC	60
	GATTTGTTTC	CTGAAGCACA	TGCACGCGCG	GAAGTACAAC	GTGACGGTGG	TGTCGCCACG	120
	GAACACTACTC	CTGTTTCACG	CGCTGCTCGC	CTCGACGCCC	GTGGGCACGG	TGGACGAGAA	180
	GTTCGATCATC	GAGCCGTGGG	TGAACCTTTC	GCTCAAGAAG	AAGGGTAAAC	TGTCTTACTA	240
	CGAGGCGGAG	GCGACGTCGA	TCAACCCGCA	GCGCAACACG	GTGACGATCA	AGTCGGTGTG	300
50	GACGGTAGCA	CAGCTGTCTG	ACCCGGACAA	CCACCTGGGG	CTGACGCAGC	AGGACTCCGC	360
	GGAGCTGAAG	TACGACTACC	TGGTGTCTCG	GGTGGGCGCG	GAGCCCAACA	CGTTCCGCAT	420
	TCCGGGCGTG	GAGGAGCAGC	GCAACTTTTT	GAAGGAGATC	CCACACTCGT	TCGAGATCAG	480
	AAAGCGCTTC	CTGTGCAACG	TCGAGAAGGC	GAACCTGTTG	CCCAAGGGCG	ACCCCGAGAG	540
	AAAGCTCTTG	CTGACCATCG	TGGTCTGTGG	CGGTGGTCTT	ACCGCTTGGG	AGACCGCGGG	600
	TGAGTCCAGG	ACTACGTCGA	CCAGGACCTG	AAAGAGATTCA	TCCCTTCCAT	CGCTGAGGAG	660
	GTGCAGATCC	ACCTGGTGGG	GGCCTTGCCC	AACGTGCTGA	ACATGT		

## 1646UP

	GATCAAATGG	GTTAGCCCGT	CTCCAACGAG	CCCTGCAACA	TAGTGGCAGT	AGCGGTCGTA	60
	GTCCTGGATC	GTCTCCAACC	CGCTCAAATT	AAACTTCTCG	TCCAGAATGT	AGTCTGCCAT	120
5	GCCGTTGCCC	ATCTTGTGTG	TGATGTCTGC	AATCACCTGC	TGGTACTCGG	GCTTCAGCTT	180
	GTGGAACCTG	GCTAGAATCG	TGCTGAACTC	CACCAGCACG	TCACGGTCCT	TCTCCGTCTT	240
	CGCGTTGCCG	TCGAAACTCC	ACGTATCCAG	CTTCAGTTTC	TGGTCGAACT	CCCGGAGTAG	300
	CGGCACCTTT	ACCTTGGGAC	TGATCGTCAT	ATCGTCTTCA	ACAGTATCCA	GCGCACGCAG	360
	AATCAGGTAG	AACAGCATCA	CCGCGTTGCG	CAGCTCGGGA	TGTAGCTCCA	TTATCACGGC	420
	CGCAAAAGAC	TCGAAGTCCG	CTGTAGCAGC	TGGTAGCACC	GCTTGAGCTC	TGCAGAGCCC	480
10	TGCGTGTCTG	CCGCAGGATA	AAGCGGTTCC	CTCAGAAATT	TGAGCTTCAG	AGCTGCCTTC	540
	AGCTCCAGTG	GGTGTGTGAA	TAATTGAACA	ACCTTCCCCA	TGGTCACGAT	TCGATTAAAGT	600
	AATTGCCAAT	TATGTCAAGC	GCCTGTCACT	TGGTGATGTC	GCGCTTGCTT	GTACAGG	

## 1647RP

	GATCCAGCTA	GATAGCGTGC	CAATTGCTGA	TAAATCCTGC	CAGAAATGCGA	TAACGCCTCT	60
	CTGAAACGCG	CAACGCCTCC	GGAGCGCCAG	GAGCTGTCTGC	GAGATGCGAG	GCGTCTGGAC	120
	TCGATGCACA	ACTAATATTG	AATTCAGTAT	CCCAGCAGTAG	GCGGGTACAT	AACTGCTTAC	180
	GTACTCCAC	TACGACACTG	CGCCCCGCAC	GCTGCACGTG	CGATGCCGGCT	TACAAAGACC	240
20	AAGTCTTTGG	CAACACCTGG	ATATGGTATC	CATCGGGGTC	TCTGAGGACG	GCGAGATTCT	300
	TGATAGACCC	CTTGTGTGTAG	CGCAACTCCC	ACTCCAGGTC	CGGGTACGTC	TCCTCGATGT	360
	CAGCGCAAAG	AGGCGCAGGG	TCACTGAGCG	ACACACCCAT	GTGGCTGTAC	CCCGTGGGCT	420
	CTGCGTTCCC	GTTGTGATAC	GAGAAGTCGG	CGTCATCCTC	GGTCCCCCAA	TTGTGCGTCA	480
	GCTCCAGAAAT	GCTCTCGCGC	TTCAACCGCT	CGTCCGCTGC	CGGATACCCC	AGGAAGTAGA	540
	GGGTGAATTT	CGCATTTGCG	TGCTCGCTCA	CCTCCAGTAG	CGACATACCT	AGCACATTCT	600
25	GGTAGAACTC	CAGCGACTTC	GTTGCGTCTT	TCACACGTAG	CATCGTGTGG	TTAAACTTGG	660
	GCCCCAGGTC	CACCTGGCTCC	GCGTCCGACA	AGTTGTACTG	TATCAACTCA	ATCCAGTATC	720
	CGTCGGG						

## 1647UP

	GATCCGAGCA	CGGTGCGGGT	GCAACAGAGG	AAATATATGG	CACTACAGAC	AGTGCACAGA	60
	TGCAGGAGCT	GCGCCGCCTG	GCGCGGCAGC	GCTATCTGGA	CCGGCGGGAG	AGGGAAAAGC	120
	TAGACTGGGC	AATACGGGAC	CTTGCATTGT	TAGAAGAAGA	CGTAAAGAAG	TACGGATGGG	180
	ACAAGCTGAC	GGAAACGGGAG	CGAAGAGAGA	TTGGGACCAA	GCGGCAGCTC	GTGCAAATTG	240
	TGCGCGAGCG	GCGATCGGGC	GCGGCGGGCG	GCGAGCGTCC	ATTCCATATG	CCCGGCGAGA	300
35	CCGTTGTGGA	GGTACTGCG	CGGCAGGAGA	AGAGCTGGGA	GGAGCAGCAG	GTGCAAAGG	360
	CGGTGCGCGC	GGAGGGGCGC	TCGGACATAA	TTGAGGTGGA	GGGCTCTGAA	CAGTACGAGT	420
	TTGTTCTGGA	CTCGCGGTCC	GTTGTGCGCT	TTACAGAGGA	AGAGACGCTG	GCTCCCGGCG	480
	AGCGTGTCTG	GAAGCAGCTC	GAACAGAAGC	TCGAGAAGGA	AATTAAGCGC	GTGGCGTCTG	540
	TTCAAGAAAC	TAGGAGGCAG	CTTCTGTGT	ATGCGTACCG	CGACGAGCTT	CTGAAGGCGG	600
40	TGCGCGACCA	CCAGT					

## 1648RP

	GATCCAGCTC	ATGCAGTGCG	CGATTCCAGC	CCTGCCCTGTC	GTTTAAAGTC	TTGAAGTAGT	60
45	TGGTGCTGAA	ATGCTTGTC	AATTTGTACA	GGTATCGTTT	CGAAGATTTT	GAGAATAGTC	120
	CTTCCACCAC	TTTCAATGGG	TTCTCTCTCGA	ACTTGTCGAG	GAATGAATTC	TCCAGCTTGG	180
	AGAATGCATG	CTGTGAAGAG	TATATACGAG	ACCCAGCTTT	CGCCACGAAT	TTGATGAGCT	240
	GATTGAAGTC	GTTGCGCATG	TCGCTCTCGG	GTATGAATCG	TGGCACAGTC	AGCGTCAAAG	300
	CTCGCTGCGT	CATAGGACGG	TATGGTCCCG	GTGGGTACTC	GTGGACATCG	AAGTTATCAA	360
	GCAGATAGAA	ATCCTTGATT	TTGCCCTTGT	CTGCGAGAGA	CCGCAGGTAC	GCCACGAAAA	420
50	GGTGGTACAG	CGCGCTTCCC	CGGTTACGGT	AGATCTTGTT	CAGAAATAAGT	TCGTGCTCGT	480
	TGCTTTCATC	GTTGGCATCC	TTGTACTCTT	CTACCGCCTT	GCAAGAGGGG	AAACACACCT	540
	GGCCCGCGGT	GAATATTAAAG	TCCATCTGCG	TCGTCTTCTC	CACCAACAGG	TCCGTACGCC	600
	CAACGATCGT	CACCAGGATT	TCCAGAAAAAG	CGTAAGTCGT	GCACATGT		

## 1648UP

	GATCTAGCAG	GTGTTGAACA	GATAATGGAA	TGGCTCTCCT	ATATTCCAGC	TAAACGTAAT	60
	ATGCCCGTAC	CTATACTGCA	GTCAGAGGAC	AACTGGGATA	GGGATGTTGA	ATACACACCA	120
5	ACACTTCACA	GCCTTATGAT	GTACGCTGGA	TGATTGAAGG	CCGCCAAGGA	CCTGATGGAT	180
	TTGAATATGG	TCTGTTTGAC	AAGGGTTCCT	TCCAGGAAAC	ATTATCAGGC	TGGGCGAGAG	240
	GCGTCGTTGT	AGGCAGAGCT	CGCATGGGTG	GTATCCCGCT	CGGTGTTATT	GCCGTTGACA	300
	CTCGTACAAT	TGAAACTGTG	ATCCCTGCCC	ATCCGGCAAA	CCCTGCATCC	ACAGAAACTT	360
	TGATTTCAGGA	GGCAGGCTTA	GTTCGGTATC	CTAACTCAGC	ATTTAAAACT	GCGCAGGCCA	420
	TAGCTGATTT	CAACCACGGA	GAACAACTTC	CACTCATGAT	ATTAGCAAAC	TGGAGAGGGT	480
10	TTTCTGGTGG	TCAAAGAGAT	ATGTTCAATG	AGGTCTTGAA	ATATGGCTCC	TTCATTGTTG	540
	ATGCTCTAGT	GGATTATAAA	CAGCCTGTAT	TCGTATACAT	ACCTCCAACA	GGTGAGTTGA	600
	GAGGTGGTTC	CTGGGTTGTG	GTGGATCCTA	CAATTAACTC	TGACCAGATG	GAGATGTATG	660
	CTGATTCCGA	CTCGCGGGCA	GGTGTGCTAG	AACCTGCTGG	TATGGTTGGT	ATAAA	

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## 1649RP

	GATCAAACGC	AAAACGTGTA	CGCAGAAAAA	AGTTTCGCTG	ACAGACGACA	TGCTCGCAGG	60
	GCACCACGGG	GTGGGCAACG	GAGCGGTCCG	GTTCCCAGCG	ATGGACCTCG	GGGCGACCAC	120
	GAATCTTTTG	CTAAACAACA	CTATCAACAA	GACCAAGTTC	AGTCAGCTAA	AAAAACGCGT	180
20	AGATAGTATC	GAAGTGCATA	ACCAGCAGCT	GCGCGCAGAG	AACAATAGTT	TGAAAATCGA	240
	ATTCCAAAAG	ATGAGTTCCA	GATATAACTC	CATGGTGGAG	AACCTCGTGT	CTCTTAAAAA	300
	CTACAATAAT	TCCCTCGTTG	AGAACTTCAA	TCTGCTGGTA	TCCACGCTGG	CGCAACAGGG	360
	CCTGAAGGTT	CCCCATCCAT	TAAACCTCGG	CAACTATGCA	TCTTCACAGG	TTGCCAAAAA	420
	TTCATCTGCT	TCCGACGTTT	AACCGCATGT	ATCGCCGTTG	GGTACTGTAG	CACCTACGAA	480
	CATACCCTTG	GCGCAGGCTA	CCCCGTCGAA	AGAAGAGGCC	AATCCTCCTA	CAAGCCTGCG	540
25	CCCAGGCTTC	CATGTTCTGC	TGGTAGAAGA	ATGATTCGGT	TGTATCCAA	CTATGTTCCA	600
	AATTCTTGAG	AAAATATGGC	TGTTCCGGTG	AAGTCGTAAC	GGACGGCCTA	TCTGCTATTG	660
	AAACAGTAGA	GAAATTCCAG	TACGACCTCG	TTCTGATGGA	TATCGTGATG	CCCA	

## 30 1649UP

	GATCGCTGGC	GCGGGCAGCC	ACATGCGGGC	GCATTTGACG	TTCTACCACA	TGCAATCTAT	60
	GGCGGCTGTG	CGCGCGTTGC	GCCCGCAGGG	GAAGTACGGG	CTGCGCGAGC	CGCCAGCGGA	120
	GGCACCACCC	CCGGCGTTGC	CCGACGTGGA	TGTGGTGCTG	ATGCCCCGTC	TAGGGTTCTG	180
	CGCCGATACC	GGCGCGCGCC	TCGGACGCGG	GGCAGGTTAC	TACGACAAC	ATGTAAGCCG	240
35	TACGCAGCAG	CTGCACGGCA	GGAGACCCTG	GCTGGTTGGG	CTGGCGCTCA	GCCAGCAGCT	300
	GATGTTGCAC	GTCCCGCTAG	AGCCGCACGA	CCAGTGCTTG	GACGCGGTGG	CCTGCGGCGA	360
	CGGACAGTTG	AGGTGGGCGC	ANCGCGCGCC	CGGGGAGATA	GTTGATATAT	AAGTGTATCT	420
	AGCCTGTAGT	GAAGCTCCCT	TTCGCACGCA	CGAATGTCCG	CGTGCCGCTC	TGGTTGATGA	480
	TCTCGGCCCTC	CAGACGGACG	TTGTTGCCGT	GGTCCTCGAC	GCGGGTGGTG	CGGACCACAA	540
	CGAACTGGTT	CGCCAGGGTC	GGGAAACAAT	ACAAGATCTT	GATGTGCTCG	GTTACCTCCT	600
40	AATCGGTGCC	GGTCACGAAT	GTGACTGCCT	CCCGCATCAG	GTGCTCAGC	ACCGTGGCCA	660
	GGA						

## 1650RP

45	GATCGTCTCG	CCGGGACTCG	ATTTTTGTGC	ACCGGCCACG	CAAGAAGGAC	CTTGCGTGCA	60
	TCATGTACAC	CTCGGGCTCG	ACAGGTGACC	CGAAGGGTGT	GTCGTTGACC	CACGCTAACA	120
	TCGTGGCGGG	CATTGGCGGT	GTTTCCGTTG	TGATCAACCG	CGCGATTGTG	AAGCCTGACG	180
	ATCGTGTGAT	CGCGTTCCTG	CCGCTTGCGC	ATATTTTGA	GCTTGTGTTT	GAGTTGACCT	240
	GTCTCTACTG	GGGCGCCTTA	ATTGGCTACG	GCTCCGTCAA	GACGTTGAGC	GAGGCTTCGG	300
	TCCGCAACTG	TAAGGGGAC	ATGAAGGAGT	TCCGGCCGTC	CGTCATGGTC	GGTGTGCGAG	360
50	CTGTCTGGGA	GGGTGTCAGG	AAGGCTATTG	TTGCGCAGGT	CACTAAGTTG	CCTCCGTTCA	420
	AGCAAAAGAT	ATTCTGGGCG	GCCTACCACA	CCAAGCTACG	CATGAAGAAG	TGCCACATTC	480
	CAGGCGGCGA	TCTAATAGGA	AGCATGATCT	TTAAGAAGGT	GCGTGAGACC	ACTGGTGGCA	540
	ACCTTCGCTA	CATCTTGAAT	GGTGGCTCTC	CATTGTGCGG	GGATACGCAA	GTTTTTATT	600
	CCAACCTGAT	TTGCCCCGTG	TTGATTGGTT	ACGGCTTAAC	GGAGACTGTG	GCGAATGGCT	660
55	GTATAGTGCC	TCCACACCAC	TTCAAGTACG	GGGTTGTGGG	AGACAT		

## 1650UP

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GATCCATTTC	TCATGGAGAT	TAACGCTATA	TGCGAGGAAA	GCAATAACAA	GAAGCAAGCC	60
AAGAAGTCTG	TTAACTTCTC	TATGCTAGGG	TTGACTGATT	TTACCAAAC	CAAAAAGCC	120
GATACTACAG	ATGTCTGGAG	AGCGTTTAGG	ATGTACGACG	AAGTACAAAT	GAAAAAGAGA	180
TTTAGTTATA	AATGGGATTA	TGATAAAGTG	TCCAGGGAAT	TGGATGAAGA	GACATGGAAT	240
AAGATTATTA	ATAGGGAAAC	TTTGAATTTA	TTTGCATTAG	TGGAAAGATA	TACGGTAAAG	300
ATTGAAAACG	ATGCCAATAT	AACCTATTGG	AGTTCTGTCTG	TTATGCGCAA	CTCCTGTCTGC	360
AAGCATGAGG	CTACAGGAGT	GAGGCAATGT	GCCAACTTCT	TCTGTGGTAA	ATGGGAAGAC	420
CACCCGAAGC	AGTTTCCCAA	GTGCCGCCGT	TGCAAGCGCA	CAAAATATTG	CAGTTGTGAG	480
TGTCAACTAC	AATCTTGGGC	ATATCATCGG	TACTGGTGCC	ATGATGTTGG	CTCTGTCTTC	540
ACGGGCACCT	CCTCAACGGC	AAACACCACT	GGGACACATA	CGCCAAATGC	TGTCCGGTCAG	600
TCGGCTGGAA	CCACGACCAC	TACTACCACG	GCGGCTACGG	AGGTAGATCA	ATCCATTTTG	660
ATGACAGCAA	GGGG					

## 1651RP

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GATGGCGACG	TTTACCGAAG	AGCAAAAAGA	AAAGTACGCG	ATGGCGTTGA	AGGACAAGGG	60
GAACGAGTGC	TTTAAGGACC	AGCGGTACGA	GGAGGCGATC	AAGTTCTACG	ACTGCGCGTT	120
GAAGCTAAAA	GAAGACCCGG	TGTTCTACTC	GAATCGGTCTG	GCGTGCTACG	TGCCCTTGAA	180
CAAGCTGGAG	AAGGTTGTGG	AGGACACCAC	TGCTGCACTA	AAGCTGAAAC	CCGACTATTTC	240
TAAGTGTTTTG	CTTCGTCTGTG	CAACAGCTAA	TGAATCGTTG	GGTAATTATG	CTGATGCTAT	300
TTTGGATTTA	TCTGCCGTAT	CTCTATACGG	CGGGTACAGC	TCGCAGACAA	TGAGCCCGT	360
GCTGGAGCGG	AATATGAACA	AGCAGGCTAT	GCAAGTATTG	AAACAGAAAC	TCTCTGGTGG	420
AGAGAAACAC	GAACCTCCCT	CCAATACTTC	CTTAGCGTCT	TTCTTCCGCA	TCTTCCCTTC	480
GGAGACATCG	TTGGAGAACT	ACGATGAAAC	TTCCGAAGCA	GACCGCATTC	TTCTCAAGGG	540
ATTGTGCGCC	CTACACGCGC	GCCAGGCAGG	CTCCTATGAA	ATTGCTGATG	AAGCCTTTAC	600
CGATGCTGTA	GAAAAGTTCA	CC				

## 1651UP

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GATCGTGATT	TTGCGGGGCT	GCATCCTGCA	GGCTCCACAT	CATGCCGTGC	GCCAGGCTAT	60
GCTGAACATC	CCCAGCGGGG	TCTACTGCAC	GTTCCGTGGG	CAGTCATCGC	CTGCGATCCA	120
GTACGGTATC	TCGTCTACAA	ACTTCATCAC	ACACGTGAAT	GAGATCGAAA	CCCCAGACCT	180
GGACCGCTTT	CTCGAGGTGG	TACGCACGAT	ACCAGACAAC	ACCTACTGTA	AAATCCGTCT	240
TGTGACCTTC	GACAACGTGC	CTTTTGCTAT	CTCCCTGAAG	ACAAACTACC	ACTACTTCCC	300
CACCAGCGAG	CTCTCCCGCA	ACTCCGACAC	CGGCCGCTGG	ATTGAGCACC	TCTGCAACGC	360
TACCCCGCTG	AAAAACTAGC	AATAGACTGA	TATCTCTTAT	AGAACGTATA	AACTATTTCAC	420
ATGTAACCCG	ATCACGTGAC	GAGCGCTGCA	CGCAGCTCGT	GCAGCATGCT	CAGTGGTATG	480
GCAGTAGGCG	CCGCAGACGC	TTCAGATGGG	CACCTCGCCG	CATGGTCCGC	CCAGAGAGCT	540
GCTTCAGCGC	GCGCTGTCCC	AGCCTGTGTT	ACCGTGGCTG	CGGCCAGCCT	TCGAACGCTT	600
GTACCTCCTG	CAGTCTTCCG	CCATCTCTTA	GCTGCGCCTT	TGTGCGTCTT	CATTAGTGTC	660
CGCACCATGA	TCAGCGACG					

## 1652RP

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GATCTTCGTT	CGTGAAAACC	TTGCACGTCT	TCATGAGCTC	AAGAATTGCC	TCTGCATCTA	60
TTCTGTCCGG	TTGGATTCTG	CCTTCCTTAT	TGTCCTGAAT	CATGCGCGCA	AAAGCGCGCG	120
GCGTCCAGTC	ATGACGGGAT	CGGCCCTTAT	AGGACTTCCC	TGCAAGCCGC	ATGAGGCTCC	180
GCCAGCCATT	TTCTTCAATA	ATATTGACAA	GTCCTTCGTT	TTCCAACACG	ACCTTGTTTCG	240
CGAGACTGTG	GAACGTGTTT	ACGTCTATCT	GCTCAAGTAT	TTCTACCCTT	TCCTCAGCAG	300
ACCATCGCAA	GTTGCAATCT	GCCTCTTGGA	ATGTCCTCCAT	AAGCTTTTCA	TTGATGTTAT	360
CCACTGCTTT	ATTTGTCAAG	GAGAGGATTA	GTATTTTCATT	AGGAGCTACA	ATCCCTTCGT	420
AAACCAGGTT	GTAGACTTTA	TGCAGTAGTG	TCACGGTCTT	GCCAGACCCA	GGTCCCCTGA	480
CCACATTGAC	AGTTGTACAA	GGCTCATATG	GATGTGTTAC	TACTCGTGAT	TGGGACGTCG	540
TCAGTGCTTT	CATTCAATGTA	TGATACATGC	TCGAGCGTCG	GCGAAGGAAA	TAAATTCGTG	600
AATTTCCGTT	TTAAGATACT	CAAAAGAAAT	GAGATAACCG	CCCGCAAGGG	CGGAGTAGAA	660
TTACAGCAGC	TATTGAATAT	ATTTAGTTTA	TT			

## 1652UP

	GATCTCCCCA	CCATTCTCCT	CCAGCGCCTT	CTGTNAGCGT	TCCCGGCGTT	GCTCTCTCGC	60
	CTTTTGCTTC	TTCTCCTTAC	GGATTTTCGC	ATACAGCGGC	TTATTTCAGTT	CGAACTGTTC	120
5	CTTCTTCCAC	TGTTTCTTCC	ATTGCGACTT	CGACATGCCT	TCGGGAACGG	GCGGCAAGGC	180
	AGCCCGTGGT	TTTGGCCGAC	TCAATGTTTT	ATCATTATTA	GTTTCAGGAG	TCATTGCCCA	240
	GTTTGAGGAC	TCTTAGCGCA	AGGTCTTGTC	ACTGAAGTAC	AGTAAAATGG	ATGCCCTTTC	300
	GCGGTGATGA	GGCAATGACC	TGGTGAAATT	TTTCGCCCAT	GGTGAGGCTG	TATAGTGGTC	360
	ACGTGACAAC	AGTTCAGCCC	ATATATGGAG	CCCCTAGGTC	ATATAAAGGG	TCAGGAGCCC	420
	GCTAAAGTCT	TTGTATTCTG	ACCTTTTATT	GGGGAGCTTT	AGGGCGTGTG	TCTCTATCCA	480
10	GAGCCGTGTG	GTGAAAAGCG	TCTCAGCTCA	GCGCGTTCTA	CTACACTGAG	ATTTAAAAAC	540
	CAACAGCGAA	GCAGCAGAGT	ATGACGTCCT	TAGCAACTAA	ACTCGAACTT	CCATGGGTTG	600
	AGAAGTACCG	GCCGAAGCTG	CTGAAAGATG	TGTGGGAAAC	GAWGAAACGG	TGGAGCGCCT	660
	GCAACAGATG	CCAGGGATGG	AAATATGCCA	CAC TTGA			

## 1653RP

	GATCTTTGAT	GCTATTTTCGT	ACCTTAAGGG	CTGTTCCGTG	CTGGAGATGA	TCTCCGGCTA	60
	TATAGGGGAG	ACCGTCTTCC	TGAAGGGTGT	TGCCTTATAT	ATAAAGCGGA	ATAAGTTTGG	120
	CAATGCTACC	ATGGAGGACC	TGTTTGGGGC	CATTAGTGAG	GTAGCAGGCC	TTGATCTCAT	180
20	GGCGAAGGCA	AAAGATTGGA	TTCTAAAGAT	CGGGTACCCG	GTTC TGGA CA	TCACTGTTGT	240
	TGATGGGAAG	ATTTCACTGT	CACAGAGACG	GTACCTTTTCG	AGCGGACAAG	CTGACGCCAA	300
	TGACGACCTA	ACCACCTGGT	GGATTCCCTT	GGAACTGACA	CAGGACTCAA	CTTGCACTAC	360
	AACAGAAATG	GTTTCTAAAT	CCCAAGAAAC	AGAGATCTCA	GCTACCGATT	TTGTGTTCTT	420
	TAACAACGAT	GCCCACGGCT	TCTTCCGGGT	GCATTATGAG	GATGAGACTA	TTCTGGCTAA	480
	CATCTGCAAG	AACATAGCGC	AGCTGTCCTC	ACGCAGTAAA	ATTGCGTTAA	TTTCGGATGT	540
25	TGATGCCACT	GGTACCTTCA	CGCAACTCAT	GGCTGTTCTG	TCTGCATTCT	CTGCAACGCA	600
	TTCGCAAGAC	TACTATGTTA	TGGAACCTCTG	CATTGTCCAT	TTTCCACTCG	GCCTGCTCAA	660
	TCATATATCG	CGATGCGTGC	CAGAGATCCG	CAAGAAGCTT	GCGGCGT		

## 1653UP

	GATCTAATAC	TGGGAGCGAC	TGGGCGTTGT	GGCGGTGTCT	ATCTGTATGC	GAACCAGCGA	60
	GGCTGTGATG	GAGACANATT	GTACTACGAT	GGTTGCGCGC	TCATTGCTGT	GAACGGCCGA	120
	GTTGTGGCCC	AAGGCTCGCA	GTTTTGCTG	AGGGATGTCG	AAGTGGTTAC	TGCAACTGTA	180
	GACTTACAAG	AAGTGAGAGA	TTACCGGATG	TCTGTGATGT	CGCGAGGGTT	GCAGGCAGTA	240
35	TGCAATAACG	TGACTTTTCA	ACGTATTCAA	GTACCTGTAG	AACTGGCCGC	GATGCAAGAT	300
	AGGTTCAATC	CTACGATTAA	CCTGACGAAG	CGGAAAGCCC	CATACTATCA	CAGCCAGAG	360
	GAAGAGATTG	CGCTGGGCCC	AGCTTGTTGG	TTATGGGACT	ACCTACGTCG	TTGCAGAGGA	420
	ACAGGCTATT	TTCTTCCACT	ATCTGGGGGC	ATTGACTCAT	GTGCCACTGC	TGTAATTGTG	480
	CACTCTATGT	GTCCGGATGGT	TGTCAACGAA	ACATCTGAGG	GTAATCTGCA	AGTAATTGCA	540
	GATGCGAGAA	GATTGGCTCG	TGCTAGCGAT	GACTGGATTG	CAACCGATGC	ACGTGAATTT	600
40	GCAAAATATGA	TATTTACAC	TTGTTTTATG	GGAACAGCAA	ACTCCACAAA	TGAGACTCGC	660
	AGTCGGGCAA	AGAAACTTGC	GGAACACCT				

## 1654RP

	GATCTTATTA	ATTTTGATGG	TGCTATATTC	TAAATTCAAG	TAATGATAGC	GCGTGATGCG	60
45	GTACGTACCT	ATACATATAA	CGCACAGTTC	TCCATCGTCT	ATGCGTGTAT	GAAAATCACT	120
	CCAGCCGTGC	GACACGCCAC	GTGTAATCTA	GTGAGTTTCA	AGTTCTTCCT	CCTCATCGGC	180
	AGAAAGTTTC	CCCGCGGGCG	TGAGGTTCTT	GAGCCGCTCC	TTGAGCTGCG	CGATAAGGCT	240
	ATTCTCCCTT	TGAGCATGCA	TGCGGATACC	CTCTAGAGAC	ATATGAGCCG	AATCTGCACC	300
	ATCTAAACCA	TGTTTCGCTGT	TGCTGCCAGT	GGCAGCTGCC	AGTTTGGGAC	TGGACAGACC	360
50	TGTCTGTCCA	TCTTTGTAAG	AATCCTCGGT	CGTTGCCGAG	TTGGAATTCA	TGGTTCCCAT	420
	AGTGTGCAAG	ATTTTCTCCT	CTTCTGTTAG	TTCCAGATGG	GTACCTGTCA	GATTGATCAA	480
	GGACCTGCCG	CTTTTACGCA	GCGAGAGCTT	GCGCAGAAGA	GAGTGCCCGG	GTTGGCGTGC	540
	CTTCAACCAAG	GTTTGTAATG	GAGGTGTGAG	ATCTCGGAGT	CCTTGGTAGT	CTCAGACA	

## 1654UP

	GATCCGGGCC	GGGTCCGCSG	CAACCAACGA	TGTACGCTGT	GGATACCAGC	GACCTGGTAG	60
	GCGTTACGCT	GGGAGGAGCA	GCGGTTGGCG	GAAAACCGGC	AGCAGAGCAA	GTACTGGCTG	120
5	AAGTGGGGGC	CGTATCTGTC	GGAGCGGAGC	TGGGCGACGG	TGCGGGAGGA	CTACTCGTTT	180
	GACGGCGACG	CGTGGCGGCA	CTTCCCGTTC	GAGCAGGCGA	ATGCGCGGGT	CTTCCGGTGG	240
	GGCGAGGACG	GGATCTTCGG	CGTGAGCGAC	AACCGGCAGC	TGGTGTGCCCT	GAACGTGGGG	300
	ATGTGGAACG	GGCGTGACGA	GCTGCTCAAG	GAAGCGGATG	TTGCGGCTGA	CCGGGCCGCA	360
	GGGCAACCAC	GGGAGGACT	GCAAGGAGCT	GTACTACTAC	CTGGACAACC	TTCCGAGCCA	420
	TGCGTACATG	AAGGCGCTGT	AYAAGTACCC	GNTCAAGCGG	GCGTTCCCGT	ACCAGGAGCT	480
10	TATTGCGGGC	AACGACGCGC	GCGGGTACGC	CGAGCGCGAG	CTCGAGGTGT	ACGAACCTGA	540
	CGGGCTGTAC	CGCGAGGCGG	CGACCGGCGA	C			

## 1655RP

15	GATCCACTTT	CCACTCTGAC	ATCGGTCAAT	CAACGCTGGG	CACTCAGGTT	CAGTTCTGAA	60
	GCAATTGCAG	TCCCCGCGAGT	TACCCCTTCAT	TTATTTAGAG	ACTTAGTGGT	GTTATAAGTC	120
	AGTCCTATCG	AACAGCTCTC	GACAGTCATC	GGAAACGAGA	AGTTACCCGC	CCTTGAGACA	180
	CAATCTGTGA	CCCGACTTTG	ATTTACATGC	GTTACCCGCT	CTGGGTACAG	TGCCGGGAAG	240
	CACATGACAA	AGGCCGAGAG	CTAGTTACGT	GAGGCTCATT	GGGGTATGCC	GGAAACTCTA	300
20	ATGACTAGAT	CATCCGAGAA	GCACCGGTAT	ATAAGACGCA	TCACGGTGGT	GCTCGAGAGA	360
	GTGTGTAAAA	TGCCAATTGC	TTAGCCACTG	ATGCCAAATA	CACTGGATAA	GAGTTACGTA	420
	CAAAACGGCC	CTTGGAGGGA	CGGGGTGTTT	CAAGGGAAAG	TGGTCTTCGT	CACTGGCGGG	480
	GCCGGGACGA	TCTGCAGGGT	GCAGGCGGAG	GCAATGGTGC	TACTTGGTGC	CAAGGCTGCG	540
	ATCATTGGGC	GCAATGTGGA	GAAGACTAAG	AAGGCGGCAG	CGGAGATCGC	GGAGTTGGGC	600
	GACTCGGCTG	ACTGCGTGCT	CGGAATTGGC	GGCGTGGACT	TCCGGGAGGT	CCCGGACATG	660
25	AAAGCGCGCG	GTGGAACAGA	CGGTTGCCGC	GTTT			

## 1655UP

30	GATCTCTCTG	ACCGCCCCCA	AACGCTGCTC	CGCGCACATT	GACACTGGTG	TTACCACCCA	60
	TTATGTCGGC	GGCCGTTTCA	TCCCAGATGC	CCTGGCCCGT	CGTCATGGTT	TTGATCCGTT	120
	CCCGTACTCT	GGCACCGATC	AAATACTGCG	TATTTGAGTG	CATATTGCTT	TATTCTATAG	180
	TCTGCGTACA	TAAGCCGGGG	TTTCAGAGGG	CGGGTAACGA	TGACGCGTAA	CGTTTCTTTT	240
	TCGTGATATG	TAAAAAGAAA	TGTGCAACAA	TTTTTCATGA	GATGAACGTT	ATACTGGCTT	300
	TTTTCTCTCT	TGAAGTCAGC	AATCTCTAAC	CTTTGAAGGT	GATTAATAGG	CTGTTGCGTC	360
	GTGTTGGAAC	ATTGACGGAG	CTTTGCTTGT	TGTAAGCGAT	TAATCTGTGT	TGCGAGTTTC	420
35	ACTTTCTCGA	ACTGGTAGCA	GGTCTGACGG	GTCTGCGAAG	GGCGTGGAG	ACTTGCAAAT	480
	ATAGGCGCAA	GACAACCTGC	GAGATACAGG	GGAGCTGCTG	CAGCGAACAG	GTGGAGTGCA	540
	GGCGGATCTT	GAGGACTAGC	TGCTCTGGGA	CGAGATGGCG	AAGGAAAGCC	TGCGGATAGG	600
	CGTAGCAAGC	ACGGAGCCCA	AGCGGGTGAA	GGTGTTCATC	CTGGAAGACA	GCGAGTGGAG	660
	AGACACTGGG	ACGGG					

## 1656RP

45	GATCTAGCGA	TCAATCGCAG	CTAACAGATG	CTCTGACATT	ATGCATGAGC	GCAATCATGA	60
	TGGACACATC	GAAGCTCAAG	CATAAAGTAG	AGGACTCGGA	CATGCAAGCG	TACGCCATCT	120
	GCAAAAGCGT	GTTGACCAAT	ATGAACGAGG	ATGCGTACTA	CAAGCGCATG	AAGGCAGCAA	180
	AGAATGACGT	AGATGGCTTC	TCACTCGATG	AGATTCTTCG	TAAGGACTAT	AAAGAGTTGG	240
	TGTTCCCGAG	CCGCACTGCA	GATCTACGTG	TTGGCGTACC	TACTGTCTGT	CGCTCTTTTC	300
	AATGGATGCG	CGAGAAGTTC	GGCGACAATG	GGACTACGAA	GCTCTGGCAC	AGTTTCCCTC	360
	TGGAGCATAA	GTTAGATTTC	CTCGTGGTGC	TCACAATTAA	GAAGGCCAAC	GAGGGTTTGA	420
	AACGGGAGTT	GGCTATCATG	GCCAACCTCT	GCGACCGTGC	GCAGCAGGTC	GAGTTCTTGA	480
50	TCCAAAGCCT	CACCCAGAG	TTGCAGTTGA	GCAAGACCTC	TGTCTTCTCC	CCCGGCTCAC	540
	TCGTCAATTG	CACGTGCGAG	CAGAGAATGC	TATCTGCCAG	TCGCAAGCAA	ATAGTACCTC	600
	TCCTCAAGAG	AACCGTGCCT	GAGTTATAGC	ATGCTTATGT	AACTAACGTT	CCAGTTACCA	660
	CTTCCACACA	TCTCAGCGGC	AATGTCGCGT	TTGTGGTCTC	CAACC		

EP 0 866 129 A2

1656UP

	GATCTCTTCC	TACCCTGTAT	TTCTACTTAG	CAGGAACCTA	AATATGTCGA	AATCATCGCT	60
	AGTAGGATGT	TTTTTCTACA	ACACAGACAT	TTACGCCAAC	CAGAACGCTA	AGGCATGCAG	120
5	TATCTCGCGG	AGTATCTGCC	TAGGATCGGC	GTAATGCTAA	TAGTGCTTGC	GGGAGAGGCT	180
	GGTGAGGTTG	AACTGGGAAA	ATTGGGTGGG	CATAGGTTGA	CTGTACAGT	AAATGGAGCG	240
	GCCGAGGTGA	TCGAATTGCC	CTGTGAGGTT	GATCCGCTAG	CGCGGCCGCG	TATTAGACAC	300
	TCCGAAGGTG	CATTTGAGGT	CCGGCTGAAG	GCGGTGAATG	GGACTGAGGG	CCGGGGCGCG	360
	GACTTCACTA	TGCTGGCTGC	AGAGGACGGG	TGGGGGCGAA	AAGACCTGGC	GCGTGTGAA	420
	CTGCGCTGCG	CGGCGTGCGA	CGGGCTGCTG	GTTACGGGCG	AACATGCAGG	CGCGTGAGCG	480
10	CGATGCCCTC	CGAGTTTGG	ACGGAGCTGA	TGGACTACTG	GCACTGCCAC	AAGCCTGCGG	540
	ACGAGTCTGC	GGGCGCACAG	CAGTACCTGA	CGAAATATAA	CGCGCTGCTG	CCTGCGGACG	600
	GGGAGCTGCT	GGTGGGGGAC	ACATTCTGTA	CGGTCGGCGA	GGGTCTGCTG	TCAGAGAAGC	660
	TGGCGATGAG						

1657RP

	GATCGATTTA	GATTTACCT	TCAGGCACAC	TAAGAGATGG	ACTCCTTACA	CTAAGGGTGG	60
	GCTGACGGGC	GGCGTTGAAC	GTGTTTTGCT	CGACGGACAG	ACTGTCTGTG	TAAGCGGTGA	120
	CCTAGTACCA	TCTGCAGCTC	TAGGTGAGGC	CGTTGTACCT	ACTTCAAACA	ATTACACTTC	180
20	GACTCCTCTA	TTGAACGCGG	AGCCATTGCA	CAGCTTTGTT	CCACCTTCTA	GCTCGGGTAA	240
	GAAGCGGTTT	TCCTTCTCCC	GCGAGCGGGG	AAACTCGTTT	GCTTCAGCTG	GTGACCACGA	300
	GGAAGCTGTT	ATCGACCAAC	CGCTGGAACA	AAGGTTGATG	TCTTCAAGGC	CACCAAAGGA	360
	GCTGTGCGCC	CCAAGTGCGC	TGAGAGAGCT	AGTCCGTGCG	CACAATCCAT	TCAGAGGAAG	420
	GAATATCTTA	TCTGTAAACC	AATTCAAACG	TTCGGACTTC	CACGCCTTGT	TCGCTGTGGC	480
	CCAAGAGCTG	CGTGCGGCTG	TCGAGAGAGA	GGGCGTTCTC	GAATTGATGA	AGGGCCGCCT	540
25	CTTGACGACC	ATATTCTATG	AGCCATCAAC	GCGCACATCC	TCTCTTTTAA	TCGCGGCAAT	600
	GGAGCGCCTC	GGTGGTAGAA					

1657UP

	GATCAAGTCC	TTCCAGCCGA	GCCAGTCTCG	CACCGCATAC	CAGAAATGCA	TTGCGGCACC	60
	TAGCGGGATA	TTCTGCGCGC	TGTACTCGGT	CCACGAAAAG	GCCCAGCGGT	GTGCCAACGC	120
	AAAGGCTACC	ATCTCCAAAC	AGAGCGCCAC	ATTGTGGTAT	ACGTAGCCCA	TGTTCTGTCC	180
	CSCGAGTCC	TGAATCAGT	TCAGGTAGTG	GAGAAGCGTG	ATKACCATAC	CCTGCCAGTA	240
	GGATGCAAAA	ATGATCAACT	TAACACATAA	GAATTTAGGC	CATGGGTTGT	ACTTGCGCAA	300
	CTCGTTGTAC	AAGCACTTCC	AGAAGAGCGC	CAAGTTATAG	AGCGACCATG	ACGCGCTCGC	360
35	GTTGTATACA	AGCGTCAACC	ACTTACATCC	CAGATCCCAC	TCCAACACCT	GGAACGCAGA	420
	CATCCCCAAG	CAGTACACCG	GCTTGAACCA	CACGTACTGT	AGAATGCCCC	GCTTCACAGC	480
	CAATAACGCC	TTGGGGTCCG	CCATATCGAC	CATGGGCAAC	ACCCAACGTC	CCACAACGGG	540
	AATCGGGTGC	TGGATCCTTT	TCTGCTCCGG	CGCAAGGT			

1659RP

	GATCAAAAGT	TGATTAAACT	AATAAAAGAA	TTATTTTATG	TATATTGATT	GTATAGTCAT	60
	TTTCAGACAA	AAATCGTGGA	AATTTTAGCG	GCCAAACATA	AAAGTCAGAC	ATTAGAAACT	120
	GACAGATACT	TTATTTACTG	CATAATTACA	CTAAAAACAA	CTGTTCTCAA	AAACTACGGA	180
45	TTATTGACCG	CCCCCTCACT	AATAATGTAC	TCCTTCTATC	GGTTTCTTGC	GGGTAGAAGC	240
	ACGTAAAGAG	ATCAGTTTCA	CTTTGCAATT	TGGGCACTTT	TACGTTTCCA	CTTAACGATC	300
	ATTCTAGTGT	ATTTTATGAC	CAGGAAAGAA	AAGGAGCCTA	AAAACCTGAA	GGCAGCCAGA	360
	CCAGCGACTG	ATCCCAAGAC	AAAAACCAAA	TATTTGTTAT	TAGAGGTTTC	TTCAGGTGAG	420
	TATATTGGG	TTATCATCAT	GATCAAAATC	AAATTGGAAA	GCATCCATAA	CATGACAATT	480
	CTAGTCCGCA	CATCACGGTA	GTGATCTGCT	TGCTTTTGGA	TAGGATCAAC	TTTTATTTCT	540
50	ACCATTTCAT	CCGATTTTAG	ACGACCTTGA	TTTCCTGGTA	TTTATTATCG	ATGTCCTGTG	600
	CCCATTCAGT	ACCCCTCAACT	ATTTGTTTGC	CACGGGGCCC	TGGGTAACCA	TAGCTTCAGA	660
	CTTTGGCTTG	GACCCCTGCG	AAGCGCCTTT	TGT			

## 1659UP

	GATCGAGTGG	TCCACCAGGT	AGTCCTGGCC	CGGCTTCACG	TTGGGCGGCG	TCGAGAAGTA	60
	GACCCGGTAC	TGCTTGCACG	CCTTCTTCAC	CTCCTCGTAG	CTGCCCCGTCA	GCCCCACGAT	120
5	GTGCGGGTGG	AACTCGGCCA	GGTACTCCTT	CAGCACCGCC	GGCGGGTCCC	GCGCAGGGTC	180
	GCACGTCACG	AAGATCGGCT	GCACGTCGAT	GCCCCGTTGT	TTCAGTCCGC	GTAGCCACGC	240
	CGCCAGCTTG	TCCAGCTCCG	CAGGGCAGAT	GTCCGGGCAG	TGCGTGAAAC	CGAAGTACAC	300
	CAGCGAGAAC	CGCCCCGAGAA	GGTCTCTCTC	CGTGAACTCG	TTGCCGTTGA	AGTCCACCAG	360
	CTGGAACGGC	CCGCCACCCG	CCGGCCGCC	GTACCCCCGG	TTGCGCTCCG	CCTCCCGCTG	420
	CACCTCCAGC	CGCCGCTTCT	CGCGCGAAAA	CACGTAGAAC	AGCCCCCGCG	CGAGCACAGC	480
10	AGCACCGCCG	CCGCCCTTCCA	CGTCGTGAAC	TCGATCGCCC	CGCCCTCGAC	CGCTGCGAGT	540
	GCGTTTCCTG	CGCCCCCAGC	GGGATCCGGC	TCAACGGCCG	CCGCTTGCCC	GGCGCCTCTG	600
	GCCCCCGGGC	GCCTCCTGCG	TCGCCAGCCG	TGTTGCGGAG	AACTCCCGCA	CCCCGCCAAA	660
	CGCTGCTCTC	TGCCCTTGCAA	TTCCCGCAGC	TTGCCCTGCAA	ACACCGAGTC	CTACTGATCA	720
	TCTCTG						

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## 1660RP

	GATCAATTTCG	ATGCCAACCA	AGATGAAGAC	CATCTGGGTG	AGTTAGCAGT	GCACTCTGCG	60
	GATACATGGT	CTGAGACGGA	TAGGAATCTA	ATTTTGAAAT	TATTGGGCAA	GTTCAAGAAT	120
20	ATCAAAGCTA	TMTACAAATC	CGAAGATGTC	CGCCAAAGGT	TGATGGAATT	ATTGGGTAGT	180
	CGAACGCTGG	AAGTGCAGAA	ACTGGCCCTA	GATGCGTTGT	TAGCATACAA	GGATCCAGTA	240
	GCTGTGAAAT	ATAGGGACAA	TCTGAAGAAC	TTATTAGATG	ACACGTTATT	CAACGACGAA	300
	GTAACAAAGT	TATTTGCTCA	GAATGAGTCA	AGGGTTATTG	TCAACACTGA	TGAAAGATTA	360
	TTAATGCCCT	TCATTTTGCG	TATTTTATTT	GGCCGTGTTT	AGACACCTAA	TACCAGTGGG	420
	ATCAAAAAGA	CAAGAAAAAC	TGCGGTCATA	ACTGTCTCTG	CAAAATTTAGG	TGAGAAGAAT	480
25	ATTACTGACT	TCCTTGGCTCT	GGGTAGTAAT	GGTATCAACT	ACCAGTACTT	CTTTGAAGAG	540
	AATGCGGTTA	TTCTTGACAG	TGAGCTTACA	GCGATAAATT	TTAGGAGAAT	GCTTGGCTTC	600
	ATAAATGTCC	TAAGTGCCCT	GTTGAATGTT	TTAGGTTCCA	ATTTCCCGGA	GGCGGTCAAG	660
	ACAACATATTA	AACCTCTCGT	TTACGCAATT	CACATGTCAG	GTCGTACTGG	ACAGAATAAA	720

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## 1660UP

	GATCTTATAG	ATTTTTCATCC	CCAAGCTTAC	AAAGAGAACG	TTATCCACCT	GTTTTAGCCA	60
	GGCTTGGATG	TATTTTTTCAA	TGGTACCCAT	GTCTCTCTGG	CCCAAGTTCT	TGAACAAGTT	120
35	AGTTAGTAGC	AGACTAGCCA	TCCTCCTGCA	TTTAGGAGAG	TCGTCATTTA	CTGATACGTT	180
	TGCTAGGAAC	ACGAAGAATG	AGGATGAAAG	TTTCATTAGT	AAAGCGGGCC	CAGATTTGTT	240
	GATCAGAAGG	TTAAGCAATT	CCATAACAGA	TTGACGACCT	TCCTTGAGATG	GATACTGCAA	300
	ATTGTTGACT	AAAAATTTCA	ATTGTTTTTTC	CAGCCTGCCT	TTACTTTGAT	CATATTTCCAT	360
	GAAGAACTGG	TAATAGACAC	TCCTGGCAAC	ATCCCTGATT	TCCTTAGCAT	GATTCGTGAC	420
	CATGACTTCT	GCAACGTTAT	CAATAATATC	GTACAGCTTC	GGAAGAACAA	TATGTTTGGG	480
	AACCAAGGAT	TTCAAAAATC	CAAAAGCCAG	ACCTTGCTTA	TTGGGCTCCA	TCAAATCTGG	540
40	TTCAATCCGA	CCCAAAACAT	ATTTCGAGCG	AGAATCCTTT	AATTCAATGT	CTTTATAGCG	600
	GATAAGCGCA	GATAAAAAT	TCAGACCGAC	TTGACAAAGT	TCACCAGAAG	T	

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## 1664RP

	GATCCTAGGG	TGGTTCATGG	CACTGAGCGG	GACGTGTTCT	TGGACCGGTC	GAACCGCAGC	60
	AAGAGTCTGA	AGTCCCTGAA	CGCGTCTCTG	GAGCGGCTGA	AGCGCAATCG	GCAGGCGGCG	120
5	TGGATTTTCC	CAGAGGGCAC	GCGGTCTGTAC	ACAACGGAGA	TGCAGCTGCT	GCCATTCAAG	180
	AAGGGGGCGT	TCCACCTGGC	GCAACAGGCG	CAGATTCCGG	TGATTCCGGT	TGTGATGTGC	240
	AACACGAGCA	CGGTGTTCAA	CCCGCGGCTG	GGCATCTTTA	ACCGCGGCAC	GATCACGGCG	300
	AAAGTGCTGG	AGCCGATCGA	CACGGCTAAC	ATGACCAAGG	ATGACGTGGA	CAAGCTTGTC	360
	AGCGACGTGC	AGGCCAAAAT	GCATGCGGAG	TTGAGGGCGC	TTGGCTACGC	GCCTGCGATC	420
	GTGGACACGA	GCCTACCCGA	AGAGGCGCTG	CGGCCGGAGT	TTGTGGACTG	CAAGGAAGAC	480
10	ATCACGGAGG	TAACGCGCCT	CTCGAAGTAA	CCTTGGTTGG	TATCATATAA	ACGTTGCGAC	540
	GAGTTATGTA	CATATAGCGC	TGCTAAGTAG	GCATTTCAGTC	CCC		

## 1664UP

	GATCCGACTG	ACGGTGAATA	GGCCACCGTA	GCATGCGCCG	CTGAGCGCGC	TGGCGAACGA	60
	TAGCAGCGGT	CCTTCCGAGG	CTCTGGTGGC	CAAGACAACG	ATCCACTGGC	CCACCACGCC	120
	CAGTAGGAGG	ACTGCCCCACT	GGACTGACAT	CGTCGACACA	CCGTTGTGGA	TGCAGAGGTC	180
	AATTATCAAG	CCCGACAGGA	AGCGCGAGCA	CGTCGAGGCA	ATCGCAAATT	CTGGCAGCAC	240
	CGACGCCTGG	CCCAACAGGC	TCGACAGCGA	GCCCATGTTG	GTGAGGAACA	TCTCCATCGG	300
20	GCCCAGCGAC	AATAGCAACA	CAAGGGCCAT	GAAGTACGCC	GCTGGGTTCG	GGAAGAAAGTT	360
	GCGCAGCCGG	CGGCGGATGT	CCTGCGGCAG	CAGCGGCTCG	GTGGGGCTCT	GCATGCCCCG	420
	GAAGGTCAGT	GTTGCGGCCT	TGACCTTGAG	CATAGTGACG	ATGCTCGTCG	CAAACCACAT	480
	GCAGAAGCTG	ATCAGCGTAT	ATGCGACAGC	TAGAGTCCTG	AATACACGAG	AAAGGTCAAG	540
	GTACGGCAGG	CCATTTCCAA	AACCATGGTA	TCTTCAGCAG	CTGCGACCTA	GCACAGAC	

## 1666RP

	GATCCTTGCG	TACTAAGAGT	TAGACTTTAA	TTAATAATAT	TATTTGTAGA	AGATAGAAAC	60
	CATACTGACT	CACGTCGTAT	TTAACCCATC	TCACGTAACC	TTTTAATTGA	CGAACAGTCA	120
	AACCCTACTT	AGCTGTTACA	ACCAAGAGGA	TAGGTTGAGT	CGACATCGAG	GTGGCAAACA	180
30	TAACTTACAA	TAGCTACTCT	ATCGTTATAT	TACCCTGTTT	AATTTTGTGA	TCATAATAAC	240
	ATTTAATTAT	TATTTCAATA	ATTCTCATT	TTGTTTCAGC	TATTTTCATT	TGTATTATTT	300
	ATTAATTAA	ACATATTGGG	CTTTCGTGGA	TATAATTATT	GTTAATCCTA	CTCATATATC	360
	TAGTCGTTGA	ACGTTCTTAT	AACTTTATAA	AAAGGATTGT	TATAAGCTTC	GCTGCAGATT	420
	GTCTCTTATT	ATTATAAAAT	AATATTAGGA	GTTCTTTTGA	ATTAACCCAA	TTTACTCAAT	480
	ATATTTAAAT	ATTGATAATT	AAATTTTACA	ATTTAATGGG	ACTATTAATT	AATCCCTAGC	540
35	GTAACTTTTA	TTCGTTATCA	AATACCATT	CAATATGTAT	ATTTTTGTTC	ATTATGCCAA	600
	ACTTACGTTA	TTGTTCTACT	TGTAGGTATT	ACAATTATAG	CACAGTTATA	CCATTATATT	660
	TATTTAATAT	ATTATCCCTA	TATTATGTTT	TATTAACATA	TAAACTGTGA	CAT	

## 1666UP

	GATCCTTATA	AAATGGGCAA	TAGACGTGTT	ATAATATAAT	ATACAAAATT	ATAAATAAAT	60
	ATTTAATAAA	ATATAAAAT	AATAATTAAA	GTATTATAAT	AATTAATAAA	ATTATTTATT	120
	AATAAGTATG	GATTTTTTAA	TGAAATTTGT	TAAAATGAAA	TAAGAATTGC	TAGTAATCTA	180
	TTAATAAGAA	AGTAATGGTG	AATACTCTAA	CTGTTTCGCA	CTAATCACTC	ATCACGCGTT	240
45	GAAACATATA	ATTAAATAAA	GAATATTAA	TAATTTATTA	ATTATTAATT	ATTATTAATA	300
	TTATTTAATA	AATATAATAA	ATATTTTAAT	TTAAATTATG	AATTAATGCG	AAGTTGAAAT	360
	ACAGTTACTG	TAGGGGAACC	TGCAGTGGGC	TTATAAATAT	CTTTAATATT	CCATTTTTTAT	420
	AAAATAAATA	TATTTTTTTAA	TATATTTTAT	AATAACTATA	ATTAAATAGT	TAAAATTTAA	480
	ATTATAATTT	AATAATTTAA	TAACCTATTA	ATTAGAGAGT	TAGGGTACAT	CCCCCTAAT	540
	GCTATGCATT	ATGGTTGGTA	CCACTCTAAT	TAATAAACTA	TAATAAAATA	ATACTAATAT	600
50	TTTATATCAA	TTAAATTATA	ATTATTTTTT	ATTAATATTT	TAATATTATT	TAATGAAATA	660
	TATAAATAAA	GTATTAT					

## 1667RP

	GATCCATCGT	GGTGTGCTTC	ATTACCTGTA	ATTCCATTGA	TATCCTGGCT	ATGCAGTGCT	60
	GGAAACGCTC	CTCCAGCGCC	TCTATTTTGT	TATTCAGCTC	CAAGTACTCC	GCGAGCTTAA	120
5	AGGTCAACGA	GAGCGACCTT	GGATTGCACC	TGACGGCGAT	CTCAAGGACC	TTCTCGTGTCT	180
	CGTTCTCGTC	CACAAACATG	GCGTAGTTGT	ACCATATCTC	CGGCGCAAAG	CACATGTGCT	240
	GCACAGCCTG	GCGGTGCACG	TATTCCACGC	GCTGGCGCAG	CACGACTTCG	GGCAGGTCGA	300
	GCTTGTTGTG	CAGCTCCCAC	TGGATCCACT	TCGTCCAGAT	CTGCAGCTGG	TACTCATCGT	360
	ACTGACCGGG	CGCAGGCAGG	TTCTGCTGTG	TCGCCTGGTT	TAGCTTCGTG	GGCAGCGAGC	420
	GCCGCAAGCC	CTTCGTCAGG	TTCGACCACT	CCTGGTACAG	CGAGCGCGCA	TTCATGTAGC	480
10	TCGCGGAGAG	CTCTCCGATG	AACTTCCGCG	CCGTCAACTG	GTTGACCTCC	TGCTCCCACT	540
	GCGTGTATTT	CTCCCAGTAC	CGCTCCAGCG	ACTCCACTGG	CAGGCACAGC	AAGGCGCTTG	600
	TACAGCTTGC	GCAGAACTCT	GACCCGGCTC	TGCTCCTCCC	ACTTGCTCAC	CGGCTTCCAC	660
	TGCTCCAGAA	ACTGCAGGTA	GTCTTGCCAG	AACTGCATCG	ACCGCGG		

## 1667UP

	GATCTAAGGG	ATGGGTGACT	GCTGCCGGTG	CTCACAGCAG	TGGCACGTAG	CTAGTAATGG	60
	TGCGAAATCG	ATCAAAGAGG	GTGCGTCTGG	CGGTACAGGC	AGAAAGCACG	CCCCCGGATA	120
	CAAGTTCCAG	TTCTACAAGC	ACCTGCAGTT	CCAGGGTACG	AGGTACCAGG	TGGTGACTTC	180
20	GCGGCCGTAT	CTGATAGAGC	GGTACGGGGA	GCGCAAGCGG	GCGACGATCA	GGTCGTTTGT	240
	CAAGTGACATC	CATCGGAAAA	TCAACGACGA	TGTGACACGG	ATCAGCGACG	AGCGGGTGAC	300
	GCACGGGGTG	TCGAAGTGGG	AGAAGTCGAA	GCTGTTCTTG	CTGCTGGTGA	CGCTGTCCGA	360
	GCGGGGCGGG	CCGGAGTACT	GGCTGGACAA	GACGAACGGG	TGCCAGAGCC	GCGCGGGCGG	420
	AGACGGCGCG	CGGAAGAGCG	ACGAGGTGGA	GGAGGGCGGG	AGCCGGCGGG	GCCAGAGGCT	480
	CGTCTGCACA	CTGGTGGAGC	AGATCATGCG	CGAGAACATC	ACGGAGGACT	ACGACGAGAG	540
	CGTGCACGAC	GAGAACTACG	TGTTCTCGTC	GATATGGGCG	AACTTCATGG	AGGGGTTGAT	600
25	AAACCACTAC	CTAGAGAAGG	TCATCATACC	CAAGTCCGAG	CTGAAGGTGT	GCCAGCAGCT	660
	GTACCAAGCC	GATGATGAAG	ATCATCTCAC	TCTATAACGA	ATACAACGAG	CTCATGGACA	720
	AGA						

## 1669RP

	GATCAACAGC	ACCTCCACCT	GCGACAGGTC	GAAGTCATCG	TAAAAAGGCA	GCGACGCGAT	60
	ACCCTGGTGG	GCGGGATGCA	CACCGGCATC	CAGCATGACC	GTCTTGCCCT	TATACTGCAA	120
	TATATGGCAT	GAGCGTCCAA	CCTCATTGCT	GCCCCCAAGC	CCGAAGAATC	GGAACGAATT	180
	CGTATCTAAC	TTCTCCTCCG	TCATCCGCAA	TTTGTTTATG	TCTGCCTGCT	GCGAGGTGCT	240
35	GTGCTCTCTA	CCCAATGCCT	GCGACACTGG	CTACTGAGAC	AATTCCACGT	AGCTGTGCT	300
	GCAACTTTT	TGCAGCTATG	GAAATACCGT	GGTTCGGTAG	ATTTGATTCT	GTGGAGATGA	360
	ACGATCAAAC	GGGAACACTG	GTTATCGGGT	ATGCGTGTGG	TTAGTACCCA	ATCACCCGCA	420
	GAGACAAAGT	CCACTATTAA	TTGTAGTACT	TACAGGAACA	CCGATCGCAA	GAAGCTTTAA	480
	CGGCTCCGTT	TACCAACGAT	CAACACTTTT	CTCCTCGAAC	GTTATGCTGT	GCGGCGGTGG	540
	CGATTGCGAA	TGATTGTTGA	ATTGAACCAG	AGAGCGGAAA	ATTTTCGTTT	TCACGTGACC	600
40	GTATCTTACA	TAAGCTACTG	AACTATATGA	AATACCGACG	TTGCTCGAGG	ACCGCTAGCG	660
	CAGTGTCTCA	AGCAGTGATC	ATGAGATTGA	GTTGTTCTGA	TGTGTACAT	GAGAGTACTG	720
	GG						

## 1669UP

	GATCAACAAG	TGCAACAGCA	AGGTGCAGTT	GCGCCATGTG	CCCTCGGGGA	TCGTGATTGA	60
	GTGCCAGGCA	ACCCGACGCC	GCGAACAGAA	CCGCAAGCTG	GCCCCGCGAG	AGCTAGCCGC	120
	CGCGCTGGCG	CAGCCCCCGG	GTAGCGCCAG	CGAACGCGAG	CTGGCGTTGC	GCACGTGGGC	180
	GCGGCAGGGT	AAGCACGCGC	AGGCGCGCAA	GAGCCGCGAG	AAACACGAGC	GCGCCCCGCG	240
	CGAACGCGAG	GAGCTCGCGC	GCGCCCGCGA	CGCGGAGGAC	GCCGAACCTC	TGCGTCAGCT	300
50	GCTCGCGAAG	CCGCCCGCCA	CCTCCTAGTG	CCCCGCGGGG	CCGCGGGGGG	ACGCAAGGGC	360
	GTCTTTTTCG	GCAATTCCAA	ATAGACACCC	TAGTCGCCCT	TGCTGCCCGC	GAGCGCAGAG	420
	CAGGCAGCTA	GCACACCACC	GTCCACGCGC	AGCGCTTTTG	CTGGCGAGTC	GTGCCGCACT	480
	CCGCTGGCTC	TGGTGTGCAC	ATGCCGCTCC	GGCGTGGCAC	CGCAGTGCAG	AGCTACCTAC	540
	GTACGTTTGC	AGGCTTCGCA	GTACGCCTGA	TACTGGCTCT	GGTGAAACTT	CCCGACAAGA	600
55	GTAAATCTC	ACCAAAGAAC	AAAAAGATAT	GTTAGTGAGG	ATATCTCACA	TTCTGTTACT	660

EP 0 866 129 A2

GGAAGTACAC AAAGT

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## 1670RP

	GATCCGGCAA	GATCGTCGTT	CAGTTGACCG	GCAGATTGAA	CAAGTGCGGT	GTCATCTCTC	60
	CAAGATTCAA	CGTCAAGATC	AACGACGTCG	AGAAGTGGAC	TGCCAACCTA	TTGCCAGCCA	120
5	GACAGTTCCG	CTACGTCATC	TTGACCACCT	CCGCCGGCAT	TATGGACCAC	GAGGAGGCC	180
	ACAGAAAGCA	CGTTGCTGGT	AAGATTTTGG	GTPTTGCTA	CTAAGCGGCT	GCTATATAGC	240
	GTATCTAGCT	CTAATGTACG	ATACTCAGTG	TCTATTACGA	CGGCCGCGAG	CTCCACGCGC	300
	CACATACGAG	GCCAGCCGGC	GACGGCAAGC	GGGAATTCAG	ATGCGTTAAT	TAGCAGTAGA	360
	TTAGTAGTAT	ATATGTACAA	ACAGCATACA	CATGAACGGC	GTCGCCGATC	ATAATCTTCT	420
	ACCTCTTCTA	CCACCCTTCT	TTCTGGTAGA	GTCCGATGGG	ATAGGAGTGA	CGTCCTCGAT	480
10	ACGGCCGATT	CTCAAGCCGG	ATCTGGCCAA	AGCTCTCAA	GCAGCCTGAC	CACCTGGACC	540
	TGGGGTCTTG	GTCTTGGTAC	CACCGGTAGC	TCTGATCTTG	ACGTGCACAG	CAGTGATGCC	600
	GACCTCCTTA	CACCTGGCAG	CGACGTCTTG	AGCAGCCAAC	ATGGCAGCGT	ATGGAGAGGA	660
	CTCGTCTCTG	TCGGCCTTGA	ACTTCATACC	ACCGGTA			

## 1670UP

	GATCTATTTG	TGCCGTCCGC	CATTAAGCAA	GCGGCAAGCA	TCGATCCAAA	TCATGAGAGT	60
	ACCCTCGGGC	TTTCACTTTC	CAAGCCTTTA	TCAACAAATC	TGGTACACGA	TACATCCATC	120
	GCGACAGCAC	ATATAACCAGA	ACGGGAAAGC	CGACAAGATG	GCACTAGACT	CTGGTAGGTA	180
20	ATCTGAGTTC	GACCATATCC	ACTTCGTTAA	TGGTGATAGT	TGATAAAAAG	AAACGATACT	240
	GAAAATTTTA	ATGGTTACCA	ATCTCATCTC	ATCGCCATAC	TGAAAGAATA	TTGTAGGTCT	300
	CGCAGTGGAA	CAAGGATCAA	GCCCAGGCTA	AGACAATAAT	GGTTGCAGCG	GAGGCAGTAC	360
	AGGAACTACC	CCCAGATGAA	GAAGAACTGG	CCTTGGCTAA	GCTAGTGTTT	GGCGACACAG	420
	CAGACTTCCA	TGAAGCGCTG	CGAAATGCAG	ACCTTAATTA	TGTTTCTTCA	GATGAAGACG	480
	TATATGGCCA	GGAGTCGTCC	AGTGATGACG	AAGAAGGGAC	TGAAATTGGT	CACCTGAATG	540
25	ATGACCAATT	GTTTTTTTGTG	GACGAAGGTG	CAGATACCGA	GGGAAGAGCA	GATGGAGAAC	600
	CGGAGGCCAT	GGAGGTGGAC	CAGGTTAGCG	AGGAAAGCGA	CTCCGGAGAG	GAAAGCGGTA	660
	GCAGCGCTGC	ATGGTCAGAT	TCGGATGACG	AACACTTAAA	CGTTACAATA	GGG	

## 1671RP

	GATCGCTTTC	AAACCATCCT	GTAACACGC	TGAACCACAC	TTTACAAGAC	AACGGCATAT	60
	CGACAATCAC	AAGACTTCCT	CGAGACATGC	CCGCCACCAA	TCTTCATCGT	GTACTGACGG	120
	ACTATAATCC	AAGTGGCCAT	TTGAATTCGC	AGCATGATGC	CACGCTTTC	AACCTGAGCT	180
	CGAAACTGG	AGATGTACAT	CGGCCTTCCA	ATTCTCTTTC	GAGTTTAAAT	GGAGCACAAA	240
	AAAGGGCTAG	CATCCCAAT	ATCTTAGGCT	CTGCTCCACT	TAGTAATCAA	TCAAGAACTC	300
35	CAGACAACCG	TTTAACACAT	GGTACATCGA	TCCATGAGAA	CCCGCGGTTA	GAATTAAACG	360
	GTGATCAGTC	TTTACTCTTT	GGCGGTAATA	CAGGGCAGGC	ATCGGGTAAC	TTGGCGGGTG	420
	TTTCACCGGC	CGAAAACCTC	CGAAGGAGCA	ATTGCGATGA	TCAGAGCCAA	TATAGATTAC	480
	ATTCCAACGC	TTTCCATTCC	ACTGCCCCCTC	CAAACGAACC	TTCTAAGAAC	ACTAGTCCAG	540
	GTACAACGTG	TGCACCTGCG	AGCGTTGTTG	GTACAAACAC	AAGGAACACA	CAACGTGGAC	600
	CCACGGGAGA	TGTCTCCCAA	GAATCAGTCG	AACAGCCGCA	ATCAGCTTCG	CGCGCATCCG	660
40	ATGAATCTAG	CGCAAGAATT	ATGTCGCCTA	GTCATCATAC	GGAGCCAGTA	GTGTCTGTTT	720
	CGACAATCTC	TTCTAACACA	CGC				

## 1671UP

	GATCAGGGAT	GCGGAGGACA	TTCCGCGACG	TTATCGGCGA	GCACGACCTA	CGCGTCTGGA	60
	ACTATGTCAA	GTACGGCAAG	AAAGCTATTA	AGGCCCTTCGG	CTTCTCGCCA	GACGCATATA	120
	TTCAACAGAT	CATCCAGCTA	GCCATCTACA	AGTATGTGGG	CAGACAATTG	CCAACCTACG	180
	AGGCTGGGTC	GACCAGAAAG	TTCTTCAAGG	GTAGGACCGA	AGCGGGCCGC	GGCGTTTCTC	240
	CGGCCTCCGC	CAAGTTTGTC	AAGACTTGCC	AGTCGCCGGA	AGCATCTCCA	AGTGAGAAGA	300
	TTGCTGCTCT	ACGTGAGTCT	GCTAAGAACC	ATTCTGCGCT	GCTAAAGATG	GCGGCGGACG	360
50	GCCAGGGTGT	TGACCGCCAC	TTCTTCGGTA	TGAAGAACAT	GTTGCGTGAT	GGCGAGGAGC	420
	ATCCTGCACT	CTTCCGCGAC	CCGCTGTTCC	AGCACTCCTG	CACGTGGTAT	GTGTCTACCA	480
	GTCAGCTATC	TTCCGAGTAC	TTCCGAGGAT	ACGGCTGGTC	GCAGGTGAAC	GAAAATGGCT	540
	TTGGTCTGGC	GTACATGATC	AACAATGACT	GGTTACACAT	CAACATTGTT	ACMAAGCCTA	600
	AGAAGTCGGG	CTATAGTGTG	CACGAGCTTT	CACTACTACT	TGACCGAAGC	AGCAAACGAG	660

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## 1672RP

	GATCGTGTAT	TTGTCAGGCC	CATCCAAGCC	CTCCCCCGCA	CCCAAACCCA	CTATGATGGG	60
	CAAGAAGTGC	TCCAACGTCG	GATGGGCAGC	CTGCAACAGT	TCTCGTCCCT	CCGCGCTCGA	120
5	GAAGAGACGA	AGTAGTCTGC	CGAATTTACA	GGCGTTGGGC	GGCGTGGTTA	GCAGGACGTT	180
	GGACAGTGCC	CAGTGAAAGG	CAGATGAGCG	CGAGTGGCTT	TTTGCATGG	CAGATCCGCA	240
	GAAGAGATCT	CTCAGGTTGT	GCACAGCCAT	GCCAGACGTT	ATTATCAACC	CGCCGAGGTC	300
	GCGGTACCTG	GACAGGAGGC	GCCCCGAGCG	ATACTGGTCC	CGCAGGTCTG	TTCCCCGCCG	360
	CAGTGATATT	TGGACCAGCG	GTACCGGGAC	ATCCCAATCG	TCATCCACGC	ACTTCGAAGC	420
	GGAGAACGCA	ACTTTTAGGG	GGACCCAAAC	GCCATGGTCT	ATGCCGCGTT	CTGTGAGCAC	480
10	AGCGCATAGC	GGGCTGCGTA	TGTGGTTGAT	GGTGTCCGCG	ATGTCCGTAA	CTAAAGCCAT	540
	GCTTGATTTG	CTATGGAAC	CCTCCTCGTA	CATCCGGGTC	GAGAACCCAT	AAAAATCGTA	600
	TATCAATTCTG	TTCTCCAACG	GGT				

## 1672UP

	GATCCAGAT	TAGATATTAC	TTAAACGTTT	CACAGCTTTT	TGATGGCCTA	GTTCTGCTGC	60
	ACGTCTATAA	TGGTCCATCG	CCCTGTGCAAT	GTCCGGATGA	CAGCCGACCG	CGTGCTCCGT	120
	ATAGAAGCCC	AAGGCATACT	CCGCTTTCCG	TAGCCGGCCT	TCGGAAGCAA	TGGATGCTTT	180
	ATACGCCCAT	TTGTAAGATT	CTGAAGCGTT	GGGTTCCAGC	ACGCCCTTGA	CACCAGTTAG	240
20	GTACCAACCA	CTCAAAGCGA	GCATAGCCAT	GGCATTTCCT	TTTGGTGTCTG	CGTTTGCAGC	300
	CTTCAAGTAC	CACACGATGG	ATTTCCTCAG	GCTATACGGC	AAGTGTAAAT	CAGCGTACTC	360
	GTAGCAGTGT	CCCAGCTTCC	ACTGAGCAA	CGGATAATTA	AATTTAATGG	CACATCTGAT	420
	GTAAAGGTCT	AGAGCCTTTA	GGGTATCTTG	TGGAACGTGC	TGCAACTTGA	CAGCCTGTCTG	480
	CAGCTGTGGA	TGCAAACAAT	CAAATTCATA	GATCTTTGCG	AGTTCTGTATA	ACGCCTGGGG	540
	AGAGACGGTC	TTGTCGTGTG	CAGCAGCCCC	CTCGAACCAT	CGTATAGCAG	AAATGACATC	600
25	CTGTTCAACA	ATAATTTTAC	CTGTGTCTATC	ATCCACCAGG	CCATTTCAGTT	GGGAACATAC	660
	CCAACCTTATA	CATGCTACTG	CTCTGTCCGG	AAGA			

## 1673RP

30	GATCCCAGCT	CTTACGCTCG	CTCAATTGAA	AACCTTTTCT	ACACTAGCTT	TCTTATCAAG	60
	GAAGGACGGC	TAGTCCCTAGA	AGATGACGAT	GAGGGCTTCC	CGGCCATCCG	ACCCAAGGAA	120
	CCCCTCCCGC	AGGATCCCGC	CGAAAAGGAA	CTGGAACGGC	AGCGACGGAA	TGACGCGCGC	180
	CAGAAGCATA	TCATCTTCCA	AATGGACATG	GCCACGTGGA	GGAAGCTTAT	AGACAAGTTC	240
	CACATCACAG	AGTCATTTTT	ACCGTGATCA	TGTATAAATA	GCGCGCATCT	ACGTATCACC	300
	CGCTGGCCGG	GCGCTGACCC	AACCAGGCAC	TGCTAGCAGC	TCATCTATCG	GCCACTTCGC	360
35	AATGGTCAGC	GCGGCAACGT	CTGTCTGTAC	GCCGTGTCCC	TCGTAGAGCT	CGATGCCCGC	420
	CCAGCCGATC	ATCACCGCAT	TGTCTGTACA	TAGATCTGGA	GCTGGATAGT	GAAAGGAGTC	480
	GAACGGTCTG	AATAGTTTCAG	TCTCGAGTCT	GGCACGCAGG	CGCCGGTTGG	CGCATACGCC	540
	GCCGGAACAC	ACAAACTGTG	CCACATCAGC	AACCTTATCA	GCATTTGAGC	CGCAGCACCA	600
	GGTTAATCTT	GGTAATCAAA	TGGTCGAAAT	ATGGCCTCCT	GAATCTGAAT	TGCTGCTACC	660
	CGGCGTTCCG	CCTC					

## 1673UP

	GATCGCTCTA	CCGACGTACT	GCATGCCTGT	CTTGGTCTTA	AGTTAAAAAC	CACAGCACCC	60
45	AATCGTTTAC	ACCGCAATCT	TAGACCAGGA	GCTAGTGCTT	GCGAGCCCCT	GTCGTTCAAA	120
	TGGCAGGACT	GTTGTTTGGT	TGTGAACCTC	GCGGACTGAG	GAAAGGGGGC	GGAAGATCTA	180
	TTTTGACCTT	ATTCGCAACC	GTTTAGATAT	TGAAAGCAGG	GCAACACTAG	TAAAACTCGA	240
	AATTAGGACA	TTCTGTGAACA	GATGTGAGCA	GAGGATTCCG	GATGCGCTTC	GAAATGATGA	300
	GGGCGCATGC	TGCATACCCT	GGCCGTGCGG	CGTAGTGTAG	ACCGTGCAGC	GCATGTGCA	360
	AAACAACGGC	GCCGTGGCGT	CGGCATGCAG	CTAGCACAGC	ACCTGCGAGC	GCGCAGGCGT	420
	GCATCCAAGA	GTAACGCCAC	ATGTCGGGCG	CGTTGCTCCG	TATGTACAAG	TTATGTCATT	480
50	ATTTCTACAG	ATATCATGTT	GAATATTAGC	CCGCGATCAT	CTACTCAATG	GTATCGTTTG	540
	GTCTATCTCG	CTTACGTCAA	GATGCAGGCT	CCGCCCGGGG	ACTACGCGCC	AGGGTGCGCA	600
	GAGCAGTTTG	GTAATGAGA	AGCATGATAC	TGCTTTGGAT	GCTGGTCCAG	ATGAACCTGG	660
	GGCCACACAC	GCTGAAGGCG	CCACCCAGTC	CCTCGTAGCG	AAGTACGACT	AACAAGCTGC	720
	GGAAGA						

## 1674RP

	GATCTCATTTG	AGGTACACAG	ACACAGCTGG	CAGCGACGCC	CACGCCTGGA	TGGACGAGTT	60
	GGCGAAGCAA	TCATTCCGGT	TGTTTGCCAG	CCCTGTCGTG	TGTTTGCTCT	TCCTCGTGGA	120
5	GCTCTGGAAC	ATAGCAGAAC	TACCAGGGGA	ATAGCCACGT	GTAGATCGTC	GGACCTAAGA	180
	TATAGTATGA	AAGTGCAAGT	GTGCCACAAA	GAAGAAGTCT	TTGTGGTATG	TTGTCCGTTC	240
	CGTAGAGAAA	GCTTCCGACC	TTATTAATAG	AGAGTGTACC	GTCGTAAACA	GAAGAGGGGT	300
	ATGTCACCCCT	GTGCAGCATG	TAGATGGACT	TGGGTATCTA	GTCAGCCGTT	GTGCTTGAAG	360
	GTGGACCAAA	CTAATCCTTA	GTGCATAGTA	TTTATGTGGG	GCGGCCTTTG	AACCAGGCTT	420
	TTGGGATGCT	CGAAGGCGGA	ATAATACTCC	ACGTGACAA	AATATACGTC	AACTATTAAC	480
10	GGCTAAATTA	TCCCTTGCGA	GGAGAACATC	CCGTAAATTA	CAATTATCAT	TCTATATTAT	540
	AAACATATTA	TAAAACGTCC	ATCTTGCTAA	TATAAAAAACA	ATCTAGGTCTG	GCTTACCAAC	600
	CATATTACAT	CAGTAGGCAG	CGCGATCTGC	ATCCGTCATG	GCGTGGAGTA	TCCAGTT	

## 15 1674UP

	GATCATCATC	AACTATATCG	AGAAGGAGTG	TGACCGCGGC	GTTGCTATGG	GTAAATACCC	60
	GTCTACCCTT	GACCGGGAAG	CGGTCCGAAA	GCTGGTGGCA	AAAGATTTGG	AGAACTTCCG	120
	CGTAACCAAC	AGCCTCACGC	TGAACAGTCT	CTCCCTATAC	TTTCGCAACC	TAACACGGGA	180
	GCAGCGGGAA	ATATGCATAT	ACAACAACCT	CACCGACTGG	AGCTTGCTAA	TCCTTCCGGA	240
20	AGAGGAGAAA	ACCAAGTACT	GCAAAAAGAAA	GCAGGGTTCT	TCGTACGAAT	AACAGTAATT	300
	GTAACATATAT	AATCTGGAGC	TTCTCCCAGC	GGTAGAAGGT	CCCAATTTGT	AATGTACTAC	360
	TACCTGAGCA	CTTGTGTCCG	CCTCATCGCT	CCTTAGAAAC	TCGTGTCAA	GAGCTCGGAT	420
	GGCATCTGAC	ACAAAGGTTG	CAGACGCAGG	AGAGTATATC	TCCAAAGCCT	TGGGTTAACT	480
	TTCTAACCTA	ATATTTTGCA	AATAAAGCCG	AGTCGCAGTG	TATCACTGCT	CCAGTCAGTA	540
	GATTCTGACT	TCGTAAATA	TGTGTTCTAT	GGGTGGAACA	TTTTAAGTCA	TAGTTTTGCT	600
25	TTTTCCCCTG	ATATACTTCC	AAATACATAT	ATCACTGAAG	TTCCATCGGA	AGCACCTCCA	660
	CAGTACGGCC	TAAGAAGAGC	AGAATAATTG	CTCCA			

## 1675RP

30	GATCCGTGCA	ATAAACCGCT	TGAATGCACT	GTGGAAGTAG	TTGCGGGTCT	CGATATCAAA	60
	GTGCACAAAG	AATATCTGCA	GGTTGTTACG	CAAAATGTCA	AGCACATATC	CACGCACTGG	120
	ACGCGAGCCC	TTATGCGAGT	AAGTTAGCAC	TTCAAATGCA	CCGAGCTTGT	ACTTGTTCGAT	180
	TCGCAGAAGG	CTTTCCAACG	TCGACAGCAT	GATCAGCTTG	TCTTCGTGGA	ACGGCTCCTC	240
	CTCTATCCCG	AGCTCCTGGC	CAATTTTGAG	AAGCGGTAGA	AGGAGAGCAG	GGTGCCCTCG	300
	CATGTTCCCG	AAGATAAACA	GATCGAAGAC	CTTCGGCCGA	ACGGTCCGAA	AGAGCGGCTC	360
35	CAGCACGTAT	AGTTGCACTC	GTTTCGCGCA	GGTGCCCTCA	AGAAGATGCT	GAACCACCTG	420
	CTGCTCCAC	AACTGCAGCC	ACATCTCCAG	TTTATCCTCT	GTATAGTGTC	GCACATATAT	480
	ATTGGCCAGC	AAACTCGTCA	CACCTCTGCC	AACCGCCGTC	GCAAGAGAGT	CCGACCACAT	540
	GTATCCCGA	GCCGTGCGAA	TGAACCTCCG	CCGGACCTCT	AGAACAATT	CCAGGTCAAT	600
	CCGCTCCGAT	AGCACGTCCA	CCATGAAGTA	CACGAACCTC	TTTGAAGGAC	TCAG	

## 1675UP

	GGATCCGCTT	CCACACCGAA	AACGCAGAGG	ACCAGGACCG	TGTCTCGAAT	GTCGTTGGCG	60
	ACGCCATCAC	GCACGTCAAC	ACGCTCTTTG	GCGACAACGG	CATTACGCCC	TACGTTTCATA	120
45	AGAACATCGT	GTTCGTCCAG	CAGTCCGGCC	TGTCCGTGCA	GGCCCTCAGG	TTCCGTCTCA	180
	ACCATAACAA	CTCGGTGCGAC	GACACCCCTG	GCTCCACCCC	CGCGCACTCC	CCGGCTGTCT	240
	CGCCCGTCAT	GACCCCGGTC	AATTCTCTCG	TGGCCATGTC	TCCAAGCACC	GCCGCATCTA	300
	AAACCCCTC	GGCCGCGACC	GCAACAGCCA	GCTACTTTAG	CAATGGCCGT	TCCACCAGTC	360
	GCGTCGAGTT	TGTCTGTGTC	ACTGGGACTT	CATCGCCGCT	CCTGGAGCCG	CTGTTCCAGT	420
	CTATCAATGA	ACTGGCCAAA	AAGGGCGACC	TGCCCTACGG	ATACACTGTC	GCCTACGGCG	480
50	ACGTATTAC	CACATACGCT	AAAGAGCAGC	TCGAAGGTTT	CAACGAATTA	TTTGGCATTC	540
	TAGACAAACT	GAACCTTCATT	GGCTGCTGAG	CGCCCTGTG	ACATAGGTTA	TTAATCAATT	600
	AAATCCTTTC	TCTGGAACCT	TATAGAGCCC	TGCACCTTGC	GCTCCGGACG	CATATCCTTG	660
	CTGACTAGTT	GTCAGCGGTA	GCCTTTAATA	AATTACGTAA	TATGTGGTAT	TATCA	

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## 1676RP

	GATCCCGACA	CCAGCATGCG	CTCGTGAAC	GGGTCGAAGT	CTGTGTCCAG	CACCTGTGCC	60
	GTGTGCCCCG	GGAACAGAGG	AATTGGTCT	GGCGCCTTGC	CCACCTCCTC	CACCGGCACT	120
5	ACCGCGAACG	CCCCTCCGCC	CGACGAATTC	CACGTAACCG	AAATGAACTT	GCCGTTAGTC	180
	TTGATGAGAT	TGGAATCCCA	AGCATTTGATT	GTCACTTTGA	GGTTCTCGTA	GAAGAGTTCC	240
	TTCTTTGTTG	ATTGTCCGAA	GACGTGTCTA	TACTTGGAAG	CCCGCACAAA	CTTCCCACTG	300
	CAGTGCCGTT	AGTTTGCCGT	CCGCACAAAG	TCCAGTCCTG	GAGAGTATGA	CATACCTCAT	360
	CCTTGCAATT	CTTTGGGGTT	TAGCAGCTCT	ATATGCGTGT	ACACCGTAAA	CATCCGTAAC	420
	TAAATATGTA	ACGTGGAACT	GAAGGGTACT	GGAATCTAAA	GGGGAAAGAA	GTACCCGTTG	480
10	ATGGTGATGG	TACTGTCAAG	ATGGCTAAAG	CGAACCTCTG	GCCTGGTTGG	AACTCAGAAA	540
	GGTCACCAGA	CTCTTCTTAT	TCTTGTTT				

## 1676UP

15	GATCGCCGCG	CTCGTGCCCTC	GCCTGTATTA	CTACGCCACG	AAGCAATTGT	ATAACCCACA	60
	TATTGTAAACG	TTTGTACTAT	CCTCCATGGC	CTCGCCACC	CGACACGCCG	CCTTTCCTGC	120
	ATTCGGGTGC	CGGTGGCCGC	CGCGTTTCAA	CCTCGGCCCA	TGGCTCGCGC	ATTAGCTGCC	180
	AGTAGCGATG	CAACCCGAAT	GGCGAAGATG	GAGCCGGCAT	TGGTGGGTAC	GAAAAAGCTT	240
	TTTACGCGTA	CTGTTTGCTG	GTCCTAACGCA	TCCACGCCAC	GACGCTAACC	AGTATGAATA	300
20	CCGACCTCTT	TGCGCAGCTG	GTACTTGTGC	CGATCCTCCG	GTCCCCCATA	GCGTTTGTGT	360
	TGCTTCTATC	ACGGTATGCA	ATGTTATGAT	GCGTGTGTCC	GCGAACATGT	WCTAACAGGC	420
	GACAGCGTGC	TCGATACGCC	GTGCCC GCCG	CTGGCAGCCG	CACTGACGGT	GTACACAGTA	480
	GTGTGTAATG	CGTGCCCTAAG	CGCCAACCCG	CGCGCCAAGC	TGGCAGGCCG	TGGACGCCAC	540
	TGGAGCAGAT	GCCGGACGCG	ACTTGCGT				

## 1677RP

	GATCTGCAAT	TAGGGCATAT	AAACTGTGGG	TACTGTGTCA	TCACTAGTCG	GCGTATGCAC	60
	TGGTAGTGCC	AACTATGCGA	ACAAGGGGAT	ATGAAGATGG	CCTGGCAGGG	CTTAATTTTA	120
	CATAGGCAGA	TTGAGCAATC	TTCTCTCTCA	AGGCCTGCCG	TTAGCTTTTG	TAGGTTCCGT	180
30	AGGCGGGCTA	GTGCCCTCTT	GTTGAACGCG	TTGGCCCTTC	GCCTCCACGA	TTTGTTCAC	240
	TCGACTCTCA	TTTTGACGCA	TCTATATATC	TCCTCTGTGC	CGCCACGGAA	ATCCATTCCC	300
	AGCTGCAATA	TGTCGCCGTC	TTTCAAGGGG	TAGTCTTTTC	ACATAACCGA	TGCCTGTGCA	360
	AGCCGCATCT	GATTAAGGAA	CGTGCCGGAC	GAGGACTTGA	CGTCGCGCAC	ATACCAATTG	420
	CCCTGCTCAT	CCACCTTAAA	CACCCCGTGT	GTGCGCGACA	CAACCTTGCT	CTTGAATACC	480
	ACGGGGTGGA	AATGATCCGG	GAGCGAGCCG	ATCGCCTCGC	GAACCCGTTT	TGTGTAAACG	540
35	CCGATAACCA	ACTGCGAGCT	GGGGCCTGCG	GTCCGCACGA	TGGGATCAAA	AAAGAGCCCC	600
	GGATTATTCTG	TGGTCGAGTG	GTCAATGAAC	GGCGTTAACC	GGAGCGAGAA	GAA	

## 1677UP

40	GATCGTGGCC	TTAAGCCCCCT	CGCCGCCCTGC	GCCTGCGCAG	CCCTCAATGC	ACTCCGTCCG	60
	CGTCGGCTAC	ATCCCAGAGC	ACTTCAGCGC	GCCGCTGCTG	TTTGCGCAGA	CGCTCGGCTT	120
	CTTTGCGCAG	CGCGGCGTCA	CCGCCAAGCT	CGTGCCCTTC	CCTAGCGGCT	CTGGCCACCT	180
	GATCCAGGCG	CTCGACGCCG	GCGAGCTCGA	CCTCGCGCTC	GGCCTCACCG	AGGCGTTCTG	240
	GCGCGGCATC	GCAGACACGC	CAGCCGGCGC	CGCGCCGCGC	TACCAGATTG	CCGGCACCTA	300
45	CGTGCGCTCG	CCACTCAACT	GGGCCGTCTC	CGTCGGCGCC	GCGTCGCCCC	TGGAGCACGT	360
	GGACCAGCTG	GACGGCGGCC	GCGTCGGCGT	GTCACGCGTC	GGCAGCGGCT	CGTACGTCAT	420
	GAGCTATGTG	CTCGCCCTGC	AGCGCGGCTT	CCGCCGGCCC	TTTGCCGCGC	ATCCGGTGTG	480
	CCACACCTTT	GCCGGCCCTG	GCGCCGCCGT	CAACGAACGG	CGCCGCGGAC	GCTTTCTGT	540
	GGGAGCACTT	TACCTCCAAG	CGCTACCACG	ACGCGGGCGA	GATCCGCGCT	CTGGGCAACA	600
	TCCCCACCCC	CTGGCCCTCG	TGGGT				

## 1678RP

	GATCCGCTGT	CGGCATCATC	GGAGACATCG	CCTCCATGTT	CCCCGATGGT	AGGATAAAGC	60
	AATTGTACGC	CCAGACTTGG	GTCACAGAGT	TTATCAAGAA	AACAAGAAGT	AACCCCAACT	120
5	TTAGTCAGGC	AACTAAGGAT	ACTGCTAGAT	GGGCTAGAGA	ACAACAAAAG	CATCAACTAA	180
	CCCTATAGCC	TTACACTCCA	GAATAATTTA	TCTTATTACT	CATTTTCTTC	TGCGTTATCT	240
	CGCTCTCCTC	CTGTTATTCT	ATAATACTTC	CCCTGCAATG	TCTTCATTAT	TGTGTCTGCC	300
	TCGCGACAGA	CCGCTTCGTT	GTCTCTCTCT	TTGTTTCGACC	CTGCACTGAC	CTGGCCATGC	360
	TGCTCTTTCT	AGTGGTTTGG	TACAGGTTGC	GGGTCTTTTT	ACACAACCTT	TCTACTACGT	420
	CTTCTATCTA	ATCCCATCTA	CTTTTCTACT	TTCTCTCTCT	ACTTTATCCG	TCGGACCCGC	480
10	TGCTCGTCTT	ACGTGGCAGC	TTGTAGCATC	TATATAATTG	TATATATCGT	GGTGGCAACT	540
	ATCTACGGCT	GCTATACATC	TGCTGCCCGG	TCTGATCGGC	CGAGCCGTTT	ACCAATGCAG	600
	TAAACCACA	TAAACTTTTA	AGAGTTACAA	GCTCAAAAAC	GTT		

## 1678UP

	GATCCGGGTT	CGAGTCCCGG	GAGGGGCTGC	AGCGCACCAG	CGCTTCTTTT	TGGCGCTGGT	60
	AGTCGAGGAT	TGTTGACTGC	TAAACCCATA	CAACCACATA	TTGCACTGGT	GGCTTGCCCG	120
	CCTAGGCCGC	CCTGCGGCTC	CCGCGTAGCC	CGCCGGCGGG	ACCCACGCAA	CGAGACCGTG	180
	CGGGCCCGGC	ACGGCGATCA	CCAGCGGCAG	CCGGTGCAGC	GTAGGCGGGA	CAGCTGAAAA	240
20	GTTACTACAA	TTTGAGGTCT	CGCATACTGA	CACAGAGGGT	CTTACACAGC	ACCAGACGAA	300
	TCAGCAATGG	CTAAGCAATC	TCTAGGTATG	TGACAGAACG	ATGGTGGCTC	CGAAACATTG	360
	GGAATGAGCG	TCTCTGGCGC	TGCGATCCGT	GGTAACTTGG	GCATACGGCC	CAGCGCGCAG	420
	GCGGACCTAG	CATAATCCAG	TGCGTGGAAC	AAGTTGGTGG	CCCGGCCACG	TACTAACATG	480
	TCTGCAGACG	TTTCTTCCGA	CAGAAGAAAG	GCCAGAAAGG	CGTACTTCAA	CGCGCCATCT	540
	TCCGAGCGCC	GCGTGATCAT	GTCTGCTCCT	CTATCCAAGG	AGTTGAGAGA	GCAGTACAAC	600
25	ATCAAGTCTC	TACCAATCAG	AAAGGACAAC	GAGATTATGG	TTGTGCGTGG	CTCCAAGAAG	660
	GGCCAAGAGG	GCAAGGTTCT	TCTGTCTACA	GATTGAAGTA	CGCTGTCCGC	GTCGACAAGG	720
	G						

## 1680RP

	GATCCGTCTG	ACGGTGGTGC	AGTTCTGGAC	AAACGCCGTG	CTCTTTGACG	AGATCGTGCA	60
	GCCACTGGGC	GAGATCATCG	ACCTCTACAC	CCAGTTACAG	GGCGTCCACG	AGATAGACCG	120
	CGCTGTGGCG	AAGACATTTG	AGGAGGCGAG	GGAGGTATTT	TTGTGCGCCG	CGATGATTAA	180
	CGAGAACAGC	ATACTGATTG	GCCACGGCCT	GGAAAACGAC	CTGAACGTAT	TACGGATTAT	240
35	ACATGATAAA	ATTATTGATA	CAGCTATATT	ATACCCGAAT	GGTAAGTTCA	AGTCTCTCCT	300
	CCGGAATCTA	GCCTTTCAGG	AGCTCAGTAG	ACGGATCCAG	ACGGGCGAGC	ACGACAGCTC	360
	AGAGGACGCC	ATTGCAGCAA	TGGACGTCGT	CAAGCATAAG	CTGGGCATCC	CGCTCGACCG	420
	CAAGACGTGG	TAGCCCTACG	GCTGCTCCTC	CAGCCGCGTG	AGCCTGTCTT	CAAGCTGGTC	480
	CTGCCTCTCA	ATTAGCGTGT	GTATAAGCTG	CTTAAGGTTT	TGTAACCTAA	TCGCGATCAT	540
	CCTATCTTCT	GGAAGCTCGA	ACTTGACGTT	CCTGCTGCGG	GTCACGATCT	GGCTCTTGCC	600
40	CACCTTGATAC	CTCGATGCCT	CCGGAATTTT	GCC			

## 1680UP

	GATCGCGGCG	CGCGGTGGCC	GGCATTTCCG	GAAGCGGCCA	CGGAGCAGAG	GTGGCGCATT	60
45	CGAATCGCAT	ACGTCTTCGC	CACGCCGGAA	AAAAAATTTT	CGGCTATATA	AGGAGAGGCG	120
	GCCGTCTTGC	TGCAGGCAGT	TTCACTTTCT	CTAAAACCAA	AGAACATCGA	TTTCTTTAGT	180
	CACTCGCTTC	CTTACACCGA	AATGCAATTC	TCCACCGTCG	CTTCCATCGC	AGCCGCTGCC	240
	GCCGTGCGCT	CCGCTCACGC	CAACGTGACC	ACGGCCACCG	CCACCAGAAA	CCAGACCACC	300
	TTGGTCACCA	TCACCCACTG	TGAGGACAAG	ACCGCATGCA	CTGCGCACGT	CTCTCCAGCT	360
	TTGGTCTCCA	CCGCCACCGT	CACCATCGAC	AACGTTGTGA	CCTTGAGCGA	GACCTGGTGC	420
50	CCACTATCCA	CCACTGAGGC	TCCTAAGCCA	CCAGTTTCCA	CCGCCAAGCC	ACCTGCTTCC	480
	TCCAACGCGA	CTGTTCTTCC	AACTGAGACC	CAGTCGTCCT	CTCCTTCACT	GGTGCCCGTG	540
	CCAAGGCCCT	ACCAGCTGCT	GGTGCCTTGT	TCGCGGGCGC	TGCTGCTTTG	TTGTTGTAAG	600
	TTTAGTTCCG	CCGCGTGAGC	CCTCGTTTCT	TTTAGAGATA	TATAGGAACT	TATGTGACTG	660
55	ATTCTAAGCT	TTTACACCAG	CATGATTTGG	TTCTGCGGCG	CACCGA		



## 1681RP

	GATCATTCTA	AACAGATTAA	CCTTCCTCCA	AATTACTTTA	TTTCCTTAAT	CTCCGATAAA	60
	TGGTTACATT	GCGACAATAA	GGTGCCCGTG	GTGCTTACAG	ATATACATCT	ACCGAGAAAA	120
5	TTTCCGCCAC	ACACTCGTAT	AGAAGAAAAG	AATTTGATTG	AAACTTCTGA	GCTAGATCCG	180
	ACGTTCAAGT	GACTCTTCCC	ATTTAAGGTT	TTCAACAAAT	TCCAAACTCA	TGTGTTTAAT	240
	GCCTTGATCC	ATACCGATGA	AAATGTATTT	ATTGGAGCTT	GTAAGGGCTC	GGGTAAAACT	300
	GCAATGGCAG	AATTAGCTTT	ATTGAGTCAC	TGGAGAGATG	GTAAGGGACG	TGCCGTCTAT	360
	ATATGTCCAT	CTCAGGAGAA	AATTGATTTT	CTGGTGAAGG	ATTGGCGAAA	CAGATTTTTA	420
	AATGTGGCAG	GTGGAAGGTT	TATTAATAAA	CTCACATTGG	AATTAACTAA	CAATCTTCGA	480
10	ACGCTAGCCC	AGTCGCATTT	AATCTTAGCG	ACCCAGAGCA	GTTTGACCTG	CTTCTCGTC	540
	GCTGGAAG	AGAAAAAAC	ATCCAGACAT	TAGAGCTGTT	GATTCTAGAT	GATCTTCATA	600
	TGATCAGTAG	TGACTTGCCT	GGCGCAAGGT	ATGAAAATAT	AATATCCAGA	ATGCTGTTCA	660
	TTCGGGGTCA	ACTTGAAAAAC	GGCCTTGCGT	ATAGTC			

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## 1681UP

	GATCAGGAAT	GATCCCTCAA	TTGTCAGGAA	TTATGGTTCC	ATATTGGTTG	AATTTGCCAA	60
	GATTACTCCT	GATGGTATGG	TANTGTTCTT	CCCCTCATAT	TTATATATGG	AATCCATTAT	120
	TTCAACTTGG	CAGACAATGG	GGATTCTAGA	CGAGGTTTGG	AAATACAAGC	TCATCCTCGT	180
20	GGAAACACCA	GACGCACAGG	AAACTTCTCT	AGCTTTAGAG	ACTTACCGAA	AGGCCTGCTC	240
	GAATGGGCGC	GGCGCAATAT	TACTTTCTGT	GGCCCGTGGG	AAGATTTCTG	AGGGAATTGA	300
	TTTTTGACCAC	CATTACGGTA	GGACTGTATT	GATGATTGGA	ATTCTTTTCC	AGTACACTGA	360
	ATCGCGTATT	CTAAAGGCGA	GGTTAGAGTT	CCTAAGAGAA	AACTATCAGA	TACGGGAAAA	420
	TGACTTTTTA	TCCTTTGATG	CAATGAGACA	CGCCGCTCAA	TGTTTGGGAA	GAGTCTTGAG	480
	GGGTAAGGAT	GATTATGGCG	TGATGGTGCT	CGCCGATCGG	CGATCTCAAG	AAAGAAAAAC	540
25	CAACTTCCAA	AATGGATCGC	ACAAGGGCTC	TCTGATGCTG	ACCTGAACCT	TTCTACTGAT	600
	ATGGCGATAG	CTAATACAAA	ACAATTCTTA	AGGACGATGG	CACAAGCAAC	TGATCCGAA	

30

## 1682RP

	GATCGTAAAA	TTTGCTATAC	AATGGTTTGG	GTAGGTCCTT	TAAAAGGTCG	TCAATCTCAT	60
	AGTCGCTCAC	ATCAAGGGGA	ATGTTTAAAA	AACGCACTCT	CTGATGTGTA	GGCGGAGGAG	120
	GCCTTGCGTC	TCGCCGGTCC	CTGAAACGTG	AGCGGCGCGA	GGGGCCGTAC	TCTCGCGCCC	180
	GATACGTGCT	TTCCCCCAGA	CCCATGCGTG	AAGCTAGTCC	ATTACGTAAG	TCTCGACGGC	240
	GATATTGCTA	TAATAACAAT	GTAATCGTTA	ATACTCACGC	TCAAGTAACC	TTGCGGTGGG	300
35	TCATGTATCA	CTTACGGTAG	TAGTGCGGTG	TGTCTTTTGT	CCGTTAGTAT	CCGATGAAGT	360
	TTGGTATCGA	GGAGAAAAAG	ATGTTTCATC	TTTCTCACCA	GTACCCTGGT	TCAAGTGTTT	420
	GTTCAACGAC	ATTGTCCCCT	CCAAACTATC	CTGTTTGAAG	GGCAAAGGCT	GTGTGTCAAG	480
	AACGAAGTTT	TCACCATTTT	TCCGGAAGGC	TCGGGACAGC	GATCGAAAGA	AATAGGATAT	540
	ATACGTACAC	CTTCTTTTAA	ATATCATTTA	AAATATCCTG	GAATTTTCGAT	ATGTGGCCAT	600
	ACTGGCTCTT	CAGCTTCCTT	ATCCATGAGA	TAGAAGGAGC	AAACTGTGCG	AAGGTGCCTT	660
40	CCACAGTTAC	TTAAGTTTCC	GTAAGCAACA	AGGAGTCTGT	ATGCGGC		

## 1682UP

	GATCCAGTGT	GTACGGCCAG	AGTCGCGCTG	GGGCACCAGC	AGTACCTGCT	CCGTCTCGTT	60
	GAAGTTTCGA	ACATTCCCCT	CCGCATCAGC	ACCGCGCCTG	AAGTATCTTG	TACCCGCCCT	120
	GAATCTGCTC	CGGCGCGTGA	TCAGACCCAC	ACTAACTGGC	GTACTCTGCA	ACACAGTGTC	180
	TACCACTTTG	ACGTAGCCGT	AGATTAGCGG	CAGAACGAAC	TCGTTTCGCCA	GAGCGTTPTC	240
	CTCCGCCAGG	TTTCGCAGCG	GCTCTGTGGC	ATAGTAGTTC	CAGAAGAACC	GCGTGTCTGC	300
	AGTGCGCCAC	GAGGCTGGCC	CCAACCCCTC	GTTGCGCTGC	ACAGAGTGCG	TCAAGTCATA	360
50	CGTGATCGAA	TAGTACAGCG	TTGCCTTCGC	GAGGTGGTCC	CGCAGTAGCG	CAAGATACCT	420
	GTTGTCTCTT	GCAGATGGCC	GGATACTGGT	GTTGACCAGC	ACCAAAGAGT	GCGCCGTCAC	480
	TTTGAAAAGA	GAATGGGCAC	CCAGGTTTCC	CACCACCTCC	ACGCGGTCCG	CCGTTAGCAC	540
	CACGCGACTA	TTGCGCAAAT	GTAATATCCC	GATCAGGCCCT	GCGATCTTGC	GAGTTTCTCC	600
	ATCTTTAGGG	AAATTGCTGG	GGTCTACGAG	TGTCACGCCC	GAATCGTGAT	GCGAGATAGA	660
	CAACACCGCT	TCACTCTGGG	AAGTATTAGA	TGGCTTGAAA			

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## 1683RP

	GATCTATATC	ACCAATCATC	ATGGTTTTGA	AACATTCCGT	GCTTAAAAAG	GGACACAGCA	60
	AACTACAAGC	AGGCAGCACG	AAGCACTCTG	CAGACTAAGG	GCAGGCCTCA	TCATAAGATG	120
5	CTTAGGGCTG	AGCTAGTAAA	TGCCATTCCG	TGCCAAGGTG	CTCAGTGTGT	CGCTGTGGTT	180
	GATGGCGTTC	GACAACTTGT	GGTGGTGCGA	AATAATAGGG	ACTTCTTGGT	GTACTCCAGT	240
	ATGGACGAGA	GAGGCCTGCG	TCTAGTTTCA	ACATATACAG	AATTGCTTGG	CCCGAATTAT	300
	GGTGTAGAAG	AGCTGCTGTA	CTCCGAACGG	CTGCGGACAA	TATTCGTCCG	CACGACCAAG	360
	TGCTTACTGC	TACTTCATTG	GAGCAACTTA	CAACATTACG	ACAAGATAGT	TGACAAACGA	420
	GGCATTGACC	ATGCCCTGGCT	GTTTGAACAT	CCATGTGGGA	AGGCTGAGAC	GTGGATGACG	480
10	GTGCTTGTTT	ACTCGGTCAC	AGGGTCGAGC	AAGATAAAGA	TGCTGACATG	GGTGGGGCGG	540
	CAGTTCCAAG	CGGTGCATGA	GGTCGCACTA	GGCACGCGAT	CGGAAGTCAT	CCAGCTCAGT	600
	AAGTGGCGGC	CCGCATGCTG	TGTGGTTGCT	TACCTCCGAC	GACTGTATAC	CA	

## 1683UP

	GATCTCGTCA	AATTCCTGCTC	TAGCATTATC	AACTTTGTGA	CCACAACCTTA	GAATTCCCCC	60
	ATCATGCATT	ATGTTTATAG	ATGTACAGTT	CTAAAAAAT	CGGTAATATA	ATGAGACCTA	120
	TCCTCTTTTC	TCATCCTTAT	AGTCACCCAA	AGTTTAAACA	TGTGACATGC	TGCCAGATTT	180
	ACAGTCATCT	GCGGCTATGA	TTTCTTGCGA	AGACCTGCCA	CAATTATAAT	GTGTTAATAT	240
20	ATTGCTTCCT	CTGAGGTTGA	AGAGCGAGAA	AAGTTCACCT	CTCCCTAATG	TTAAATTCTT	300
	CTGGCAAACG	TAGCAGCGGT	TATCTTTCATC	TACCACCAAA	AATTCAGATA	TGATCTGGGA	360
	TAAGCGATAG	GTGCTTCCGA	TGAGGTTGAC	TTTCAAAGA	TTGTTCTGTA	TACGCGATTG	420
	GTTTTTCTTC	ATGGACGCAC	TTTTAATCCT	TCTACTTAGG	AATTCGTTAA	GCGTGTATTAT	480
	CGGAATATTG	GGCGGCAGTT	TCTCAAACAA	TGTTATCGCA	TCTAGCTTCG	AACCATTCTC	540
	TAGCAGAAAC	AGATGAACGT	TTCTCCATCC	GCTAAATTCT	ACCTTCGCAA	GCAGCTTTTC	600
25	AAACAAGTTC	ATGAGAGCTG	CTGTGCCTGC	ATTTTTGT	GTGGCATAGA	GCTCATTACA	660
	ATATAGAGAA	GCTTGTTTAT	AATTCCCTAG	ATCATCAACT	AGGATCCCTA	ACGCTGTT	

## 1684RP

	GATCTGTACA	CTTCAATATC	GAACGAAGTG	TCACCGGCAT	ATTCTGCAGA	GATTTGAAAA	60
	AGCCACCAAA	GCAATATGAC	ATCAGGGTAG	AGCTTCGAGC	GAGTAATCTC	CGGTGATTCTG	120
	TCGATCTCCT	TTAACCAAGC	AGCAAACCGT	GTCTCATGTT	GCTTTTCCCA	GCTAATAATC	180
	TCATGCACCA	CAGCCATAGA	TTCAGCATAA	TGAAGGTATG	TTGCGCGCGC	CTCATTACAC	240
	CATTTGATAT	ATATTTTCCC	CAGGCCATCG	ATGAACTTCC	CTTTCGTCTG	CAGCTTCCCA	300
35	AAAATAGGTG	TCAAAGCAGC	TTCTTTGTGC	AAGTCAATCA	GCGGATAAAA	GATGTCAAAG	360
	GCAAGAGAGG	CGAAGTTTTC	GTCCGTGGGC	AGCAACGCCG	GCGAGAATTG	TGCGCCGTAG	420
	ATTTCTACGG	CAGCATGGGC	CAGGTTTCTG	CTTTTCTCTT	CGAGCACAAT	AAGGTCAAAT	480
	ATGTAGCTCT	GGCGCTTTAC	TTCTCTAGGA	TTAATCTCTG	AAAGCTCCTC	GTCCGTCACT	540
	TTCCAGTACT	CGGTCCAAAG	TCCCAACGGG	CGGCTGA			

## 1684UP

	GATCCATGAC	GAGCAGCTGG	ACCTCGTCTG	CGCTCTGGGC	CTGGCGCCAG	AGAACAAGGA	60
	AACGCTGCAG	AACCTCCCGC	TCGCGCGCGT	CAGCGTCACG	TTCAAGGACG	TGGTGACGGA	120
45	CTACTGCGAG	GCGCACGGCC	TGCTGTCTGA	AAAGACGGGC	GACGTGCGCA	CCCTCCGCGT	180
	CTACCAGCAT	GCACGTACTG	TCCCGGTCTT	CACCGTCACA	CACGTACACC	GCCGCCGGCG	240
	TGTAGCTCTG	TGCGAGGACG	TGCTTTGGGT	TCAGGAAGGG	ATAGGCTTCA	AACCTACGTA	300
	CTTATACGAA	CTAGAAACTC	TTCTAAAGAG	CGCTTAGTCTG	TCTCATATAT	ACAGGACCTA	360
	GTACTCTTGG	CGCACTCAGT	GGCCCTCGTC	GCTTTTTCGG	CTCTCGGCCG	CGGCCTCCGT	420
	CTCGCGCACG	GCCTGTCTCT	CGCTCTCCAG	CTGCTCCGCG	TAGTGCTCGG	GGTGTGCGCG	480
50	GAAGCATCCT	GCATCACCTG	GAATTCTCCA	CGCAGTCAAT	CCCCTTAGGC	TCGGCCTCTG	540
	AGTACACGAA	GCACGCGAAC	GCAGCCTTGA	ACTCCTCGCC	GACCGGCCCG	TGCGCCATGC	600
	CGCCAGGCA	TGGGCAGTCC	CAGTTGATCT	CGCCCGTGTG	GGGATTGTAT	GCTCCTGCTG	660
	CCCTGCGCAG	CCTCACCCGC	GCTAGCTTTG	TCCTCCGCGG	CGCTCGG		

## 1685RP

	GATCAACTTC	GCCTAATCCC	TTAATCATTG	TCACTGCTAA	CTTGAACTTA	GTCTGTGTGT	60
	ATGCCATATAG	TGAACGTTTA	ATGTGATGGT	TTTATAGTAA	TCGATGGAAC	TTTATCCGCG	120
5	AAGCCTCAAG	CTGATCATCA	CGTGAGTAAC	CGTCGATATG	CAGAACAGAG	GATACCATAA	180
	ATTGCTATTTA	GTAATCAATT	AATAGACTTA	CATATAGCTC	AAAGCTGATC	ATTGATGCGT	240
	CTCAAACCTCT	TTTCATCGTC	TGAACCTTTC	GGATTTCAC	TTCTGTATC	ATTATACCAT	300
	GTATAATCCT	CTAGTACGCT	AGTAGTCTAG	TATCTCGGAT	AACCCCCCTA	TATTACATAT	360
	AATATGAGTA	AAATACAGAA	TGACGTTAGC	GGATAATCTA	AGGCTAAGGT	TGCCTACACT	420
	AAGTTAACGG	GGGGCTTCTT	ATCTTGACAG	TTGTCTCTCT	AATCAATAGA	ATTCTGTTTC	480
10	TTTTTCCACT	ATTTGGTCCC	TGGCAAACCTG	CGAGCCACCC	CGCGTATCCT	TAGCCTCTGA	540
	GGTGTCTCTCT	TCGACATCAC	CTTCGTCTCT	CGGGATCTCT	CGGGACGTGG	TTCAACTGTA	600
	CGCTCGGTGC	ATATTTAGTG	TGCTCAAGGT	TGCTGAAAAT	AGATGCGAGC	ACCTTGTTCA	660
	GATATT						

## 1686RP

	GATCCTCTCC	GAGGTCAAGA	GTTGTGTCAT	GAATTAACCT	CATTTTAGGA	ACAAACTTGT	60
	CTAGGGTTCC	CGCTACTAAT	TCCTGCTCGA	CTTTGAAATC	CCAAAATTTG	ACAGTCTTGT	120
	CTGCGGACGC	AGTCACTAGC	CTCTTCCCAT	CACTAGTTAG	GTCTAAAGAC	CAGATTGCAG	180
20	CGGTGTGTGC	CTCTTCAATA	TTTTCTAGCA	TAGTAGAAGA	TGCGAGATCA	AATAGCTGAA	240
	GTTGGCCCGC	TCTTGTAACC	AGAATAACCA	AGGCGCCACC	TGGTAAAAAC	TTACAGCATA	300
	AAGCATAGCC	ACAGTCAAGA	TTGCGGATAC	AAGTTTTAGT	CTTGATGTTT	CAGACCTTTA	360
	GGTTTCCATT	TGAAGCAGTT	GCTAGTAGCT	TATCATCGCT	ACTGATGTCT	GCAGCACGTA	420
	GATCAGTCCCT	ATGGCCCGGC	GATTCGATAC	TATGCAATTT	GATCGCAGTA	GGCTGGAGCG	480
	GTTCTTCTTT	TTTGTATGGG	ATTGAGTAGT	ACTCTATAGT	GTTGTTTGCA	GTCTGTATCA	540
25	CCAGTTCCAA	TTTAGATGGG	GTACAGACCG	TCCATGAAGA	TGCTTTTAGC	TTAAATAGGG	600
	ACCTTACGAG	TTGGAAAAGG	ATGCAAAAGT	AAGTTCGCAT	AC		

## 1687RP

	GATCAGGACA	GTAGCAGCTT	GACTGAGTAT	CAGCAGGAAA	AGCCTAGCTA	ATTGGCGCGA	60
	GTACAATTAC	AAGTACCTGT	CTGACTACTT	CTTTTGTGG	GATGCCATAT	TTTTTAGGAT	120
	GGCCTGCAAC	GGCCCGGTGG	GGGCGCCATC	CAAATTTATG	GAGTTGAAGA	GCTGTTCAAT	180
	GCCCTTTATC	CCATCTGCAC	CGTCTTTATC	GCCGAACATG	GCATGCAACT	CTTCAAGCAT	240
	GATATCTTCT	TCCTCGTGCT	CTGATCCGGC	GTTGTCTGTC	TTTGCGCAGT	CTTCGTAGGC	300
	GCCATTTCTG	TAATGTTGAA	GCTGTTCTTT	GTTCATCTTC	AGACCCTCCG	TCAGGAAATA	360
35	TTCAAAGAAA	TCGTCTTCAC	TAATATCTAC	GCCTTCACTC	TCGAAAAATG	TCCGAGCCTC	420
	TTCAATCCCA	GCTGAAGACC	CCTGACCAGA	AACATGCTCA	TTGCTACCTT	CATCGTCATC	480
	TTTAATATCT	GTCAGGAAAG	TCTCCAGCGA	CAGGGCCAAG	GCATCCATAG	ACGCCTCTTT	540
	GTCCGCAGTC	GGTACCTCCG	TAGTTAATTC	AGTCGTAGAG	AACTCCACCG	GGCGCTCTAG	600
	CTGTTTTGTA	TGTACCAGAG	CGCTTACTAG	GTCACCCTCT	AACTTTCTCT	TGGGTTTACG	660
40	TGTCGTTAAC	TGGCC					

## 1687UP

	GATCCGTTCC	AGTTTGGCCA	GCGGAAGCTG	GCGGACGAGG	CGGACATCTG	GGCTCATAAC	60
	GCGTGGGATA	ACGTAGACTG	GGGTGACGAA	CAGATCCGGC	TCGCAAAGGA	GAAGATAGAA	120
	GAGCAGAAAG	AATACCCGGT	GCAGGAGTTT	GACAAAAAGC	TGTATCATAG	CAACCCCGCA	180
	AGGTACTGGG	ATATATTCTA	TAAAAATAAC	AAAGAAAAC	TCTTCAAAGA	CAGGAAGTGG	240
	TTGCAGATTG	AGTTTCCCTC	TCTATACGAA	GCTACCAAGA	AAGATGCTGG	TTCAAGTACT	300
	ATCTTCGAGA	TTGGGTGTGG	TGCGGGCAAT	ACCATGTTCC	CGATCTTATC	TGCAAACGAA	360
	AACGAACACT	TACGCGTTGT	GGGTGCGGAC	TTCTCCCCGA	AGGCCGTGGA	ATTGGTAAAG	420
50	ACGTCGCAAA	ACTTTAATCC	CGCGAATGCC	CACGCGACGG	TATGGGACTT	AGCCAACCTT	480
	GATGGTCTTT	TGCCCCGATG	TGTCGAGCCG	CATTCCGTCG	ACATCGCAGT	AATGATTTTT	540
	GTTTTTAGTG	CCTTGGCGCC	CTCACAGTGG	GCCCAGGCTA	TGGATAATTT	GCACAAAGTT	600
	CTAAACCAG	GCGGTAAGAT	CCTCTTTAGA	GACTATGGCA	GGTATGACTT	GGCTC	

## 1688RP

	GATCTTGTG	AGAACA	ACTCA	ACATCGGCGT	AATTGCAGAG	CCCCCGGTGA	CCATACCGAT	60
	TTTCTTG	TAC	GCATTTC	GCA	CATAGCTGAA	CCGTCCCTACA	GGACCTTTGA	120
5	TTGGCCTGGC	TGTAGCCCAG	CAAACCATTT	GGATACCTTA	CCGTGCACAT	AAGATTTGAC		180
	AATGATATCG	AAATGGCCCT	CGGCAAATTT	GTTGGAGATA	GGCGTGTAGT	AACGCACTTC		240
	TTCTACACCA	TCCAGCATCA	CCTTCGCAGC	TAAATGAAAG	CCAGTAGGTA	TATCAAGAGT		300
	TTCCACGCTT	GAACGGAGCT	TGAATCTGTA	TATCGCAGCA	TTTTTGCTTA	GAACGATCCG		360
	TTCTTCCAAT	TCTAATGGCG	TCCACTCATT	TGGAAGAATT	GAAGTCCTGC	TTCTGTATGC		420
	TAGTAGCAGG	CGTGCACCTA	CAAACATTCG	CAAAGCTAGA	ATGCCTAGAA	GGTACCATGC		480
10	GTTCCCCGCT	GACCAGGCGA	TAACAAGAAC	GCCCAATGTA	AAGATGCCGC	TGGGGATGAA		540
	GATCCCATGA	ATGGGATCAT	CCAATATCTC	CATACCTCTG	CGTTCGGTCA	TACTAATATT		600
	TTGAAAGCTC	GTCGTAGCTA	TCGTCTAGTA	AGGATGAGAA	CGGTTAATAT	ATGCTTCCTC		660
	CTAGTTCTAT	AAGCACGGAC	TCCTTTGCAA	CTGGTGAAGT	ATCGTCTAAC	GGTCAT		

## 1688UP

	GATCAGGCCG	GACGGGTACT	TGCAGGAAGG	CCTCACGAAA	CCCAAGGGGG	GCGAGGAGGG	60
	CTTCTCGACG	TTTTTCAACG	AGACGGGGCTC	GGGCAAGTTC	GTGCCGCGCG	CGGTGTACGT	120
	GGACTTGGAG	CCGAACGTGA	TGCAGCAGGT	GCGCACGGGC	GCGTACCGCG	AGTTGTTCCA	180
20	CCCGGAGCAG	TTGATCAGCG	GAAAGGAGGA	CGCGGCGAAC	AACTACGCGC	GTGGGCACTA	240
	CACGGTGGGG	CGCGAGCTCT	TGGACGATAT	CCTAGACCGC	ATCCGCAAGA	TCTCGGACCA	300
	GTGCGACGGG	CTCCAGGGCT	TCCTCTTCAC	GCACTCGCTT	GGCGGTGGTA	CGGGCTCCGG	360
	CTTGGGGTCT	CTGCTTTTGG	AGCAGCTTTC	TATCGACTAC	GGCAAGAAAT	CGAAGTTGGA	420
	GTTTGCCGTG	TATCCCGCGC	CACAGGTGTC	CACCTCGGTC	GTGGAGCCAT	ACAACACCGT	480
	GTTGACCACC	CACACCACAT	TGGAGCATGC	CGACTGTACG	TTCATGGTTCG	ACAACGAGGC	540
	CATCTACGAG	ATGTGCAAGA	AGAACTTGGA	CATCTCGAGA	CCTAGCTTTG	CGAACTTGAA	600
25	CAACTTGATC	GCCCACGTCG	TCTCCTCGGT	GACCGCGTCA	TTGCGTTTCG	ACGGCTCCTT	660
	GAACGTGGAC	TTGAAC					

## 1689RP

	GATCGTGCAC	AAGTTTGACG	AGCTAAAGCT	AAAGGAGGTG	TTGTTGAGAG	GTATCTACGG	60
	TTATGGTTTC	GTTGACCCAT	CTGCCATCCA	GCAGCGTGCG	ATCTTGCCCTA	TCATTGAGGG	120
	CCACGACGTT	TTGGCGCAGG	CCCAGTCCGG	TACCGGTAAG	ACTGGTACCT	TCTCGATTGC	180
	TGCGTTGCAG	AGAATCGACG	AGAGCATCAA	GGCCCCACAG	GCGTTGATCC	TAGCTCCTAC	240
	CAGAGAGTTG	GCGCTACAGA	TCCAGAAGGT	TGTGATGGCG	CTTGCGCTGC	ACATGGACGT	300
35	TAAGGTCCAC	GCTTGTATCG	GTGGTACGGA	CCCTCGTGAG	GACGCCGAGG	CCTTGAGAGC	360
	CGGTGCGCAG	ATTGTCTGTCG	GTACCCCCGG	CCGTGTGTTT	GACATGATTG	AGAGACGTTA	420
	CTTCAAGACT	GACCAACATCA	AGATGTTTCAT	CCTGGACGAA	GCCGACGAGA	TGTTGTCCCTC	480
	CGGCTTCCAG	GAGCAAATTT	ACAAGATTTT	CACCATGTTG	CCACCAACCA	CCCAGGTCTGT	540
	GCTATTGTCT	GCCACCATGC	CAAAGGAGGT	GTTGGACGTG	ACCGACAAGT	TCATGAACAA	600
	GCCCGTCCAG	AATCTTGGTC	AAGAAAGGAT	GCCTTGACCT	TGGGAGGGTA	TCCAGCAGTA	660
40	CTATATTAAC	GTCGAGAGCG	AAGAGTACAA	GTACGACTGT			

## 1689UP

	GATCGCGCTG	AACCTCAGCG	AGGCACGGCT	GGTGATCAAG	GAGGCGCTGC	AGCACCGGCG	60
45	GCGGGTGTTC	GGGCAGTGCG	GGGACGGGCT	GGAGGAGGAC	GAGGCGGACG	GGGGAACACA	120
	ATATGACGCA	GGAGAAGGAG	CTGGCGATGC	TGGACAAGCT	GCTGGAGAAG	ACGACGGGGG	180
	GACAGAACCA	GGCGCTGAAG	CAGACGATGG	TGTACCTGAC	GAACCTTCGCG	CGGTTCCGGG	240
	ACCAGGAGAC	GGTGACGGCG	GTGACGCAGC	TGCTGGCGTC	GACGGGACTG	CACCCGTTTCG	300
	AGATTGCGCA	GCTGGGGTCG	CTGGCGTGCG	AGGACGCGGA	CGAAGCCAAAG	ACGCTGGGTGC	360
	CGAGCCTGGG	GAACAAGATC	TCGGACGAGG	ACCTGGAGCG	GATCCTGAAG	GAGCTGTCTGA	420
50	ACCTGGAGAC	GCTGTACTAG	ATAGCTATAC	AGACAGGAAG	AACCTTGCCGC	CGCCGCGGCG	480
	CCACCAAGTG	TCGAGACAGG	AGTGCATAGT	GTGCTCGATG	TCGACGGCCT	CGCGGCCGAA	540
	GTTGCAGACG	CAGCGCTGCG	CGAGACGCGC	GACGTGCGCG	GACGGGCACG	TGCCGTAGGG	600
	CACGTGGAAG	TTACCGATCT	CCTCGAAGTG	GTGCACCTCG	TCCGCGCGCA	GGAACAC	

## 1690RP

	GATCTGAAAC	TAATGTCATC	CGCGGAAGAA	CATACTAAGA	GCTCATCGTT	ACATCGAGAT	60
5	GAGACAAAGT	ACCTGATGTA	TAAGAGTTTT	ATTGACATAT	GCGCTCGGAG	GCAAACGGCA	120
	GGCTACCGCC	TGCCCCGTGT	TCCGTCTACA	CATGACAACA	TAATTGTGGC	AATGTCAGGC	180
	GGCGTGGACT	CTTCAGTATG	TGCTGCTTTA	TACGCTCACT	TCCCAAAAGT	CCGTGGGCTC	240
	TACATGCAGA	ACTGGTTCGA	GACGTCGGGC	TCAGGGCCTG	TAGAGGGTAA	GGCCGAACCT	300
	TGTTACGAGC	AAGATTGGAA	GGATATTGAG	AAAGTGGGCG	CGTACCCTTA	TATTCCCGTC	360
	GAGAGAGTCA	ATTTTCGAACG	GGACTACTGG	CTGGATGTTT	TCGAGCCTAT	GTTACAACGG	420
10	TATCAACAGG	GTTATACTCC	GAACCCAGAT	ATTGGCTGCA	ACAGGTTTGT	AAAGTTTGGA	480
	GCGTTGCGGG	AGCACCTGGA	CAAGGAGTAT	GGACGCGGCA	ACTACTGGCT	GGTAACAGGC	540
	CACTATGCGC	GAATCCTATC	CCCCCAGACT	CGCAGAGAGA	CCCACCTGCT	GCGGAGCCAT	600
	TATGCGCCAA	AGGACCAAAG	TTACTACTTA	TCCCAAGTCC	GGCGGGAGGC	CCTCGCGGAC	660
	CTCTTTAATG	CCCATGGGAT	TTCTAACAAA	ACCGGAAGTC	CGACAATGGG	CCGCAGAA	

## 1690UP

	GATCAGAAAC	ATCACCATAT	GGTGTCTGAA	GACCTTACGG	CGACGGTCGA	TACACGCTAC	60
	CATCTCCAAG	CCGATGATGC	CGGCTATTAT	GGACACCGCC	GACGCCGTGA	TTGCCAGGAT	120
	TCGCAGCTTC	AGCAGCTGGC	TCGAGGTGAA	CGTCGAGAAC	ATCCCCGGCA	GTCCGAGCAC	180
20	GAGGTTCAAC	GTGGTTGTGT	TGTAGGACCC	GAATACACAT	GTGTAGTTGC	TGTCCATGCA	240
	CTGTATCTGA	GACGCGCCCT	CCATCTTGCA	CGTGCCTGCG	CTACACGTCT	AGCTCCCGCT	300
	CGCACCTATA	CTTTGTATCT	GTTTCGCCCT	TGCTGCGCGC	TAGCCCCCTC	GCGCTTGCCT	360
	CTTATCCCTT	CTCGAAGTCG	TCTCCCCTAA	GTTGGATCCC	AGCGACCTCC	TAGTCGAAAA	420
	CTGCTGTCTA	CGTTCGCCAG	GCACTAGTTG	CCTCCCCTG	CAGGTTATCG	ATAAGTCCTA	480
	AAATACCACC	AAGCAGGCGT	TGTACTGCTT	CTATACGCCA	ACCCTCGCTT	TTCGTTGGGC	540
25	TGACACACTC	AAGTGACTGC	AAGAAGACTA	CCCTACTCAC	AGATACCGTC	GTCCGTTGTA	600
	CGCACGCTAA	AAGACAAGTT	AAATCTACGA	CACATATAGT	GCCTCGCAAG	CTCACCGCAT	660
	CCGGAAGGAA	CAAGCTATTA	GAAACTGAGA	CACCTC			

## 1691RP

	GATCTTCTTT	GTATTCCTCG	TCTTACCTGC	CCCAGACTCC	CCTGTTACTA	ACACCGACTG	60
	GTCTTGCCTC	TGTGTCAACA	AGTTGCGGTA	TGCTTGCCTC	GCTACCGCAA	AGATATGCGG	120
	CTCGTTGTCT	TCCTTGGGTG	ACCCATGGTA	CAAGTTCACA	TAGTCCTGCG	TGTACACCTT	180
	GATGTTGCTG	TACGGATTCA	ACGCGACGAG	GAATAGCCCA	GAATAAGTAT	ATATCATATC	240
	GTCCTTGTAT	CGGTTCTCCA	AGTTGTACAA	CACAGACGCC	TCGTTCAAGT	GGGTCAACTC	300
35	GGACATATCG	TCTATCTTGT	CAAACGTTGA	CGGATTCAAC	GCCGCGGTCT	CCACCTCCAG	360
	CACTTCTCGT	TCCTTGCCAT	TCACTCTCAC	AAGACAGACC	TTCTCATCCT	TGTTCTGTTT	420
	GTTTTTAATT	GTCTTTGTGG	AAACCAACTG	TCCTTTTACA	AACACCTCCT	CAGCATCTGG	480
	AACCCAAATC	ATTTGACATT	GTTCACTCAT	CGGGACAGAT	GCTCTTGAAC	TTATCTAATA	540
	TGCAATAACC	AAATTCAACT	TTACTTTAAT	CACCTGCCTG	TTACACACGA	AGCAATGTTG	600
	GATCTCATAT	TCACACGACC	TACTTTTTTCG	AAACACTTAT	TTGTTTATGT	CGGGCTCGAG	660
40	CATACACGTC	GGTCACGTGA	CAAGCGCATG	TAC			

## 1691UP

	GATCATTATG	CAACCGAATC	TGGTATCTCA	GAAGATTACC	GTAGGACTGT	GCCTGTCCGA	60
45	TCGATTACGT	TAGTGGGGTA	GAGAATGAAG	TAAGAAGCAG	CTCTGCGATT	ATTGTGCGTT	120
	TGCGCCTCAT	GTGAGGTAAA	GCCCTATCCC	GCGAGGTGGC	GGCTTCTTGC	AAGAAAATCT	180
	GGGCATCAGC	CCCCCGAAAC	GAAATGCGAT	AGTCACCTGT	GCCATGGCGA	CGAGTCATTT	240
	CCCCATTCTG	ACAGAAATGA	ACGGGCAGAA	TCGCGTAATG	GATTTTCTGT	GGCGTTCGTG	300
	CCAAAAGGTG	ATCTCCACCT	GCGTGTCTGC	CTGCGGGCGT	GGTTGAGCAG	AGCACCTGGA	360
	AAAAGAACAG	CACAGAAGGC	CAATGCAAGT	GGCCAATTGA	GGCAATAGCC	GAGCAGGAAC	420
50	AGTCGAAAGT	GGGTGTTCTG	GCGCTGTTGG	ATCTGAAAAA	TGCAGGAAGT	TACAAAAAAC	480
	AGTGGGGCAA	TACATAGAAA	CCGGCGACCC	GGCGATCGCC	TAATCATCTG	CCATGGAGAC	540
	GCGGGTCCGG	CGCTCGAACC	AGCGGTGCAA	ACCTTGAGGG	CATGGTGATA	CGGGCCCGTC	600
	GGCGGGGCAC	TCAAACAGGC	ACGTGTTAAT	CCTGACAAAA	CGCAGCGGGG	TAATTCCTTT	660
	CCGCAAGCCG	GACGGGTATA	TGAATCGTAC	GATACCAGTT	GTCGA		

## 1692RP

	GATCTAAATA	TATATAATTT	AATTTATAAA	GATTAATATA	AACTTTTTTA	TTATAATATT	60
	TAAGTATTAA	ATTATTTAAA	CTATTATTAT	CATTATTTAA	TAAATTAATT	ATTTGATTAT	120
5	TAATACTTAT	TATATAATTA	TTATATAAAT	TACTTAATTC	ATCATTATTA	ATATTTATAT	180
	AATTATAAAA	ATAATATTTA	ATATGAATAC	TATTTAGTCT	ATGTTCAAAT	TTTAAATTAG	240
	TTATTAAAAF	ATTATTAGAT	ATTATTATTT	TCITTAATAA	ATTATTAAAT	AGATTATCAA	300
	TAATTAATAT	ATTATTTATT	AATTGTTTAT	TAAAATAATA	TATTTTATTA	TTATAAAGAT	360
	TTAATTTATT	TAAATATTGT	AAATTATTAT	TTTTATTATA	ATATCTATTT	TTATAAATAT	420
	TATGTTGATT	TATATTATTT	AATCTTTTTA	TAAGAATTAT	TATTAATAAT	AATTTTAACT	480
10	TTAATTTCTT	ATTATTAATT	TTTATATTAT	TTAATAAATT	ATATTCATTT	TATTTATTTA	540
	TTTATTTAAT	TAAATTAATT	ATTTAATTAA	TATTTTATCA	TTATTTAATT	AATTAATAAA	600
	ATATTATAAA	GAATGTAGTT	AAAAATACTT	ATAAAA			

## 1692UP

15	GATCTTGATA	CTAGAGCTTA	TTTTACTTCA	GCTACTATAA	TTATTC TTAT	TCCTACTAGT	60
	ATTAAAGTAT	TTAGTTGATT	ACTAACTATT	TATGGTGGTT	CATTAAGATT	ACTAACACCA	120
	ATATTATATC	TATTATCATT	TTTATTTTFA	TTTACTGTAG	GTGGTTTAAC	TGGTGTAGTA	180
	TTAGCTAATC	TATCATTAGA	TGTAGCATTTC	CATGATACTT	ATTATGTAGT	ACTACATTTTC	240
	CATTATGTAT	TAAGTTTAGG	TGCTGTATTTC	TCTATGTTTG	CTGGTTATTA	TTATTGAAGT	300
20	CCTCTTGTTT	TAGGTTTAAA	TTATAATGAA	AAATTATCAC	AAATTCAATT	CTGATTAATT	360
	TTCTTAGGTC	TTAATATTAT	TTTCTTCCCT	ATGCATTTC	TAGGTATTAA	TGGTATACCA	420
	AGAAGAATTTC	CTGATTATCC	TGATCTATTTC	CTAGGTTGAA	ATTTAGTATC	TTCAATTGGT	480
	TCTATAATAA	CTATTATATC	ATTAATGTTA	TTCTTTTATA	TTATTTATGA	TCAATTAATA	540
	AATGGTTTAA	CTAATAAAGT	TAATAATAAA	TCTATTAAAT	ATATAAAACT	ACCTGATTTT	600
	ATTGAATCAA	ATAATATTTC	CTTAATGAAT	ACTACTAAAT	CATCATCTAT	TGAGTTTATA	660
25	TTAAATTCAC	CACCTCTTAT	TCATTCATTT	AATACTCCTC	TAATTCAATC	TTAAAAATAT	

## 1694RP

	GATCCGTTCC	TTGAGAAGCA	CCTAAAGCCT	GAAGTCTGG	CAGAAGCGAT	CAAGGGAACC	60
5	TCTTGGGAGG	GTAAAGTTAG	TATTAAGTTG	GTAGACGGAT	TCGACCACTC	GTATTACTTC	120
	GTCAGCACGT	TCGTGCCGGA	ACACGCAAAAG	TACCATGCAG	AAAAGTTGGG	TCTAGTTTGA	180
	GATTTGACGT	TGCGCCTGTT	AATTGGTATA	TACTTACATA	TTTAGTCATA	TGACGGCTTC	240
	AAGTACTCTG	ATTCTGCATT	ATAAGTGCAG	CCGAATGCCA	GCCTCCGGCA	GTAATGGCAA	300
	CGCAAACGTA	ATTTGCCGGT	AGTTCAACCT	TGGCCGGTTG	CAGCACGCGT	ATGCTCCGAG	360
	CAGACTCAAA	CGTCGCTATT	TGGCGGGTAT	CTACAGCCTC	GTCGGGATCT	CCCTGCCCAA	420
10	GACAGCCACA	GATATCACTC	TCCAGCCCCC	AGGAGTAGAG	TTCACCTTTG	TCGGTTAGAG	480
	CTAGGTTGTG	GTAGTCTCCC	GCAGATACAG	CAATAAACTT	CTGGCCTTGT	TCCAAATTCA	540
	TCCTCATGAA	TGAGTCCCTG	ACGATATCAC	CATTATTCAC	CTTCAGGGTG	TATGTGCTAT	600
	TCCTCGGTACA	TAAAACCAGT	GTCATGCAAG	ATGCCTCAAT	CTTCGTTAAC	CGTCCATCAA	660
	ATGGCAAAAT	CAA					

## 1694UP

	GATCAGCCCC	CGACCGAAGA	ACACTCGCTT	CCCTCTGGCG	AGCGCCGAAA	TTCTTGGACC	60
	GAGTATCAAC	AAATCCAGTT	AGATAACGAT	CACATGATTG	CAACACTGCG	GGAATTTCATT	120
20	AGTTACCAGA	CTGTTTCCCA	ACTCCCAGAG	CCCCAAAATA	TCATCGATTTC	GCGTAGGTGT	180
	GCGAACTTCC	TGCAAAATCT	CTTCACTAAG	CTCGGTGCTA	ACCATTTGTGG	GCTTATACCT	240
	GTCAGTACAG	GCAGCAACCC	GGTGGTTCTC	GCGCAGTTCA	AGGGCAATGC	AGCCGCGCCC	300
	AAACGCATAC	TATGGTATGG	CCACTACGAT	GTGATATCCG	CGGACCACCC	GTGCGAGTGG	360
	GACAACGACC	CCTTACGCTC	CACCTTGCAG	AATGGGTATC	TTAAGGGAAG	AGGCGTGTCT	420
	GATAACAAAG	GCCCCGTGCT	TGCCGCCATC	TTCAGTGTAG	CCGAGCTTTT	CCAGAAAGGA	480
	TACCTGAACA	ACGACATCAT	CTTTCTAGTC	GAGGGCGAGG	AAGAAAATGG	CTCTCGCGGC	540
25	TTCAGGGAAA	TTTTGCTTGC	CTCCGAAGGG	CTTCTCAATC	AGCGGTGGGA	CTGGATCCTG	600
	TTCAGCAAAT	CCTACTGGCT	GGATCAGAAG	GTGCCCTGCC	TCAACTATGG	CCTCCGAGGC	660
	GTCATAAACG	CCGAAA					

## 1695RP

30	GATCTGCCCC	CAAAAGATTT	CGGTGCCGGC	TACCCCAAAA	GATTTTCGGT	GCCGGCTACC	60
	CCATCACGAG	ATGGCACTGG	CTCATTTGGC	AGCTCCTGGG	CATTTGCCTA	TGACAGAGGA	120
	ATGAGTCAGC	TTTACTCCGC	CACACCATAC	TCCCGGGCTG	TCAACAAGCT	TCTGTTTGCC	180
	ATCGGTCATC	TGGCCAGTTC	TTACACTGCG	GCCCCACCTG	CATCGGCCGT	CATCGCAGCC	240
	GTTTTGTAC	AGTTCTCCCT	CCGCAGGTAT	CGTCTCCGCA	CCGGTAACGG	ACGCGACTAC	300
35	GCAGCGGCTG	CCGCACTCAC	GTGCGGGCGG	GTCTTCTCTC	CCACCGTGAT	AGTCACTTTT	360
	CAGTAGTGTG	TGCTGCCTTG	AATTGGCAGG	GCAATCGTTC	AAGCTGCTCT	GGCGCGGACG	420
	ACGACCCCAT	CTCCGCAACG	GCGTTGGCGG	AGAAAGGGTG	TTTCGGACCA	GACATCGGCC	480
	ATCTGCCGCA	GTCAGCAGCT	GCCTTGGTAC	GGAGCTACCT	GTCTATATTA	TCCCCTTAAT	540
	AAACATTGGA	TATGCCTGTT	ATTGTATGCC	AACGGTTCTC	CGGGTACAAC	GGGGTAGTCC	600
	CGCCCCCTCC	TGAGCTATCC	TGGCCGATGT	GAAGTGCCCT	TGGTTAAGTG	GTCTGCTTTT	660
40	CCGGGCCACT	TGTAAACACT	ATGGCGGATC	ATACAGCCAG	GACTCAAATA	C	

## 1695UP

45	GATCTGAAAA	GCAGGAAGTC	GCAGTGGGAG	GCGCCTGCGG	GCACGTCGTG	GCCAGCGAAG	60
	GGTGCGCCGG	ACGCGCCACC	GGCGTACGAC	ACGGCCGTG	CACGCGCCGC	CGCGCACGGC	120
	GCGCAGGCCG	TTGCGCCCCA	GCCCGACTAC	GGCACACAGG	CCGGATACGC	GCCCCAGGGG	180
	TACGGCGCGC	GGGCGGGGTA	CACGCCCCAG	CCCGGCTACG	CGCGACAGCC	CGGCTACGGC	240
	ACACAGCCCG	GCTACGGTGC	ACAGCCCGGC	TACGGCGCAC	AGCCCCGGCTA	CGGCGCACAG	300
	CCCGGCTATG	CGCCGCAACC	CGGTTACGGA	TACGCGCCGC	AGCCGGGCTA	TGGTGCCGCG	360
	CCCGGGCCGT	ACGCGCAGCA	GCCCGCGCAC	GGTTACCCGG	CCGGCGCAGC	CGCCGCGCCG	420
50	CAGAACGGCG	GCCGCAACAA	CATGATGATG	GGCGGCCCTGA	TGGGTGCCGG	CGTGGGGTTG	480
	ATGGCCGGGT	CACCTAATGAC	CACAGCCATG	TATAACCAAG	ACAAGGACGT	GGCCGATGCT	540
	GCCTACGACC	GCGGCTATGA	AGACGCTTCA	TCGACGGCGA	CTTCTAGGCC	GCACCCCGTC	600
	ACGTGCCAGA	CCCGTAGAGA	GCTAGGACAA	CTTACGTAAC	GCGTCGACGT	ACGC	

55

## 1696RP

	GATCTTGTTTC	TCCATTGACA	TCGAGGCGT	TGAGAGCAAC	ACATCTGTCG	TCACAGAGGT	60
	GGGAATCTCG	GTCTACGATC	CCCGCGAGAA	CGAGGACACG	CTCGTGCCCC	ACTTCCGCAC	120
5	GTACCACCTC	TGTCCTGAGG	AGTCTCTCGG	GTTGATAAAC	AAGCGGTTTG	TTCCGAATCA	180
	CAAATGCGAG	TTTCTCCATG	GTGAAACCAT	GGTAATGCCG	CTCTCCGAGT	GCGTTGAGTT	240
	CATTAACGGG	CTTATCGAGT	ACTACCTGTA	CCCACCCACG	GGCGTGGACG	ACAAGTACTC	300
	GCGGGCAATT	GTGGGTCATG	GTGTCTCTGG	TGATCTGCAA	TGGCTTAGGA	GTCTGCTCAT	360
	CGACCTGCCC	ACGATCGCTG	GCCCAGGCAA	CTCCCATCCG	CGCGACCATG	TTTCTGTCTT	420
	AGATACCGCG	CATTTATACC	AGTACTTCTA	TGGTCAGAAG	GGTTCATCCC	TAGGTAAGAG	480
10	CTTAAGATTG	CACGGTGTCC	CACATAGCTA	TCTGCACAAT	GCAGGCAACG	ATGCATATTA	540
	CACATTACAA	CTGCTCATGA	AGATGGGCGA	TGTGCAGCAA	CGCATCCGGC	ACCAATGGGA	600
	CGATCTATAT	GCTGTCTTCC	ACACGTTGAA	GCAATGGGAA	GAGTATGAGA	ACTCCACGCC	660
	CTCCACTCAG	CACGCAGAAT	CCGTCCATAA	CAGCACCCGC	GCTACCGGGA	A	

## 1696UP

	GATCCGTCAG	AAACCCATCG	CCTCGCTCGC	TCGTCTGCTA	ACGCCCAGAA	CGCCACCTGT	60
	GGTCTTTTCA	CTGCCGCTGG	TTCCTTATTC	CGCCAGGGGG	CCTCGTGGGC	CCGCCAGCGC	120
	TCGCCAGCGC	GGTTGTCTGC	ACCCGCAGCA	ACAGGACGAG	AACTCTCCGC	TTTCGGCCTC	180
20	GTGAGATTTT	GGATTCACTC	ACGTGATTCA	CGTAGAGGTT	ACCCGGAAAG	AGCGGCTTGG	240
	ATGCCAGTAA	TCACCGCCGT	TATCCCCGGC	CTTCTTAAGC	ATTCACTCTG	AGCCGCTTCT	300
	CCCCGCTTCC	TTGTTCTCCT	GGAATTTCAA	AGGGCGGGCG	GTATATAGGC	GGCGAGAAAA	360
	ACACGGTGGC	GAACGTTGTT	GCCGCCAAGC	GTTATCGTGA	AGAACAAGCA	TAATGGTTTC	420
	CCCTTCGGTT	ATTAAACAGG	TGCAGGCGCT	AATCCAGCAG	AACCGCGTGT	TCATTGCATC	480
	CAAGACGTAC	TGTCCGTATT	GCCAGGCGGC	AAAGCGTACG	TTGCTGGAGG	AGAAGCGCGT	540
25	CCCGGCAAGC	GCAGTAAAC	TGTTGGAGCT	TGACACCATG	GGCGAGGAGG	GCGCGGTGAT	600
	CCAAGCGGCG	TTGCAGGAGC	TGAGCGGGCA	GCGCACCGTG	CCCAACATCT	ACATCAACGG	660
	GCGCCATGTG	GGTGGCAACA	A				



## 1698RP

	GATCTGGTGC	TTTTCAACGC	GCCGCCCCAG	ACAATTTCCG	GAAGCATACA	TATCGCCATT	60
	ACATAAACAG	ATTTTATGAC	TAGTACAGTT	AGGTATGTGG	GAGATCACCG	GAATAACTCC	120
5	TATATCTTAT	TTCTGTATTG	TCAGGTACTG	ATCGCTGTGG	ATGAACGGGC	AACCCTGTGA	180
	CTTGGGGATT	AACACTGTAT	GAAGCCGGAC	GGGGGGGTAG	CACATTGGTA	CTAGGCTGGC	240
	TGAATTCATA	ATTGGAATAA	GGTGTGCTTT	GCCCCGATGG	CTGGTATGTC	CGGTGTGGG	300
	TTGAAGGCAT	AAAATTGCTC	GAGCTGTAGC	ATGTTGCCTT	CTCTAGCATC	ATGTTGTATG	360
	TAACCTCCGC	ATTGGCCAGA	ACCTCGCGCA	ATGATGCAAG	ATCTTCCTTC	TTCTGCGCAT	420
	ATTTACCGAT	GAGTTTCGTG	ACATGTGGTC	TAAGCGGTGT	GACGGTAGAG	TAAAGTTCTG	480
10	ATATCTCGTC	TTCTGTGTGC	ACATCCACAT	TCTGGGAGAC	CCTTAGTTTC	TGGAGCAAGT	540
	TCTCGACATT	GCCGGCTTGC	GCAAAGACAG	CATGCTCCTG	AGCAGCCTCC	TTAGCTACCT	600
	CCTCTGCAGT	TGGCTCAGGG	CATACGCCGA	CATAATTAC	TGGGAAAAAT	ACCAACCTTG	660
	CCGCGCA						

## 1698UP

	GATCAGCAAG	CTGGCCGCCG	CAGGTGTGCA	TCTGGGGCAG	TCTACGTCGT	TGTGGCGCTC	60
	CTCCACTCAA	CCATACATCT	ACGGCTCTTA	CAAGGGCATC	CACATCATTG	ATCTAAACCA	120
	GACGCTGTTT	CACCTGAAGA	GAGCTGCGAA	GGTCGTTGAG	GGTGTTCGGG	AGAATGGTGG	180
20	CCTGATCTTG	TTTTTGGGTA	CCAGAGAAGG	GCAGAAACCA	CCTTTACGGC	GGGCTGCAGA	240
	GAGGGTGCGT	GGCTGTATG	TCGCCTCGAA	ATGGATACCG	GGGACCTTGA	CAAACCCAAT	300
	TGAAATATCC	ACTGTCTGGG	GCAGGCATGA	AGTTGACTTC	GAGGGCAATC	CAACTGGCAG	360
	GGAATTGACA	GAAGAAGAGA	ACATCCGCAT	CATAAAGCCG	GACTTAATTA	TTGTTTTGAA	420
	CCCAACAGAA	AACATGAACG	CGTTGAGAGA	GGCTATGCAG	GCTAGAGTGC	CACCTATTGG	480
	GATCATTGAC	ACCGACTCAG	AGCCTTCAAT	GGTCACATAC	CCGGTCCCTG	GTAACSAACG	540
	ATTCGCTACG	TTCTGTAAAGT	TTACTTGTA	AC			

## 1699RP

	GATCTGCGTG	TATATTTGGA	TGTATATGGA	CTTCACACTT	TCGGAAGCAA	TGGAAGTCGA	60
30	AAGCTGGTTG	ACCACTCTGC	TGTATTCTCG	TAGTCTTTCT	GAAACGACGG	TAAGAAAATT	120
	AACCTTGAGC	GGCGATAGGG	AAGATGCAAC	TTTAAATTTT	TCTACTTGGT	TACTCAAATA	180
	CTGATATAAT	AATGCAGCCT	CAAATATGCT	GTGGAAAACA	CCACTTTTCG	CGTTCGGAAC	240
	ATTGGGTGGG	ATTTCGATAA	CCTGATTGGA	GATCGGGAAC	AAACTCGACG	TAGTAGCCAG	300
	TAACGTGTAG	GAAATATACT	TTAAAACGTC	GGCCTCGGGC	ACCATGTTGC	TGTAGTATGG	360
	GTTAGACAGA	TATGCCAATG	GAGTATCGTG	CTGCTGCGGC	CGCTTGGGGA	CCGGGCCGCC	420
35	GTAGGCAGAG	GTTACCGCCG	ACCGGCGCTC	TGAAAGCCGC	TCCACATTCT	CGAACGACTC	480
	TGCATAGACA	CTAACCGCCC	TCGACGGCGT	CATCAGCGAG	TTGTGCCGTT	GCAGCGTGGC	540
	GTTCCGTAAGA	TATCCAGACG	CGGTGCGCCT	GTGTGCGAAG	GGCGTGCTCT	CCTGCGGCAC	600
	GCTGTTTCAGC	ACCGTCAGGT	ACTTCAGCAC	CTGCTCCTTG	CTACCGAAAC	TCTCCAGCAC	660
	TTTC						

## 1699UP

	GATCTCCACC	GCGTCCAGCA	CCACGATCCG	GTCACCGTCC	CACCGCGTCA	TCGCCACTGT	60
	CCGCGCGACG	CTTTCGAAAA	CCGCCCGTCC	CTCCGCCGTC	GCAGCCCCTC	CCCCGCTGTC	120
	GTGCGTCCGG	TGCTCGGCCT	CCCGCGACCG	CAGCGTCGCC	ACCACCCGCT	CTATATTAC	180
45	GCCCGCGGGC	TTCAGCGTGT	CGCGCTTGAT	GCCAGGGCTG	GTGGGTTTCT	CTCCCACCAC	240
	CTCCAGGCTC	TTGATAAACG	TCGTCTTAAT	CACCTTAAAG	CTCGCAGTAT	GGCCCTTGCG	300
	CCCACATAGT	AGCGTCAGCG	TATGGTTTCC	CGAATCGTAC	GCGTATATCT	TGCCCTGTGT	360
	TACACCGTCG	AGGACGTTGG	TCACCCGCAC	CTTGAATCCA	AGGATATGTT	CCAAGTTGAT	420
	GCTCATTTCTG	CTCACTTCCA	AGCCCCACAC	GCTATCCTGG	CCACCTTAGA	ATGCCACGCC	480
	TGCTCCCCGT	CCACTGGCTG	ACTCCCAATC	GTTCAAGTTG	CGGTGTGGGT	ATTTTTTTGA	540
50	AGTGGCGCTC	TAACGATGAA	GTAGGATTTT	CTATGTATTA	CTATGTCGCA	CAAAGGTTAG	600
	TTCCAATAGT	GCTTGCAACT	ATCAGGTGCT	GTGGAATTCC	AA		

## 1700RP

	3ATCAGCAAC	CGCAGCGGAT	GAGGGAGTCC	GCTCACGCAC	GGTCTTGTTT	TCAGCGCTTG	60
	3CTTGCTTTT	CTCCTTTATG	CGTTGTACTA	CTTCTGTGAT	GTGCTCGGCA	TCCAGGCCCC	120
5	TTTTCTTAG	CCTGCTTCGT	AACCTGCGCA	GGCGGCGGTT	GCTACGAACA	CGCAACTTGG	180
	CTTCTGGATC	AGCAAGCTGC	GCTCGGTGTT	TGCGCAGCCG	TTGGCATGCT	CGCGGATCCT	240
	CGCGTTCAAT	ATACCAGAAT	GCATCATGCT	TCGCTGGCTC	TATATTGACC	TGGTGGCCAT	300
	ATATGAAAAG	GCGGTCCTTG	AAGTTTGTGA	AAACTCGTC	TGCCTGAGAT	GGCGTAGCGA	360
	ACCCAAGGAA	GCATTTATTG	CGGCATTTAC	GAGGCCTGGA	AACACTAACT	ACCCCGTACT	420
	TCATCATCTAC	CAGTGGGAAG	GGCACGTCTG	CGGAAGGAAG	CGGCTCTGGC	AACGTTTTCT	480
10	CCGCCGATAG	AGCATATGGG	TTATCCTTGT	TGATGGACTT	CAACAGTTGT	CGAGCATATT	540
	CTATCCTGGA	GGCATTTGAC	GCTGGCAAAT	TTGACAGGTA	GACACTGGAT	GGCGGGGTTA	600
	3TATCGAATC	GACAGCAGTA	TAGC				

## 1700UP

15	GATCACTGGG	CCTGGAGGGG	CGCGCCTTTT	TGCGGCTGTT	GTAGAACAGC	ATGCCGCGGC	60
	GGACCTTGTC	ATAGAAGTGT	TTAGACTGTA	GGGTTCCCAT	CGAATGGGAG	CGGCGGTAGC	120
	TGTGACTTTT	CATGATAATG	GGGGTGCAAA	GCTTGAGGTG	GTCGTCTGTAC	GGGGAGGAAA	180
	TGAGGTTGCG	GCCGAGACGG	AGGTCGTCCG	CGCGCGCGAG	CGACGAGCCG	CCGGATGGCC	240
	ACTTCCAGGA	CTTGCGCGAC	GACGGCGCGT	GGCGCGAGGA	GTAGGAGCGG	ATGGGGAGT	300
20	CGCCGCCAAG	CTGCGAGCCG	CGGAGCCACG	ACGTGAGCCG	CTTCAANAAA	CGGCGACGGC	360
	GGTTGGCGGG	CTGGAGCTGG	CCGGCGACAA	ACGCAGAGCC	GCTGTCTGGC	AGACCGGTGG	420
	GCGCGCCTGC	GCTGCTGGTA	AGCCCAGTGG	CGGACTCAGG	CAAGCCGGAC	ATGCCCGGGA	480
	AGTAGCGCGC	GCTGTTGGCG	CTGAGCTTCG	GAAACATCTT	GGAGAAGAAG	CCCGGCTCCG	540
	TGGAGCGCAA	CACGCGGTCC	GCCTTGGAGA	TGTGCTCCTG	CGTGGAGTGC	GCCAACTGCT	600
25	CCA						

Ann x to the des ription

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: Novartis AG
- (B) STREET: Schwarzwaldallee 215
- (C) CITY: Basel
- (E) COUNTRY: Switzerland
- (F) ZIP: 4058
- (G) TELEPHONE: +41 61 324 11 11
- (H) TELEFAX: +41 61 322 75 32

(ii) TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHEYA GOSSYPHII  
AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 1152

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: EP 978 110 20.3
- (B) FILING DATE: 24-DEC-1997

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: CH 0016/97
- (B) FILING DATE: 31-DEC-1996

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTACTAGA TATTTTATAT CCAAGAAGCA ATAGATCAAA ATGGCTGCGG TAAAGAGAAT 60

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGGAGCTCC ACCGCGGTGG CGGCCGCTCT AGAACTAGTG CGCCAACGTT GCGAGATATA 60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: AgLEU2

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25	ATG GCT GCG GTA AAG AGA ATT GTG GTG CTT CCG GGC GAC CAC ATC GGC Met Ala Ala Val Lys Arg Ile Val Val Leu Pro Gly Asp His Ile Gly 1 5 10 15	48
	CGC GAG GTC GTG GAG GAG GCG GTG AAG GTG CTT GGC GGC GTG GAG CAG Arg Glu Val Val Glu Glu Ala Val Lys Val Leu Gly Ala Val Glu Gln 20 25 30	96
30	AGC CTG TCG GAC GTG CAC TTT GAC TTC CAG TAC CAC CTG GTC GGC GGC Ser Leu Ser Asp Val His Phe Asp Phe Gln Tyr His Leu Val Gly Gly 35 40 45	144
35	GCG GCC ATC GAC GCC ACG GGG TCG GCG CTG CCG GAC GAG GCG CTG GGC Ala Ala Ile Asp Ala Thr Gly Ser Ala Leu Pro Asp Glu Ala Leu Gly 50 55 60	192
	GCG GCG AAG GAG GCG GAC GCG GTA CTG CTG GGG GCA GTT GGC GGA CCG Ala Ala Lys Glu Ala Asp Ala Val Leu Leu Gly Ala Val Gly Gly Pro 65 70 75 80	240
40	AAG TGG CAG GGC GGC GCG GTC AGG CCG GAG CAG GGC CTG CTG AAA CTG Lys Trp Gln Gly Gly Ala Val Arg Pro Glu Gln Gly Leu Leu Lys Leu 85 90 95	288
45	AGA CAG GAG TTG GGC GTG TAC GCG AAC CTG CGT CCC TGC AAC TTT GCG Arg Gln Glu Leu Gly Val Tyr Ala Asn Leu Arg Pro Cys Asn Phe Ala 100 105 110	336
	GCG GAC TCG CTG CTC GAG CTG TCG CCG CTG GCG CCC GAG ATT GCC CCG Ala Asp Ser Leu Leu Glu Leu Ser Pro Leu Arg Pro Glu Ile Ala Arg 115 120 125	384
50	GAT ACC GAT ATT ATG GTG GTG CCG GAG CTG CTG GGC GGG AGC TAC TTC Asp Thr Asp Ile Met Val Val Arg Glu Leu Leu Gly Gly Ser Tyr Phe 130 135 140	432
55	GGC GAG CCG CAC GAG GAC GAG GGC GAC GGA GTC GCG TGG GAC ACC GAC Gly Glu Arg His Glu Asp Glu Gly Asp Gly Val Ala Trp Asp Thr Asp	480

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	145		150		155		160	
	AAG TAC ACC GTG AAG GAG GTG CAG CGC ATC GCG CGC ATG GCG GGG TTC							528
5	Lys Tyr Thr Val Lys Glu Val Gln Arg Ile Ala Arg Met Ala Gly Phe	165		170		175		
	CTG GCT CTG CAG CAC GAC CCG CCG CTA CCT GTG TGG TCG CTG GAC AAG							576
	Leu Ala Leu Gln His Asp Pro Pro Leu Pro Val Trp Ser Leu Asp Lys	180		185		190		
10	GCG AAC GTC CTG GCC AGC TCC CCG CTG TGG CCG AAG ACC GTG GAG GAA							624
	Ala Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu	195		200		205		
	ACC TTC CAG AGT GAG TTC CCA AAC GTG CAA TTG CAA CAC CAG TTG ATA							672
15	Thr Phe Gln Ser Glu Phe Pro Asn Val Gln Leu Gln His Gln Leu Ile	210		215		220		
	GAT TCA GCT GCA ATG ATT TTG GTC AAG AAC CCG CCG GCG TTC AAC GGG							720
	Asp Ser Ala Ala Met Ile Leu Val Lys Asn Pro Arg Ala Phe Asn Gly	225		230		235		240
20	GTC GTG GTG ACG AGC AAC ATG TTC GGG GAC ATT ATC TCT GAC GAA GCG							768
	Val Val Val Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala	245		250		255		
	TOG GTG ATC CCA GGG TCC CTA GGG TTG CTG CCA TOG GCG TOG CTC GCG							816
25	Ser Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala	260		265		270		
	TCT TTG CCG GAT AGC AAG AGC GCC TTT GGC CTC TAC GAG CCC TGC CAC							864
	Ser Leu Pro Asp Ser Lys Ser Ala Phe Gly Leu Tyr Glu Pro Cys His	275		280		285		
30	GGC TCT GCG CCC GAT CTG CCC GCC GGG AAG GCG AAC CCG ATC GGA TGC							912
	Gly Ser Ala Pro Asp Leu Pro Ala Gly Lys Ala Asn Pro Ile Gly Cys	290		295		300		
	ATC CTC TCT GCT GCC ATG ATG CTG AAG TTG TCG TTG AAC ATG GTT GCT							960
35	Ile Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Met Val Ala	305		310		315		320
	GCC GGC GAG GCG GTC GAG CAG GCA GTG CAG GAG GTG TTG GAC TCG GGA							1008
	Ala Gly Glu Ala Val Glu Gln Ala Val Gln Glu Val Leu Asp Ser Gly	325		330		335		
40	GTC AGA ACG GGC GAC CTG CTC GGC TCG AGC TCC ACT TCG GAG GTT GGC							1056
	Val Arg Thr Gly Asp Leu Leu Gly Ser Ser Ser Thr Ser Glu Val Gly	340		345		350		
	GAC GCC ATT GCG CTT GCA GTT AAG GAA GCC TTG CCG AGG CAA TCC GCA							1104
45	Asp Ala Ile Ala Leu Ala Val Lys Glu Ala Leu Arg Arg Gln Ser Ala	355		360		365		
	GCT GGT CTG AGC TAGCCTGAG GACCCCTCTC TTTAGACTAT TCTACTCTTA							1156
	Ala Gly Leu Ser	370						
50	TGCACGTAAA AAATTCCTAGG AAATATGTAT TAACTAGGAG TAAATAAACC GGCTAGTGGC							1216
	ATTTCATATAG CCGTCTGTCTT ACATCTACAT CACACATTTT GAGTGTATAT CTGCAACGT							1276
	TGGCG							1281
55								

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## (2) INFORMATION FOR SEQ ID NO:4:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ala Ala Val Lys Arg Ile Val Val Leu Pro Gly Asp His Ile Gly
 1           5           10           15
Arg Glu Val Val Glu Glu Ala Val Lys Val Leu Gly Ala Val Glu Gln
          20           25           30
Ser Leu Ser Asp Val His Phe Asp Phe Gln Tyr His Leu Val Gly Gly
          35           40           45
Ala Ala Ile Asp Ala Thr Gly Ser Ala Leu Pro Asp Glu Ala Leu Gly
          50           55           60
Ala Ala Lys Glu Ala Asp Ala Val Leu Leu Gly Ala Val Gly Gly Pro
          65           70           75           80
Lys Trp Gln Gly Gly Ala Val Arg Pro Glu Gln Gly Leu Leu Lys Leu
          85           90           95
Arg Gln Glu Leu Gly Val Tyr Ala Asn Leu Arg Pro Cys Asn Phe Ala
          100          105          110
Ala Asp Ser Leu Leu Glu Leu Ser Pro Leu Arg Pro Glu Ile Ala Arg
          115          120          125
Asp Thr Asp Ile Met Val Val Arg Glu Leu Leu Gly Gly Ser Tyr Phe
          130          135          140
Gly Glu Arg His Glu Asp Glu Gly Asp Gly Val Ala Trp Asp Thr Asp
          145          150          155          160
Lys Tyr Thr Val Lys Glu Val Gln Arg Ile Ala Arg Met Ala Gly Phe
          165          170          175
Leu Ala Leu Gln His Asp Pro Pro Leu Pro Val Trp Ser Leu Asp Lys
          180          185          190
Ala Asn Val Leu Ala Ser Ser Arg Leu Trp Arg Lys Thr Val Glu Glu
          195          200          205
Thr Phe Gln Ser Glu Phe Pro Asn Val Gln Leu Gln His Gln Leu Ile
          210          215          220
Asp Ser Ala Ala Met Ile Leu Val Lys Asn Pro Arg Ala Phe Asn Gly
          225          230          235          240
Val Val Val Thr Ser Asn Met Phe Gly Asp Ile Ile Ser Asp Glu Ala
          245          250          255
Ser Val Ile Pro Gly Ser Leu Gly Leu Leu Pro Ser Ala Ser Leu Ala
          260          265          270
Ser Leu Pro Asp Ser Lys Ser Ala Phe Gly Leu Tyr Glu Pro Cys His
          275          280          285

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Gly Ser Ala Pro Asp Leu Pro Ala Gly Lys Ala Asn Pro Ile Gly Cys  
 290 295 300

Ile Leu Ser Ala Ala Met Met Leu Lys Leu Ser Leu Asn Met Val Ala  
 305 310 315 320

Ala Gly Glu Ala Val Glu Gln Ala Val Gln Glu Val Leu Asp Ser Gly  
 325 330 335

Val Arg Thr Gly Asp Leu Leu Gly Ser Ser Ser Thr Ser Glu Val Gly  
 340 345 350

Asp Ala Ile Ala Leu Ala Val Lys Glu Ala Leu Arg Arg Gln Ser Ala  
 355 360 365

Ala Gly Leu Ser  
 370

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATGATTACG CCAAGCGGCG

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCAAGCACAT TTCACCTGCG

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1489

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	GATCGTAACA TTGCCAATA GCTTGTTTAG CTGTCATCG TTCTGATGG CTAGCTGTAG	60
	ATGTCCTGGG ATGATTCTGG TCTCTTGTT GTCTCTGGCG GCGTTACCGG CCAACTCTAG	120
10	GATTTCCGCG GCCAAGTATT CTAGCACAGC GGTAGGTAC ACAGGCGCGC CGACCCGAT	180
	TCTCTGTGG TAGTTGCCCT TTCTGAGCAA TCTGTGGACT CTACCGACAG GGAAAGTCAA	240
	ACCGGCTTGA GCGATCTCG ACTGCGAAGC CTGCGCGCA GAACAGCTT TACCTCCTTT	300
15	ACCAGACATT ATTTGTGTTG TGTGTGTGTG TGTGTGTTA GTGTGAAGTG CGTGTGCTAT	360
	GAGAAAACAC TACGCTGAAA CTGCTAAATA ATCCAGACAG GTCCCCCAC CGCAAAGGAT	420
	CCACGCTATA CTCTCTCTA CATATTTATA CTGTCTCTT TGCCCTCTAA TCCTCGATCG	480
20	TACCGCTCTG ACGCTTCAAC AGACGCTTCA CCTAGACGCT CGACCTGTGC GCGCTGGTTT	540
	TTTCGCATGA CATGTCCGTG CTGGTTTTTT CCGCTGAAA AGGAAAGCGC GTGGCTCCCA	600
	GCACCAGAGC CGTACTAGCT CTTTCGCGTG CTGTCTATG TGCAAGGAA ATTTTCATAC	660
25	TGTAGAGTGT GCCATCAGCT TCACAGAGTA CAAACGGTAG GCGAGTGGAT ACGCGTCTG	720
	TAGCCGGACG TGAATGGCAG AACTTTTTGG CAGTCGGTA ATCTTAGATT GAAAGTATTT	780
	AAGTGGAAAG TATAAAACAA AAGTTCGGC TGAAGAGGAC CTCTTTTGSC GTCTGCTACT	840
30	TCCCAGTTAT CTGTTGGATA CTAAGCATAT CGAACTCTAA TTGCAATTCT AAAGATGGCA	900
	CCAAAGGCTG AGAAGAAACC TGCTTCCAAG GCGCCAGCG CAAAGAAGAC CACTGCTTCT	960
	ACCGACGCTT CTAAGAAGCG GACGAAGACT AGAAAGGAGA CCTACTCCTC TTACATTTAC	1020
35	AAGGTTCCTA AGCAGACTCA CCCAGATACT GGTATCTCG AGAAGTCTAT GTCCATTTTG	1080
	AACTCGTTTT TGAACGATAT CTTTGAGAGA ATCGCGTCTG AGGCATCCAA GCTTGGGGC	1140
	TACAACAAGA AGTCTACGAT CTCTGCTAGA GAAATCCAGA CTGCTGTGAG ATTGATCTTG	1200
40	CCCGGTGAGC TAGCCAAGCA CGCGTGTCT GAGGTACCA GAGCTGTTAC CAAGTACTCG	1260
	TCTTCTACCC AAGCCTGAAT GGAATCATT CTTAGAATGA AAGAACTCC TTCAAGAAGG	1320
	TTCTCGTCAG CTAGTGCTTG TGGACCCGC CTCTTATTC AGAGCAGCTG CGGCAGAGCG	1380
45	GTATGTGGTA CGTTCGTTT CATCATTTTG TATTATTAGT ACATGTAGAA ATAGGGTTTT	1440
	CTGGTTTCAT AATTCGGTAT AAATCCAAC GTAATGTATA TTAGATAAGT TTAAACTAG	1500
	TAATCGGAGA GCTTCTTTTC AACCAGTCT ACCTTGCTT GCGAGTCTG CTGTTTGCT	1560
50	GTCTAGTTC CGAGCTCAT TTGCGTGTG ATTCTAACG ATCCAATTC GTGCTGTAT	1620
	TCGTGCAACT GCGGATGAG GCTCATGACC TCGTCCCAAG GCGCTCAAT CGTGTGCA	1680
	AAGCTGTGCA TAGTGCTTTT CAAGTACTC TCCCTAATTC GTTCTCAAT CTTGGTGACA	1740
55	TAGTCTGAGA CACTTGGTGA GCTAGTACCT AGCTATGATT CAAAAGTTTA GTATATTGTT	1800



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	TTATATATGC AGCTGGAGAT GTGAACATAC CGGCACCATG CAAATGTCCA CTAATGTGTG	1860
5	CAGCTTCGAC ATTTTGATTT CTACCTTCAG AGTATTGGAA TATGTTCTTG TATGTAAOGT	1920
	CTACTAATTT TCTGGTTTAT ATCGCTGATC TTAAGGGAGA TAATTTGGTT CACCCATCAC	1980
	ACAGAAGTTT TAAGTACAAA ACTTGTCCCC AGATATAGCA AGTCATCAAT TCAGGTATAA	2040
10	TTGGTGTGCA TGCTAATTTG AAGGCTGTT ATATAGTTGA AGTTGTTCTT TTGGCATGGA	2100
	GCCAAATTTG GATTCATTC AGTAGTATTG AACATCAAGT CTCCAAAGCT GAAGTCTGAA	2160
	GCAAACATC TCAATAGCTA TAGAACTCTA GCAAACAACA GACCAGAGCT TATATCATGA	2220
15	CACATTATAA GCTCAGCTAT TACTCTGAGT GATAGAGTGA CCTCAATTA GTTGGTTCAT	2280
	TTTATATATA AAAATATAAA ACTATAGCTA TTTCAAATGA CTACTAACTA ATACGAGAGA	2340
	AGAAAACAAA TTAAACACGA TGGTCTACAG ATAGCTTGAA AGAGACACTA AGAGAAATTT	2400
20	CAGGAAACAG TTCAGAAAAT AGCCATTCAG CTCTACAGCT CTCTTTATTA TCAAGAGTAC	2460
	AGTTTCTTTC ACTAATATCG CTTAATTAAT TATATTTCTT GCCATTAAAT GCGACGGTGA	2520
	CGGGATAACA ATTTTGGCA ATTCTTCATA TTTTGATTGA AAAAAAAAC AATTTACCAG	2580
25	AATTAGACGA AATAGTGGCT TACTACAAAC AGGTTGAGCC ACTGGATAAA TCTCATAGTT	2640
	TAAATATTG AGTTACAGAA ATTGGCTTAC AGAAAGCACT AGCGATTAGG CCATTTGCCA	2700
	TTGATTTAAA CATGAACATA CGAACCTCCA TGAATTACAA TAACCACAAA TTAAACGGGA	2760
30	CAATTAAATTT TATGTAGCAG GCTCTGCCAT GGGAAATAGCT TTACGTGAAC AGGATATTTA	2820
	ACGTATATCC TTGTTATGAT AAAGACTTTG ATAGGTGCTT ATACTTGCAA GTTCATATTT	2880
	TACAGTTAAA TATCTAAATT TAATATATTA CGCAGTTTAC GCAATGTAGC ACGTGACATA	2940
35	AATATGAAAT TFACTATGTG CTGCTTTTAT TTAAAATAAG TTTATAAAGT TAGTAAAAAT	3000
	ATCAGAGTAT ATATATTTAA TAAATAATA TCCTAAAATA TACTAATACA ATTTATCAAT	3060
	TAAGCTTTAT ACACTTTATA AATAGTTATA ATTATAGATG TGTATACGAT TTCCGAAACA	3120
40	TAAAAATATT TCACTGCTTT CGTGAAAAAT AATTTTTTTT TTATAAAACA ATCCCTAATA	3180
	TAGTATTACC TOCAATTATG AGTCTATCGT AATATATGAA GTACTACCAA AATTTACCAC	3240
	TGATTTTICA AAAAAAAAC ACCATTTTTC AAAAATATTT TATTAACTGA ATTTTATATA	3300
45	ATTAAATTTT TTATATCTAT ATAGAATATC TATTATACGC AAGAAAAACC AAAAAGTACC	3360
	CTATAAGTAG GTACCGCTTG TCCACATTAT AATAAAAAAA GTGAAGTACT CATCAATACT	3420
	TTTATTTAGG ATACCTGCAG TCTAATATCC CTTCACGTAA GTTACTTAGT GCACAATATT	3480
50	CACAGTGAGT TAGTAACCCG GTTCAGATCA AGGCATACCG AGCTTTCTCT TCTGGCTTCA	3540
	TATGCTTAAA GAAATATCA GGGACGGTGC AGTTAGCTAA AGCTCTCTTA GCATAAGTAT	3600
	TCATAAATTT CAAACCTAAG ATATAACTGG AATTGACCCA GCCAAATCCT TCAGTAGCAA	3660
55	CACCTTTAAA GCTGCACTT TGGTTACCAT ATTGCGCATC AACTCTATGA GGATCTGTGC	3720

CTCTGGTAAC GTCTGTTTTC TCTACTACGA TACCATTGTA GTGACAAAT GCCTTGGTCA 3780  
 TTAAAAATAA CCACCTATAG GCGAACCTTC TTGCAACTCC TGTAATCCG TAATTATCTA 3840  
 5 ACCCGGTCCA AGCAAGCATT TGATGAGGGG CCCAACCATA AGGGTAATCC CATTGCCTGC 3900  
 TTGGTCTATT CATTGTTATC TCACCCGAG ACTCCTCAGT ACAGGCAACC AGGCTCCTA 3960  
 GCATTTCAG CTTGGCAAT GCCTTCTCGA CCATAGCGTT GGCTTGTTCC TGGGTTGCCA 4020  
 10 AGCCTGCCCA CATGGCCAA AATGTTGTTG CAGAATCGTA AGATGTTCTC TTCCAATAT 4080  
 GGACATGTGA GTCATAGAAA AAGCCTGTTT CCTCGTCCCA CAAATATTTC GTGATTCTTT 4140  
 GCTTACGAAT GTCTGCAAGT GCTCCCAAT GAGAAGAAGT GGTGGTTTCA CCAGCATAAT 4200  
 15 CAGTAATACT ATCATCGAAG TACTTGGAAA CCACATATGC AATATCTTTT TCGTACTTGT 4260  
 ATAGTAACGA ATTCAAATCA ATCTGCGTA AGTAAGCACA GACGTCTCT AGACGGTAAG 4320  
 AGGTGTCATG TCCACTCTCA CGTACAGCAC GATCATGCAA AAAGAACTCA TCTAGTTCGG 4380  
 20 GCTCGTGTAC TTGCGCGCA TCGTACATGC ACCTGAACCTC CGGAATCGTT ACATTGTGCT 4440  
 TTTCGCAAA TTTCGGCAA ATTGCGTCAA AGTGGTCAGG CTCGGTTTCT GGTGGGAAAC 4500  
 CGATACCATC TGGATGATAA CATGAAAGAC CCGTGGTTTT GTGTACCGC GGTTCGCCA 4560  
 25 TCCATACACT CTTGTATTCC TTAATGGCTG CGATGAATGC TCTTTTCAAG AAATCCACAG 4620  
 CGGTAGGATT TTGGTCACCA CCGAATTTT CGAAGACCTT CAAAGCCATG TCGGTTAGGA 4680  
 ACCGGGGTTG TGACCGACAG AGGTAGTAGC TCCTATTGGC GTTCAATATT TTACCGTAAT 4740  
 30 GCTCTATCTC AAAGATGAAA TGCTCAACCA TCCCACGTGC TATGTCCACT TTGTTACAGT 4800  
 CTAGAAGACC CAAAGCCATT AGGTATGAGT CCCAGCCGTA AAGTTCATTA AAACGACCGC 4860  
 CCGGAACAAC GTAGGGAAAA CCAACCAATG TACTCTCACC GGTAATTGGG TCCTGTGAC 4920  
 35 TCTCCATCGC CAAAGCAAGC AACCCCGGC TTTCGTTCAA TGATTGCACG TGCTCCGGCG 4980  
 TGATC 4985

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTTAGTCTG ACCATCTCAT CTG

23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCGCAGACCG ATACCAGGAT C

- (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTAGGGATA ACAGGGTAAT

- (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGCATGCAA GCTTAGATCT

- (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTITTTTAGAA TATACGGTCA ACGAACTATA ATTAACTAAA CATGGGTAAG GAAAAGACTC 60

A 61

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTATATAAA AATATTATAT GGAAGCAATA ATTATTACTC TTAGAAAAAC TCATCGAGCA 60

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAGATCTG GTGTATTTC CAATAAT 27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGAGATCTG ATGAGGCGGT CTTTGTGTG 29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1001RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTGATTGCTC CGAGATTGAA AAGTCCCTAA CAATCAAAAA CAACGGGAAG GCGTACGAGG      60
AATGGCTGGA CCTGGGTAAT GGGTGCTTAT GTTGCACTCT GAAGGACGTA GGGGTGAAGG      120
CCATCGAGGC GATGGTTTCG CCGTGGCCAG GTAAAATCGA CTACATCATA CTGAGACAA      180
CGGGGATAGC GGACCCAGTG CCGATCGTGA AGATGTTCTG GCAGGATGAG GGTCTCAATA      240
GCTGCATCTA CATTGATGGG ATTGTGACGG TGCTGGACGC AGAGCATGTG ATGACATTGC      300
TOGACGAGGT GGCCCTCCCG CGCCAATTGC GCGGCGACCA GGTGCTGATG GAAAACCAGA      360
TGACCCNNGG GNATCTTCAG GTTGCCATGG GGGNGCGGG GNGTTGATTA AATCNACCCC      420
TGNAGGCTGN NTAAAAATCT TGGNNGGAA AANGGTGANT ATAAGCGGCC TTTTTOGGCN      480
AATNCGGGAN TTTNGNTANN AAAGNINT      508

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1001UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

TGATCCGACC AAGAGCAGGG CTTTGGTGG GTGAATCTCG AACTCCTGCC CCTGTGTCAG      60
CTCACCCCGG CCGAAGTCCT TCCAAAGAAG AGCTTGTTAGA AAGTGTTCCT CGAACCCTC      120
GAGCTCAGCC TTGTGCGGCA GCGGCCGCA GGTCAAGGTG ACCGTGGACA GCGCGGATC      180
ATGGTAAGCC ACGTGGGCAT CCGGAATGTC AGAGGCACCA AAAGCATGGA GATTCAAGTA      240
CCTTGTTTAT CTCCAGATCG CCGAACTTGG TCCGATAGA TGGGCGGAC TGCATTAAATG      300
CTACGCATT TTTCTCCAA CCACAGCGAT TCGTCATCAA NGCCTCCAG CCNGTGGAT      360
TTATCAAAAC AACCNNGTCC GCCATGGCNA GTTGNAGATG GCANGGCACT TTNTTCCAC      420
AGACTGGNGG CCGGCAATGG GGGGGGCACC CGGACATTA NAATTNTGTC AGACCNAAAC      480
CNCAATTGNN      490

```

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1002I1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATCTCCGCA AATTCTCCCA AAATGGTAAG TCGTTATCCA CCTTAAATGC TTGCTGGGGT 60  
 AGCTTGTGTC CCAATAAATA ACGTGACCCA TCATTGAGAT CCAATACCTG GGGGAGCAGT 120  
 TCGCTCCAAT CGCGTACTTT CTTTAAAAAC GGAAATAGTT CATGATGGAG AGAGTACAAG 180  
 TTTATGTCTT CACCAAAAAC CTCACGAAGA CCTATATCTC CTTGCATGAA ACAAGTGTGG 240  
 AACACTCGTA GTGCTTCCAG CATGGCAGCT GTCACCGAGG CATCCTTCAT GCGACCAAGC 300  
 GACCTTTTGA TAATTTCGTT CAGCCATTGT TGTCTCTTTT TCTTTGCGAA AGTACCACTG 360  
 GCATTCTTTT CCAGGGGGCA TCTCCCGAAC TGGGTTGGTC AACAGAATGT ACTGTINTGGG 420  
 GNGGGGTTTG GTGTTGGACG ACNTTTINGTG AAGATGGGGC ACAGTTINTGC CGTTTTTTGAG 480  
 GNCAGGCAGA TTTGAAACAA ATTNNCGNNA ANTTCCGTTT CCNACGCAC GGGGCCCGAN 540  
 TTCAGGCAAC CTNGACATTN TOGAAGTACC N 571

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1002I2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATCTTCGAG TGGGCGAGGG ATAGTAGCGA CCGTGGCAGA CATTCATCTT GATCAATTGA 60  
 AGCGCCTGCT CCATGTCCTT GATGAACTGG GGAATAAATT GCCTATAGAG TTGGTGTACA 120  
 AGGGTAACGA CTTCTCTCGA TTGCCTATCA AAAGACTGAA AAGGTACGTT CGGCAGCACA 180  
 CAAAACAGCG AGTTCGGCTG GTGGACTGTT CGCGTGTACT ACGCAGTACA CATATACCTA 240  
 AGATAAAGAG GTTCATGAAT AAGTGGTTAG CCACTATATT CAATTCATTT GGAGGAAATA 300

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ATACTACTAG ACGTGGATTG TTGGTGCCAC TGGGTTCCAA TCGATAGCTA CTTCAAACTT 360  
 CCGGCTACA CTAAAAACGG GCGCTCTTGT CCTTCAAGGA TAGAACGCTT CCGGAGTACC 420  
 5 TCCCTGTTTC ATGCACAAAA GCGAACTACT CTTGCCACCA CCGCCGGAGG AGACAAACTT 480  
 TGGGGCAATC CTTTGAGATT TCGACACCAN TGNAAAAGNT N 521

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 518 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1002RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GATCTACTAA GGAATTATGG GAATCGTGTG TTTTCTTCTT AGAAATGAAT TTGTTTGCAG 60  
 25 TCGAAGACGA GGTGGAAGAC GAGCGCGACT GTTTACTCTT GGGGAAGTTA GTCAAACAAT 120  
 CGCTAGATTG TATCCGCATG GTATCACCTG AGTTTCTATC TATAGGAATG CTACTATYAC 180  
 GGAAGTTGCG ATGCTGATGG GCATGGTTGT CATGAAAAAT AGGATGTTGG CTCGCGTTAG 240  
 30 ATGACTGACC GAATACCTCT TCTATGATTA ATTCTWCAA GCGGGTATTG ATTAATGTGG 300  
 ATCTGTGGC GTATGATGAA ATGACTGCGC CGTCATTGCC GGTACGCCCT TGGAGTGTTT 360  
 GGANITGACA AGAANNOGCT CTTAGGTGCC NGGATTCCCN GGGTTGGAAA GATGATNGCG 420  
 35 AATNCCAATT TNGGTCCAAT AGGGAATCTG GNATTATTTG TTATTGCAAT NAGGATNCCC 480  
 GGGAGGGGGT TNCNCTACGA AGAAGGATTA GGTNNNC 518

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 441 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1002UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATCCACGKG AGTCGCAGCG CCAAAGGCGG CTGGGCGTCA CGATGCAGGT TATGCTGTGG 60  
 CGTCGACAGA GTGCGCCCCG CTGGATGAAG CCCATAAGAC TATTGAGCCA CTATATAATA 120  
 55 CCAGCTGGTT ACATGATACT ATATGGTCAT AGCATCAATT GTAGTAGCCA GGGCAGTGAG 180

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GCTATAGCAG CTGGAAAGGC GACTCTGAAA AGGGATTATAT GCCAAGAGCT TCAGAAGTGG 240  
 ACTCAGGCCA CGCATCCAAC GGATTCCTCC TCAATTOCTC TATATTGAGC CAGAGCTCCA 300  
 5 TCTTGACCGA GGTCCCTCAT TCATATTCAT ACGAGTTACT TGAACATCCA ACAGGTGCCA 360  
 TATTTAGKTT GGGGGGGTAA GTACAATANC GVTGNNGGCC GTGGAACCCC GGTCGGTTCC 420  
 CNGGGTTTTG GAATTTTTING G 441

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 513 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1003RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCGCTCAT GACCAAAACA ACGAAATCCA CTACATTTG CTGOCCTG CTCACCCAGC 60  
 GAAGTTTGCG GACGCTGTGA ACGAAGCTCT CTCTCTTAC GATGACTACA ACTTCGATGA 120  
 CGTCTTCCA GACCGTCTAA GACGCTTAGG TGACCTTGAG AAGAGAATTA AGTACGTGGA 180  
 30 CAACACCGAC GTTGATGTTA TCAAATCTAT CATGAGGAG GAACTGATTA ACATGGGCAT 240  
 TTACAATCCA TAGATGATCT GAACTCTAGA TGATTTATAG ACTATCTAGT TAGCCTTCTA 300  
 GTCCTATATA CCTAATTOCA ATAGGCAGGG GGGCCTATGT CAAGTTTAAA TCCATTTTGC 360  
 35 CTTCTACTGC CGCAACGTGG TTTTGTGCAA AGCCAATTTT GCGTGGGGG CCAACTTCAC 420  
 CTCANTACCC AGNCTCTGGA GTCATCANCA TTCCCGCTIN TAGGCCCCAG TGANTAGAAG 480  
 TGGTCTAGGT CGTTTCAAGA GGAACATNAA TNT 513

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 504 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1003UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCTTTAGA CAATTATGAC ATCCAAGTTT GGTCGGTTCA GACTGGTCAG TTGCTTGACA 60



CACTCTCTGG TCACGAAGGC CCAGTCTCTT GCTTGTCCTT CAGCCGGGAA AATAGCATA 120  
 TAGCCTCTGC CTCTTGGGAC AAAACTATAA GAGTGTGGCC GATATTTGGG CGGCCCCAGC 180  
 5 AAGTCGAGCC TATAGAAGCA TACTCTGATG TGCTGGATAT TTCCATGAGA CCTGATGGTA 240  
 AGCAGGTOGC TGTCTCCACG CTGAATGGTC AGCTGTCATT CTTCGACGTT TGAAACCTCA 300  
 CGGCAGGTTC GCAACAATTG CTGCAAGAG GGACATCATA TCAGGACGCC ATTTAGAGGA 360  
 10 CCGGTTTACT CAAAGAACTT CGGCAACGGC CCAAATATTC ACAACAATCC ACTACAGTTC 420  
 GCGGCTTTC AATGNTGGAG NIGGGANAAA ATCTNTTGGT NTAGAATCCN ATAAGGGTAT 480  
 AANCGTCATG TTCCANAAAT NATC 504

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1004RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCTTAAAG AGGCTCAGTA TGCAGAGGCA GTTTCAGAA GAAGACAGGC TGGGCTTCGA 60  
 AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA 120  
 GCAAACGCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGGC 180  
 35 GTCGTCCACT GGTGCAGGCC AAAAGCGOGA CTACGACTAC TCGTGTTC AATGAGAGCAG 240  
 GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCGCAA CGCACAAACG 300  
 CGTATTCCAC CCGGACCGC CCCCACGAG ACAGCTACCC GCCCCGACTT TGCAGCCCGC 360  
 40 TCTGCTTGG ACAAGCTTCG GACGANGAGG GAGAGCCCCN CCCCCCTCNC AGAGNGGCN 420  
 TTINGACCC CCNIGGNTG TTCATCATCC CCCCANTCCT CCAGGAGAGT TTINGAAAGG 480  
 GCGCCCCNA NACNCCNTAG GATTGTTGGA GGATGGAGTN GGGCCCTTTT 530

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1004UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCACCGAG OCTAATGAGT GGTGCTAGGG TAGCGGTAT TACCGGTACT AATAGGTATG 60  
 5 TTAATATGCC ATCAGTGTCT GAGCTCACGA CTGACATATA TTAGCAATCT TGGCCTGAAT 120  
 ATCGCATACA GGTGATTGA GCAGTTTACT GATGACAGCA AGTTGGTAT CGTGGTAACA 180  
 TCGCGTACGC TGCCAAGAGT AAGGGAGGTG GTAGACCTAA TCAAAACATA CGCCGAGAAA 240  
 10 TGTGGYAAGT CTGGAGCAGT AGATTTOGAC TACCTGCTGG TGGATTTCAC CGACATGGTT 300  
 AGTGTGCTGG GCGGGGCATA CGAATTAGAA AAACGATATG ACGCTATACA TTAATTCTAC 360  
 GCTAACGCTG GCAGGGTGTG TATTCCCCGA ATTGATTGGT TGGGTGCACC NGGTGTTTAC 420  
 15 GGGATCCNCG GGTGTGTGAT ATCCNCGTTA GNCNCGGTGG ANNAATCAGG ATGGINGGTT 480  
 AGTTTCAAGC ANTC 494

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1005RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATCTCCCC AGGAACCGCG ACGGGTAAGC AGTCGTGCTT CTTCOCAGCG TGGTCGTAC 60  
 35 GAATTCCATC AGCATGTGGA ACTTCAGGC GAACATCTCC TCACGCAGGA TCCGGTCTT  
 CCTCTCTCTC TGCGGCCACC GAGAGCTCCG CCAGCTGCTG GCACCCGGTC AGGAAGCACT 180  
 CCGCGCGGTT CCCCTCGGC CCCACCTCC TGAAGCAGCC CACCAGGAGC CGCCACACCA 240  
 40 TATCATCCCC GAGCCCTTCG TTGAGGTGA AGTTGTCTGC OCTAATGCAC CGCACAAGCA 300  
 CCTTCGGGAT ATCCCAACCC AAATCTOCCA CGAGTGCAGG GTGCTCCCG AGCTGCTCCC 360  
 ACAGCGCCTC CAGGAAGCTC GCCAGCGGC CCGCGTTACC GCTGCAAGC GCCTGCTCCG 420  
 45 CGCACAATC GATCCCCGCT GCGAGCGAGA TCTGCTCCC GCCTGCTCCG CGAATAGCAC 480  
 GCCCAGACTC TCACCTTCCG TATTGCGTGG CGTTTCATAG AATCACTCT 529

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1005UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

	GATCTTGCAG TTAACGGTTC TTCCATCAAG GGACAAATGG GCGTACCGAA GCTCTTAGCC	60
10	CAGCCAAGTA TCCACAGCT GCACAATGCT AAGGGTGAGG TAATTGATGT TCAGTCCCAG	120
	CCCCCGCGG GCTGGCGGCA GGTGCTACTA NAGCATGGCC CAGAAGTATT TCGAAGAAG	180
	GTGCGTGAAT TCGATGGAAC ATTGCTTACA GACACTACAT GGAGAGATGC CCATCAATCA	240
15	TTGTTGGCAA CTAGGGTGGG TACTTATGAC CTAGCTGCTA TTGCACCTAC CACTGCACAT	300
	GCATTAGCAG GAGCCTTTGC ATTAGAGTGT TGGGGTGGCG CTACGTTTGA CGTTGCCATG	360
	CGGTTTTTGC ACGAAGACCC ATGGGAGCGC TTGAGGACAC TGGGAAATT GGTGCCAAAC	420
20	ATCCCATTC AGATGTTGCT TCGTGGTGCC AACGGTGTG CTTACTCCTC TCTGCCTGAT	480
	AATGCGAATG ACATTGCTCA AACAAGCAAA GGAGAATGGT GTC	523

(2) INFORMATION FOR SEQ ID NO:28:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 567 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1006RP

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

	NNNNNGNNN NNNNTGTGGG GCGTGGTAGA NTAGTGGGTC TCGTAGACAA TGGATGCCTG	60
40	TAAGCATGTG TAACGGGTAT CGTGGAGGGG TCCCTTCCCG CCTCCGAGC CTTCTTGGT	120
	TTCTCAATTT CCCATAGCAA TGGCGACTCG CACCAGTAAA TTCTCCTCTG GGTAGGCTCC	180
	GCTCATTAGT CGAACGGTTC TCCGTAGCCC ATCCTCGTCC AGTTGCGGCG CCGCGAAAAC	240
45	AAACAAACAC TGGCCGCGCG GATAACGTCA GTAGCTATGT TTCAGCAGAT TCCGCGGAAA	300
	CGGTCCAACA GATCGTCTGT AACCGGTGCA GATACGTCTG GGCAGCGGGT TTAACTGCA	360
	GCCAGTGAG ATTTAACGTG CGATGGAAGC CTGCGCGCGG TTCTGGCTGC CCGCGGTGG	420
50	CTCCAGCGGA GCGAGCGCGC GCGTCGCGAT GCGCGCGTA AGTCTGTGAT CGCGGGGAGC	480
	TGAGTAGGCG TAGCGAAGGT CACACGGAGC CCGATAGTA GATGGAGCAA GGGGCTCTT	540
	TGGACGGTTT GGTACGAAA TNCGGG	567

55

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1006UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCTCTGTT	CTTTTITTTAC	CTCTGAAGGT	GCCGAATGTG	TGCGCGTGAA	ACCACTCTTT	60
CGCGATGGGA	TGTTTCTCGA	TCTCCCTCGC	GAGCTGTTTC	ATGTACTACT	TCCTTGTAAG	120
GCAATCGCCA	CGCAGGACAG	ACCGAGCTGG	TGCCAACGGT	TTCTCCGGGG	TGCTTTTGCT	180
GAGATGCGTT	CGCATGTTTT	GACCCAGCT	CTGGAATATG	CGCGGGTGC	GATGCTGCGT	240
GTGCTACGAT	GCAACGTCAG	CGATCCCGCA	GGCGGGGGT	GCAGGGGTGT	ACTTCGATCG	300
TAGGCGCTG	TAAATGCTCC	TCTGGGAGC	CGCTCCCGCC	GATCTTACTG	TCCGCCATGA	360
ACGATGGGAC	AGAGTAGCOG	GGATGGTTCC	CTTTGCAGAT	AGGAAATCTG	GAAGAATTIG	420
GTCCCGCTCC	GCCTGATTIG	TTTATACAAA	AAATTGGCCA	TACATTCTTT	G	471

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 518 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1007RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCTTCTCG	CCGAAGTACT	GCACCATGTC	ATTCTCTCTC	GGTTCACCAT	GAACAAGGAC	60
ATCTAGGCCG	ACCTCTCTCT	GGAAGCGGAT	GACTTCTCTCA	ATCTGAGAAT	TGATGAAGTT	120
GGTGTACTCC	TCCGIGGAAA	TGCCCCCTT	TGCATGCTTG	TTTCTGTIGA	TCCGAATGTC	180
CTTAGTCTGT	GGGAAGGAAC	CGATGGTGGT	GGTGGGAAT	AGCGGGAGCT	TGAAAATTGG	240
CTGCTGCTCC	TTGAGACGCT	CCCCGAATGG	TGCGGCTCTC	GTGGATAGCT	TCTCGTTCAA	300
ACCAGCAACA	CGTTCTCTGA	CAGAAGGATC	GTTGGGTGAT	CGCAGAGGCG	GGACGGGCAG	360
CAATCGAGTC	TGCAFTTGGC	TCCAACCTCAG	AGGAAAAGTC	TTGCCAGAG	CGTCTTAGC	420
GAGGAAACAA	ACTCATGCAG	TTCTTGTTTG	AAAAGAGAAC	CAGCCTGGCT	TNTTGTCCAA	480
GGAGATCGTT	TOCAAGTAAC	TGNNNTGAA	NAAGGAGC			518

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1007UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCTTGTGCG AGCTGGCCAT GACAGATGAG AATCCGACAG CACGTTTCAC GGCATTTTAT 60  
 GCGCTGGGGC TAATTAGTAA AACGGAGGAA GCGTGTGAAC TATTGGACGA GTTGGGCTGG 120  
 GACTGTTGCA TCGATGTTG TCGCCAGCCA GTTGGTATTT GGGTACCAA TAACATCACC 180  
 ACCTTTCTCA GTTATCTCA AGAGAGCGTC GAGAAAACAA CCGTTTCGGA AGGTATOGAC 240  
 CAATTTGGAC CACCGAATTT CCGGAGGAGG GACTTCCCC CACTGGAGGG TATCACAAT 300  
 ACAAGTTGAT ACAATACTCT GAAAAGGTAG GAAAGGGATG TCCTGACAGA CAACCAAGAG 360  
 CTTAAATCCA TCCTCGACA CAGGGGTAGA CAAGTGANTG NAAGCGNGA TTGATCTTCC 420  
 CATGGAGNTC CAGGATGACC AGCTCCCCAA GATTTCCGTT CGTGGGAANC GGAATCATTT 480  
 NTACACAGNG GA 492

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1008I1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGAGTCATT TCCTGTAGTC CAGTGACATG ACAAAGTGT CTGCTTCGCC GTTGGCATA 60  
 GTTATTTGCG TTCCATACTC GGCAATCA GCGTCTCAA GCGCGACTG AGACAATCC 120  
 TGGCGCAACT TTGTCTGGC GCGAAGCATC TCCAGGGGAC CCCTGCATTG ATAACAGGAT 180  
 CCGGAGCGAG TCGGAATGG CCTTGAGGTT CCGCGAAGA GCCTTGATTT CCTTGTTACC 240  
 CCGCGCTGC AAGGAATCTA GGTGAGGAGC ACGCAGTGA AGCAACCACT TAAACCAACA 300  
 ACGGATCGCT GAGCTTTCTG TCCTAACGTC AGAGGCCACC CGCTGGCTCA CGATGACAAA 360

ACAGTTCATT GNANOCGNAT GGAAGNGAT NCATGTGCGN NANATTCTTT NNITCTTTCC 420  
 TOGGACCANG NGTNANAAC TACAGTCCCT GACGANTTCC TCACCTANGT CNGCGCAGGG 480  
 5 GATNMTTICA ACGCGGNCOC GTCTNNCCCC CTGNCNCTCG NNACCTTCT TTGTNNNGG 540  
 TTTTCTTTIN CCNNCNCOC TNNNCNCAC TINGGTTTT NNACNCCNTC NNAC 595

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 680 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1008I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TOGAGACCGC ATCAAATATC TGTCAATTATG TAAATGTGCA TATTATAGAC TTCTATTTC 60  
 AGTACCAGGC AATTGTGTCC GATAAATGAG GTGCAATGAG CACCGTCAT CACCGGACGC 120  
 25 GATAAATTTT TTTTGGGGG TCAACCATTA AATCTACGTG CATCTAACGC AAGGAGCAAT 180  
 TTAGCTAACA ACTCTTCTTA TCTTAAGAAT CGGTATACC TCCTCTTCGC ACATCTTCGC 240  
 CTTCCTTAGT CTCGAGTCTT AACTACGTC AACAAATGCA GCTCCGATA AGATGTACAT 300  
 30 GTCGTATAAC AACATACACA AACTGTGTCA GCAGGTAGCT GGCCAAATTA TGGAGCGTGG 360  
 TGACAGACCG GACGTGATTA TGGCATTAC CGGCGGCGC ATGATTCTTG CAAGAATCAT 420  
 CCGGTGCTTC CTCAAGGTCA AGGGCCAGAA AACATCCCC ATCCAGGCGA TTGGGTCTTT 480  
 35 CTTTGGTACG AGGACTTGGG TTTGGAAGAC GGGACGAAA GCATCGGCAA GGAAGTTATC 540  
 CGGATCAAGT GGCTAGACTT TGGGGGCTT GGGCAAACAC TTTGGACTCA ACTGATTGGA 500  
 AGAAGGTGTT GGATTGGCGC CGAGTTGGNC GANACCNGA CACGTCCCTA CGTTGTINAC 660  
 40 CGANTTGGCG AGGGGNCAN 680

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 509 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1008RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

# EP 0 866 129 A2

GATCTGTCTT GGACGATATC AAGTCTATG CCATCTTCCA AACGTCCTT TCCACATTGC 60  
AACAAAATGA CTCTACAAAA TACCAGTTAG TCCTAGAAAA TATGTCACAG GACGAACAGA 120  
5 TGCACTAGC ACATATTACA TCGTTATGAG CACCATAAAT CTCATAGTCT TCCTACTTTA 180  
TCTTTAATAT TAATAGTATG TGTATGCCAA TCGGCGCGTT ATGCCCGGGT AACAGTAGTT 240  
TCTTTTCTIN GAACATCTGA AAAATTTCAC CCGATGAGCT CTCTGTGTC AATGGGCGAT 300  
10 CGAGCTACAA GTGCAGGTGT ACCATTCCACA TCCTATOGG NATTOGGCTG TTGNTAGAGC 360  
TGTTAAAATG ATTGCTTCAG AAGATACGAG GTCTTGGGA GTTTTGGGC CGATGAACGN 420  
GGTGCATTC CAAGCCAATG CGTGGAAAGG ACTCATTGAA TTTTCANNGA CCNGNAGAAT 480  
15 TAANGGNAAA GTCANNGTA ACCNATTGT 509

## (2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 500 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1008UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCAAGCGG GAATTTGGC GCAAATGCAC GTTAATGCTC ATATTGTAA CAAGCTGGG 60  
GCAGAAGTCC GCGTTTGGG GCTAGAAATT TCCACATTGA AAGGTTCAA TAACACATTA 120  
35 GAGGAAGAGA AAGCTGTGC AGAAGATGAT ATTTTGAAGC TGCTAGAGGA AAATCACACT 180  
GTGCATCATT TGAAGACTAC CAACGAAGCG TTGACTACCA AGGTAGCGA CTATAGCAAT 240  
AGACAAGATA CGATTCTCCA GCTGTTGGG GAAAAGACGG AACGTGTAGA GGAAC TTGGA 300  
40 AAATGACGTC GAGGACCTCA AGCAGATGCT GCGGATGCAA GCACAGCAAC TTGGCCGACA 360  
TGCAAGAGAG GTTAAGAAAT TAGATTCCCA TATCTTATTA ACATTATINA TNCANCGGC 420  
TTGGGTTNGT TAATCAACTT CNCCAGATGC NTAGATTGG GTAGTTAGNC ANTTTTTGA 480  
45 NTGGNTCAA ATGGNGGCC 500

## (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 506 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1009RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

5 GATCTTCGCT TGGGGCCGTG CGTTCACGGT CTTAGAAAGC AAGCGTGCAA GCGATGTCTT 60  
 GCGTACCCCT GGGGGGGGCC ATAGTATCAT CGAAGGTATT GTTCCCTGGC TCACATATTT 120  
 10 GTATAGTGCC CGCTTTTCTT GGGAGAGAAT ATGCTGTGTC CCCACGTACT CCGGCAGCTC 180  
 GCGGGGACGA AGTTTCTCAC TTAAGGGCAA ATGTGCCATT TTCTGCAGCT CACGCTGATC 240  
 TGAGTTCACC GCGCTGTG GACGTGCCCC CTTCGGTGG GGAGAGTCGT CCATCTCTAT 300  
 15 CACCTCACTA TCCTCCATAT TAACGTCCGA GATCAGAC ACCTATCTT CATCTCCAG 360  
 CTTATGCTTG CGCCCCAGCA TCTCAGATAC GGACGTGGTC CTCGCTCCTT TCGGCTCCTC 420  
 CTGCAGGGAT GCATCTAGAT GGTATGGATG TGATGAATGG AAAGCGTGCA ATCTGGNAAT 480  
 20 GGTAAGTCTC CCCCCGTAT CATTIN 506

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1009UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

35 GATCATGCTA GTTCTGCAGC TGAGTTTITA AAAACGCACT ACTGGAGATG TTTCGCTTTA 60  
 TGGTATCGCT CCACTAGCGC ACGGACTGAC TTGGTTAAAC GGCTTAGCAC TGATGCGGT 120  
 ATTTGGAACG CCGCTCTAA GAAGCTTGAG TTGCACCAT CAATGAAGGG AGCGCAAGTC 180  
 40 GAAATTTCCC AGCCTAGAGG CATGTCAGTA GGTCAAATA CGTCTGTTC TGGATCGCTC 240  
 TGCATCATGA TATCGACATA GTAGTCGCAC ATATCGATGG AGACGACCTT GCGGGGTCA 300  
 AATTGTATA APTGGTTCAA TCCTCAGGC ACTTGGGTGA TAACTCAAG TAGGGCATT 360  
 45 TCTTCAGGGA AATGCCCCG TAGGAGGGCA TCGAAGNCAG AGTTNGACGA ACCNCAGGCG 420  
 GGGGANTCT TTGAAGGGAG AAAGAGGCGG GGAANTGGTA CCACTCCGCT CCCCNCANA 480  
 AGTTGGCCCC AGCCTCAATN 500

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1010I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

10  TOGAGGCGCT TACGTGGGTC CACCTGAAGA TGCGGCAGAC GCGGCACGGG GAGCTGGTGC      60
    GGGCGAAGCC CACCGTGTTC CCGCTGCTGC TGGCGAAGTT TCTCAGAAAC GATCTGTGCG      120
    TGACCGGGGC TGGATGGAG GGCAGGAAG CGAAGTGCAG CGACGTGCAC GTGCTAGTAC      180
15  CGAAAACACA CGCGCGCTG GCGTCTCTCC TGCTTGCACA TAGTCCCGTG GCGCGGGGTG      240
    GCGATCTTGG CATCACCCCTT GCGACATTT TATCGTGTTC CCTGCAGGAT GCACTAGACG      300
    CCGGCCAGTT AACGACAGCT GAACCCAAAG GAAAGTTAGA GGGTGACCTA GTAAGCGCTC      360
20  TGGTACATAC AAAACAGCTA GAGCGCCCGG TGGAGTCTTC TACGACTGAA TTAATACGGA      420
    GGTACCGACT TGGGACAAA GAGGCGTCTA TGGATGCCCTT GCGCTGTGCG TGGAGATTTT      480
    CTGACAGATT TAAAGATGAC GATGAGGTAG AATGACATTT CTGTGCAGGG TCTCAAGTGG      540
25  GATGAGAGGT CGGCATTTTC GAAGGAGNNT GGTTTATNAN NANATCTTGG ATTTTCTGAG      600
    GGGGCTNAGN TNCAAGAAAG TCANATN      627

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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 628 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1010I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

40  TOGAGGTGGC GGGCGGGAAA CCGCTGCGCA ATCCTGGCCT CCAGCGCCCG GCTGACTGCG      60
    GGTACCGTCA AGCACTTGAA GTGGCTCCGC TCAAGATAAT CCACCGCCTC GTTGGCCCGC      120
    AGCCCGCGAC TCCCGTGCAC ATCCCGCGGG ATCAGCTTGA ACTCCCCCGC GCTCAGCCAG      180
    AGTGGGTGTG TCCCCACCGG GTAGTGTGAC TCCTCTGGCA GCGCCTCGCT GCTCATCATC      240
50  AGCAGAAAGT CGCCCTCTGT GTGCACATC TTGATGAAAA CCTCCGCGCC CTGAGCCCCG      300
    GAGAATGCT GCAGACCCC TGCCACCAGC GCTCCTCCT CCTCGGGTTG TCCGCGACTT      360
    CCACTCCGCC AAGCACCATC GCTTGCCTC CCGCGCCCG CACCGCCCGC AGGTGCACCC      420
55  GCTGTACCCC TGNACGGGT AGTGGTCATT CCACGGCCGG AACACTCCTC AAGCTGAGCA      480

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TGTCTTGGG ATCTTTGTTT GGACGTCATC AAAATTGTG ATTGAAAAA CGATACAATA 540  
 NAGNGGCTCN GGGTINGAAA GTCACACCNA TCACTCTGGT TCAAAGCATG TCTCAATNIG 600  
 CGGGGCATAA CCAATTGCNC GGTANGCA 628

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1010RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GATCCGGCTC GCAAAGGAGA AGATAGAAGA GCAGAAAGAA TACCCGGTGC AGGAGTTTGA 60  
 CAAAAAGCTG TATCATAGCA ACCCGCAAG GTACTGGGAT ATATTCTATA AAAATAACAA 120  
 AGAAACTTC TTCAAAGACA GGAAGTGGTT GCAGATTGAG TTCCCTCTC TATACGAAGC 180  
 TACCAAGAAA GATGCTGGTT CAGTGACTAT CTTCGAGATT GGGTGTGGTG CGGGCAATAC 240  
 CATGTTCCCG ATCTTATCTG CAAACGAAA CGAACACTTA CGCGTTGTGG GTGCGGACTT 300  
 CTCCCGAAG GCGTGGGAA TTGTTAAAGA CGTCGCAAAA CTTTAACCCC TCGAATGCCC 360  
 ACGGACGGT ATGGGACTTT AGCCAACCCCT GATGGTCTTT TGGCGATGG TGTGAGCGG 420  
 CATTCGGTCG ANATCGNAGN AATGATTTIN GTTTTAGTGC CTNGNGCCC ACAGGGGGCC 480  
 AGGNTNIGGT TATTGGANAA AGTCTTNANC AGNGGGT 517

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1010UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCAGGACA GTAGCAGCTT GACTGAGTAT CAGCAGGAAA AGCCTAGCTA ATTGGCGCGA 60  
 GTACAATTAC AAGTAACCTGT CTGACTACTT CTTTGGGTGG GATGCCATAT TTTTATAGGAT 120  
 GGCCTGCAAC GGGCCGGTGG GGGGOCATC CAAATTTATG GAGTTGAAGA GCTGTTCAAT 180

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GCCCTTTATC CCATCTGCAC CGTCTTTATC GCGAACATG GCATGCAACT CTTCAGCAT 240  
 GATATCTTCT TCTCGTGCT CTGATCCGGC GTTGGTGTG GTTGGGCAG TCTTGTTAGG 300  
 5 CGCCATTTCT GTAATGTTGA AGCTGGTCTT TGGTCATCTT CAGACCCCTC CGTCAGGAAA 360  
 TATCAAAGAA ATCGGCTTCA CTAATATCTA CGCCTCACTC TCGAAAAATG TCGAGGCTC 420  
 TTCATCCCCA GCTGAAGGAC CCGTACCAGA AAAATGTCAA TGGTACTCAA CGCAACTTTA 480  
 10 ATNTTNCAG AN 492

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1011I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCTGCGCG GCGGATGTTT AGCAGOGACG CGTATCTAAA CAATTTCGAA GTTGTCCAAG 60  
 GCGTGACCGT TCCAATAGAC CGCTCTAGCT ATTCCAGTA TGACAAATGG TTAAATGCG 120  
 30 TAGATGCAGC TGCAGAACGT ACAACTGCCT GGTTAGAGCT GTGGGATGCT TCGGCCCTGC 180  
 AAAACTTCTA CGCTCAGGAG GCCAGGATGA TCTGCAAAAA AATCATCCAG ACCAATGGCC 240  
 CCACATCTTT AATCACTGA GTGTAATGTC CATACTCCA GTACTCACCA GTCTTTTGGT 300  
 35 TTTCTGGATG TCAGATACCA GACTATGTAC TGAATAGCGA CAACATTAGA TATCTAAAAA 360  
 GTCTGTGGT TTACAATCTT AAGGTCCGCT GAAAGAAGAG AAACAATCTT CGAAAACAAT 420  
 ACTAAGGCGA ATATATCAAC GTAATATGAC CGCTCAGGCT TGGATAACA TTCCGATATC 480  
 40 AGAGGGAGAA GACTCCGCG NGTCTTGNC NNTCNGCGN AAATTGCNCA GTNTTNATCC 540  
 CGGNAGCCNC CCACNGGTTT TCANACCCCT TTTINGNGT TCNCGNCAAT NAAGGGNGNC 600  
 45 CTCTGCANT TACCCANNA 620

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1011I2

# EP 0 866 129 A2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

	GATCTCTTGC ACCAGTCCAA ATCAGCGGGG TCGTCCACCT TTCTCCATA TATGATTTTG	60
5	CCGATGGTGT CGCTGACAAG CTTCAGGGC ACCAAATCGG GGTGACATG CTCTTGCCG	120
	TTACTGCTCT GTTCAAATAT GTGGTCCAAA AACTTGCTAC CTGGGTGGAA GTCACCATCG	180
	TGGAAGTCGT ACTTCTTGGT GAATCCAATA GCGCGAGAC GGCACCTGGC CATGATAATA	240
10	GAGTGGAACC ACACGAGGAT GAACTTGCTA TGAAGTTTTT CTACTGGTTT GACATTCTTC	300
	AGTTCTCTG ACTGAGTCGG CCACAGCTCG CAGACTGTGT TTAGAACGCC GGGCTCACCC	360
	TCGTACGCTA TCTTATAGTT CTGCTGAGCA AAGGAACCAC TAGAGGCTTG CTTTGGGATC	420

## (2) INFORMATION FOR SEQ ID NO:44:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1011RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

30	GATCCAAAGC AAGCCTCTAG TGGTTCTTTT GCTCAGCAGA AGCTATAAGA TAGCGTACGA	60
	GGGTGAGCCC GCGTTCTTAA ACACAGTCTG CGAGCTGTGG CGGACTCAGT CAGAGGAACT	120
	GAAGAATGTC AAACAGTAG AAAAAGTTCA TAGCAAGTTC ATCTCTGTGT GGTTCACCTC	180
35	TATTATCATG GCCAGGTGCC GTCTCGCGCC TATTGGATTG ACCAAGAAGT ACGACTTCCA	240
	CGATGGTGC TTCCACGCG GTAGCAAGTT TTTGGACCAC ATATTTGAAC AGAGCAGTAA	300
40	CGGCAAGGAG CATGTGACC CGATTTTGGT GCGCTGGAAA GCTTGTGAGC GACACCATCG	360
	GCAAAATCAT ATATGGGAGG AAAGGTGGAC GACCCGCTG ATTTGGACTG GTGCAAGANA	420
	TCTGCGCGGC GGATGTTTCA CAGCGACGCG TATCTAAACA ATTGGAAGTT GTCCAAGGCG	480
45	TGACCGTTCC ATAAACCGCT CTANCTATTC CCAGTATGAC AAATGGGTTA AATCNCTAAA	540
	NGCANCTGCA GAACGTACAA CTGCGCTGNT TANANCTGTC GGATGCTCGG CCTGCAAACT	600
	TCTACNNCNC GAGGCCAGNA NGATNGGCAA AAAAATCTNC AGANCNANGG CCGCTCCTT	660
50	TAATCCCTNG ANIVINATNT CCAACCNCCN TTNCCCATC TTTTGNVTTT TGTINTTAAA	720
	AACCAAATIN TC	732

## (2) INFORMATION FOR SEQ ID NO:45:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: 1011UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCTTCACA CGCACTATTT GTCCAAGGGG CTTCAATGTT CATTCGATTA CACGAAGAAA	60
CAATACTTAC ATGAGAATGG AACATAATA AACTAAGCGT ATGGTGCCTA ATGATTGTTC	120
AGATGGGCGT TGCTGTTTCT GAACAGTAAA TGCTTGGCAA ACTCATAAGA TGTCACCGAT	180
ATAGCAGTTG CAGGCATGTT GCTGATAATT CTGGGTTTTA GGGCCGAAA GAAACCGGAC	240
CAACCATATG TTTTGTGGAT TGCAGATGCA GCGTTGGGA ATGTGTCAGC CTCCTTGAAC	300
AGCTGACTTT GAACAGAATC TGCACCGCGA ATCTGCAATA CTGTCTTCAC GCAGTCTAGC	360
GGTGTGGGTT ATGGGCGCAC ATGTTGGCGC CCGGATATCC CACCGCACAG ACAATGTATC	420
CAGGGGTTTG TAGCTGGTTA CTCGGATTGA TTATTTTGGT GGATGATTCA ATAAATTACA	480
AAAATTCAAC GCTGCGACGG ATTGTTCATA GCAATAGTTG TCCGGTTATG ATTAGAAAAA	540
CGCTTGAAAT GGGCTCGTG GGTCAATCCG CACGGGGCAT CCGCAATGG ANCANITGGG	600
TGAANTGAAC TCTTTGGTGG GNGNNANOGG TCCNNAGGA C	641

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1012RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCCTAACC CAACTGCACA AAATTGTCAG TCATATGTTG GGAGGCAGTT TACCCCTTCOG	60
CCGCAAAATA CATACTTCTC CTTAGGAAAC GCTCCTCGCT CAGGACTGCA ACTGCATTGA	120
CGAGCAGCAG AATAACGTAG AATAGCTTTC CCAGGCCAAA TATCATCOCT CCACGTACAG	180
TCTATCAGCA GTGTACTCGG CTGTGCGAGA AGTGGCATTC ACAAGATAAG CAGAAGTAGT	240
TCTAAAAATC AGTGGTCACC AACGCGAGGC TGCAAAATCG TGTGTTCAT TCCCATCTCA	300
AAGCATCGCC TGAAAACAAA GGCTCAGAT TGCAGGTGCC CCGCGTGAT AACAGATGAT	360
AAATTATATT TTAAGTTATA TTAACACACA TATACAAAAA GATTTGGTAG TGGATTAATG	420

ATGATTGCT TAATCAGGT TACGTCCTGC GGCCTTCTTA GCCAATCTCT TACCGGTACC 480  
 AAAGACCTTC TTACCTCTGT TCTTCTTTTG CTTTCTCTGT TGCTGGAAG CCTTCTCAGC 540  
 CTTCTCAGCC ATGCCGTATC TGACCAATCT GTANGTTGGC TCGAACTTCT TGGCGTCNGC 600  
 AACAGAGTTG TAGATCAAAC CGAAACCGGT GGAATTGACA CCACCAAACT GGG 653

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 650 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1012UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATCTTCTC GAGCGACCA CGCGCCCCA CACAGACTCC GAGAACCTGC TCTTCTGGA 60  
 GGGCACCAA ACATGCTTCC AGATGTTTAC GCAGCAGGTG GAGGTGCGG CAGGCTCGGG 120  
 CCAGGCGAAG ATCCTGGTGG GGTGCTGGA GGCCTTCTGC AAGCTCTGT TCGAGGCGCA 180  
 AAGCCACTGG ATGCAGGCCA TTTCGTCCGA GGTCAGAAG TGCTTCCAGT ACAACCACAA 240  
 GTATGAGAAA GACCCCGACA ACATCGCGCA GGAGGAGGAG TGCGCGGGCG GCTGTGCGA 300  
 GTACCTCGTC GCGGTGCGCA ACGACCAGAT GAAGGCGGCA GACTAGCGCG TCGCCATCTC 360  
 GCAGAAGTAC GGCTCCATGG TCTCCAAGGT GCACGAGCGC ACCATCAAGA ACCGCATCGA 420  
 GGAAGACCCCT CGACGGCTTC GCAGAGGTGG CCAAGTGAG CAACAGGGC CTCGTGCGCC 480  
 TGATCTTGA CGACCTGCGC CGCCCTACG CCGAGATCTT CAGCAAGGCC TGGTACTCGG 540  
 GCAACCAGGC GCAGCAGATC GCAGACACCC TCTACGAGTA CCTCGCGGAC ATCCGCAGCC 600  
 AGATGAACCC TTCGTCTACT CCACCTCGT CGAGTCCGTC ATCGAAGAGA 650

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 727 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1013I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TOGACGCGGA CAGCGTACTT CAATCTGTAG ACAGAAGAAA CCTTGCCCTC TTGGCCCTTC 60  
 TTGGAGCCAC GCACAACCAT AATCTCGTCG TCCTTTCTGA TTGGTAGAGA CTTGATGTTG 120  
 TACTGCTCTC TCAACTCCTT GGATAGAGGA GCAGACATGA TCACGCGGCG CTCGGAAGAT 180  
 GGCGGCTTGA AGTACGCTT TCTGGCCTTT CTCTGTGG AGGAAACGTC TGCAGACATG 240  
 TTAGTACTGT GCGGGGCCAC CAACTTGTTC CAGCACTGG ATTATGCTAG GTCCGCTGTC 300  
 GCGCTGGGCC GTATGCCAG GTTACCACGG ATGCAGCGC CAGAGACGCT CATTOCCAAT 360  
 GTTTOGGGAG CCACCATGTT TCTGTCACAT ACCTAGAGAT TGCTTAGCCA TTGCTGATTC 420  
 GCGTGTGCT GTGTAAGAAC CTCTGTTTCA NNATGTGNAN AATCTCAATN GTGNAACTT 480  
 TTTCANNITG TCCGNTCTAC GCTGNACCCN CTNNCNNTG TNAANCNCN NNNNNNNCN 540  
 CAANCGTTTC GCTANNVNNN TCCTANANAC NNANANNNT CNNNNNNAAN NCCNNNNN 600  
 CACNNNTTC NACCNCCNN CAANNNNNN NNNNNNNN NANCCNNNN NATNNTCAT 660  
 NCCCTTNC NNNACTNNN ANCCNNNNC TNNNNNAN NTNNNNNC ATNNNAACNA 720  
 NAACNCC 727

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1013I2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TOGACAAGGT GACCAAGGAG AAGTCCAAAG GTGCTCGT GCCATTGGAC GTCCACCCAT 60  
 CCAAGGTTGT CATCACCAAG TTGCACTTGG ACAAGGACAG AAAGGCCTTG ATCGAGAGAA 120  
 AGGGTGCAA GTTGAGTAA ATGCATTCCA CAGGTCAGCC AGCATATTAT AAGTAATTAT 180  
 GTTCTACCAA CTCTCTCGA TATATAGTAA GTTCAGAAAG TCGTGTTC TAAGTGTTTA 240  
 TCAGTGGGCA TAATGACTGC TCTGGTCTC CGCTCGTGG CAGCCATTCT TGGGGGACAG 300  
 CCACTACTCC CGGGACAG TGAACAGGCG CGAAATTCG TTCTCGGGC CGACCCNT 360  
 TGGACTCTTA TTGATTTCT TCCGCCCTAA GAAAGTAGAC AGCGCTACA TATATGACAC 420  
 ATCCCTGTCT GGGTGTTTAA GGAGCACGCG TCTGAAGAGC AGGGAAAACA CGGAGTCACT 480  
 AGGCTCTGCT ACGGCTCGAG GTTTTGAAG TGAGTTTGN ATTATTGTC CNNTGAGAAN 540  
 TGANAGGGGT GGAGGCGTC ACCCGATCAA CAGACNANCA GGCAATGGTN TGAGTGNAA 600  
 CACAGCNCGG CGAGAAGTG GCAANCNTCN ANGNA 635

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1013RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ANAATGGCTG GTAGTATTG TTAACCACTA GTTCTCTCCC GAAGTTGAAG TACTTCACAT 60  
 AACTCAGCCC CTCCGAGGGA CTCATCTCCT GTACAGAGG CCTATTCAAC TCAATGCGCT 120  
 GCTTGTAGTC CTCCAATGCA TCCTGCCTAT TCCAACCCCT GTNGTCTGCA GAGGCTGCTG 180  
 CCATCTCCAC TGTGCGCGCC CTCAGAATTG ACTCGCTCAC GACAGACTCA ACGAAGAATA 240  
 CTTTACATT AAGAGCAGCA AACTCTCTGG CGAGCATTCT GCGCTCTCG CGCATGATGT 300  
 TCATCCCATC ATAGACAGNA AGCTGTCCCT GCTCGAAGAA CTTCTTCATG TCCGCTTGA 360  
 TCTGGCTAT CAGCGTGGC CGCAGTCTGA TCCCTTCGG CGTAACTGGT CTGGTAGAGA 420  
 AGTAGTCCAG CGGTAGNTTC ACCATCCCTT GCGGGACCCG NGNCCNCGA TACTGGACA 480  
 CANTGAAGGA TTGTGTGNGC ACCCCNAGCC ACCCCCGTAT TGGTGTATT GNCACCGNAA 540  
 CAANNNTTTT GGGTGTCTGT TGNAGGCAC CCAGGACGNA CAAAATTTT TCCGCTTTG 600  
 GAAANCCCC CAGNTCCAN NNGNAAAT GGNCCCCGGG AATTTTNG CCGTNGCNC 660  
 CNGCNGCNG 669

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1013UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATCGCTTAC CAGCCAGTA GTGCGCACA GGAACITGAG GTTGGCTATC CGGCTGACAC 60  
 GAAGTATATC GACCTTTTG CAGAAGTGA CATATGTAA CCGGATTTGC CGCATTTGAA 120  
 AAAGCTCGGA GTCAATACCA TTGTGTTTA CTCAATTGAT CCAACCAAGC CACATGACGT 180  
 TTGCATGGAG GAGTTGAGCA AGCTGGGAAT CTACGTTCTC ATCGATTTAT CAGAACGAGA 240



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CACCTCTATA ATTAGGGAAA CACCAACATG GGATGTAAAA GTATTCCAGC GGTACAAAGA 300  
 CGTAGTAGAC TCCATGCAGA AATACAATAA TGTTCCTGGC TTTTCTGCTG GTAACGAGGT 360  
 5 CACTAATGAC CGCACGAACA CAGACGCATC GTCTTTTGTG ACGCGGGCTA TCAGAGATGT 420  
 CAAAACTAC ATCAAGCAAA TGGGATACAG AACTCTTCCG GTTGGTTACT CACCATCGAT 480  
 GACCAGGAGA CGAGGGATCA CTGGCCTGAT ACTCCCTTTC GGTNGCGTAT CTNCAGANNC 540  
 10 TTTTGGCATA ANTTGTCTCG ATTGGGCGCG CATCCACCTN CNGACGANCG TTCAAGAGAG 600  
 NGGCTTNCNA TTNNGAACT CCCCTTGGCG CC 632

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 602 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1014RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAAACTG CCGTCTTGGC GCAGCACGGG GCGCGCGAG TTGGATACGC GGTCCCGGTC 60  
 30 AAAGGCCACG CCGAGCGCGC CAAACTCCGG GAGGGGCTGG CCGCGGTAGC CCAGTGAOGT 120  
 GATAAGCACG TCCAATTGCT AATCCAATTG CTGCTCCAGG TGAAGTACAA CCTTGTMTTC 180  
 AGGGGTCAGG GAGTTTGTGC AGACGGTCAG CGCAGATATC GCGCGGGCGC CGTCCCTGGC 240  
 35 GATGTAGAGC GCGTCTTGA GATAGTCGGA CACCCAGGCC TTGGAGTAGC CTTCCGCGCG 300  
 AGGAGGGTAT TTAATCGCGG ACTTGCTGCC GCGGGCGGGG TACGGCAGCA GGTACTGCTG 360  
 GCACATGTCA ATGCGCGGTT TGTGCGCGG GTGAGCGGC AGCGCGGCC ACGCCCTGGG 420  
 40 CGTGAAGTGC TCGGGCGCGA TGTGGCGCG CACGCCGAG CGCTCGAGCT CCCACATCTC 480  
 GCGCAACTCC TTGNTGTGA ACTTGCTGCC GAGGAAGTCC CGGCGCCGA TGAGACGCAC 540  
 CTCTCGAGC GCGCGCGCC GCAACGCCCTG CAGCGCGTGC GGGTTTGATG TCGGTCTGGC 600  
 45 CC 602

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 627 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1014UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

5 GATCAGTGTG CGGGGCGAGC CGGAGAGCAT ACTGCTGTCA TGCTATAACC AGGAGCTGCT 60  
 CTCGGGGGTC AATTGAGGAGT CCAAGGTTT TGCAGACAGG GACAGCACCA AGCACATCAC 120  
 10 AGCCGAGCAC CTAGATGAGG CGGTGGAGGC GTTGCTGGGA GATGTAGACC GAGGCGGGGA 180  
 CGGGGCATGG CCTTGATGTA AGTCTATGTA CAGGATATTA GCTTTCAAAA TGCATGGTTG 240  
 GGGTACTTCA GCGTTTCCAC CATGGAAAGG GCGCTGGCGG CGTCGTTTTT GTTGAGCAAG 300  
 15 AAGAGGCOCT GGAGCTGGCG GGTCGACACT GGGAGCOCTA GCGCGACGGC CTTGGCGACA 360  
 AACTCCGGCG AGAGCGCCGA GTGTCGGGG TAGAAGCGCA GGAACATCTG CTCGATCTGG 420  
 TCGGGGTTG CGTTCCCCAC AAGGAOCTTG TAGTCGATGC GGGCGGGGG CAGCAOGGCG 480  
 20 GGGTCGAGGA OCTCGGGATG GTTGGTGGTC ATAAAGGTGA TCATCTTCTC ACTGGAGGCG 540  
 ACGCGTCCA GGGCGTGGAG CAGCGCGCTG AAGTGACGC CGTTGGTGTA ACGTCGTG 600  
 TTCTTCTTGC GCTTGACAAA GCGCGT 627

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1015RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

40 GATCCAATTC CAAACGTAAT AACCATGGAG ACTGATGCTT CAAAGACGCC TGGTCTCTT 60  
 CATCCATCAA AGAAAAGTGC AATTGTATTA TTTCCTCATC CTCCTCAATC ACAGTAGAGC 120  
 TAGGATCCCC CGGGCTGCAG GAATTGATA TCAAGCTTAT CGATACCGTC GACCTGAGG 180  
 GGGGGCCCGG TACCCAATTC GCOCTATAGT GAGTGTATT ACGGCGGCTC ACTGGCGGTC 240  
 45 GTTTTACAAC GTGCTGACTG GGAAAACCTT GCGGTACCC AACTTAATCG CCTTGCAGCA 300  
 CATCCCCCTT TCGCCAGCTG GGTAAATAGC GAAGAGGCC GCACCGATCG CCTTCCCAA 360  
 CAGTTGCGCA GCTGAATGG CGAATGGACG CGCCCTGTAG CGGCGCATTA AGCGGGGGG 420  
 50 GTGTGGTGGT TAGCGGCAG GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCGCTCTCTT 480  
 TCGCTTCTT CCTTCTCTT CTGCCACGT TCGCCGCTT TCCCGTCAA GCTCTAAATC 540  
 GGGGCTCCC TTAGGGTTC CGATTTAGTG CTTTACGCA CCTCGACCC AAAAACTTG 600

ATTAGGGTGA TGGTTCACGT AGTGGGCCAT CGCCTGATAG ACGGTTTTTC GCCTTGACGT 660  
 TGAGTCACGT TCTTTAATAG TGGACTCTTG TCCAAC TG 698

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1015UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATCCTAGCT CTA CTGTGAT TGAAGAGGAT GAGGAAATTA TACAATTGCA CTTTTCTTTG 60  
 ATGGATGAAG AGACCGAGGC GTCTTTGAAG CATCAGTCTC CATGGTTATT ACGTTTGGAA 120  
 TTGGATCCAC TAGTTCTAGA GGGGCCGCA CCGCGGTGGA GCTCCAGCTT TGTTCCTT 180  
 TAGTGAGGAT TAATTGCGCG CTGGGCTTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT 240  
 TGTATCCGC TCACAATTCC ACACAACATA CGAGCCGGAA GCATAAAGTG TAAAGCCTGG 300  
 GGTGCCTAAT GAGTGAGCTA ACTCACATTA ATTGCGTTGC GCTCACTGCC CGCTTTCCAG 360  
 TCGGGAAC TGTGTGCA GCTGCATTAA TGAATCGGC AACGCGCGG GAGAGGCGGT 420  
 TTGCGTATTG GCGCTCTTC CGCTTCTCG CTCACTGACT CGCTGCGCTC GGTGTTCCG 480  
 CTGCGGCGAG CGGTATCAGC TCACTCAAAG GCGTAATAC GGTATCCAC AGAATCAGG 540  
 GATAACGAG GAAAGAACAT GTGAGCAAAA GGCCAGCAA AGGCCAGGAA CGTAAAAAG 600  
 GCGCGTTGC TGGGTTTTT CCATAGGCTC CGCCCCCTGA CGGCATCAC AAAAATCGAC 660  
 GCTCAAGTCA GAGGTGGCA AACCCGACAG GACTATAAAG ATCCAGCGTT TCCCT 716

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1016RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GATGTGAATC GATGTGTGGA GAAGAGTGTG ACTAGACACA AGCTGGCGAT GCAGCGAGAT 60  
 CTAACAGGAA AGGTGCTGGT TGGGAGAGAA AGGTACTAAG AAGAGGTAGT CACTAGTGTG 120

ACCTACAAGC CTACACACCA CCAACTGCGT TACGAAAATC TAAATACGTA CCTCTATCCT 180  
 ACAAACTACG AGGTGCGCGA ATTCCAATTC AATTTTGTCC ATCGTGCGTT ATTGAAAAT 240  
 5 GTGCTCTGTG OGATTCCAC AGGTATTGGT AAGACCTCA TTGCCAGTAC GGGGATGCTC 300  
 AATTACTATT GGTGGACAGG GGSCACAAAA ATTATTTTTC CTGGTCCAC ACGACCACTT 360  
 GTTGGGCAGG AAATTAAAGC ATTCTGGG ATTACTGGT TTCCCNNTTA TGATACGGGA 420  
 10 ATNCTTCTTT GACAAGAGCC NNNNGCACAG GGNACAGATT TGGGNC AAAA GAAAACGTTT 480  
 TTTTTCGN NAACGCCCC CANIGGGGG GNAANTTTC CCNNGAGAG GGGGGACTTN 540  
 NNTCCCNNA GANNINGGN TTTCTINGG NNTNNGNGA NGGNTCCACC CCNGCNGG 600  
 15 GGGGCCACN NCCCCNCNN NNGGNTTTT NNGNNNTTN TTTTACAAA ANTTNC 656

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1016UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATCCATCGA ACGTCCATTT TATACGAGA CATTTTTATA CAATTTTTAT TTAATAATGA 60  
 GGATTTGGCA TTCCCTCAA CTGCTGACT AGAAGTTAGC TGGTGCTAGT AGTGTAGCTG 120  
 35 GGCTAATGTC GACTGAATTG CGGTGCGG TGCTGGAGGA TTATTTGTG TCCGCAGCTA 180  
 ATGCCTTCCT GCCAGATGAA TTCCAGTGA AAGAATTGCA AGATGAATAC TATCGAOCCT 240  
 GGGAAACGAT TGTGAGTAAT CTACCCGCGC TATTGTTGGC GGCACAGCTG CCGGATGTGG 300  
 40 TGGACCAGCT GAAGGTGCTG GAGGTGAAGA AGGAGCTGTT CGACGATATT TCGGCAGGTT 360  
 CGGCGCGCAT ATTGCGGTT GGCCTCAAC GTCAATGCGT ATGTGTGAG CTACGACGAC 420  
 GCGTTCGACA CGATT 435

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1017I1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

5 GATCTTCAAA TGGGACAAAT GCAAGGCTAT TGATCTTATT OCCAGCAAAC AAGTGCGACA 60  
 TGTATGGTGT ATTTTGTGTG GGCAACCGAC TGCTGGTGAA AACGGGCTTA AAATCTGAGC 120  
 TAGTTTTAAA GGCATCCTTC CAAAGTGTCA CATGTGGTCC TCTCGACACT GCAAGCAAGC 180  
 10 CCATGTCAGA GATTTTCACA TTGCTTGCTG GTATAGGCAG GTTTTCAACG GAATGTAACT 240  
 CCTGAAGTT OCTGATATCC CACAGTCTCA TGGACTTATC TGCTCCGGTN TGTAGCCATA 300  
 TAGTAACCTT GCCTATCTAC CCGACACCA GTGACGGGCC CGGTACC 347

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG101712

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

30 GATCTTCTTG GGTGCGGCA TCAGACAGGC GTAATAATT TGATCATTCC TGGTGCGGCT 60  
 GAGGCTAACT ATGATGCATT GGAAGTTAAT CTTACGAGA CGACGAAGCA AAGGAAAGAG 120  
 CAGGAGGTTA GATCGCTACT GAACAAATTA CTTGCTGATT CTATTGCATT AGATCCAAAT 180  
 35 GTGATTGGTA CGTTCGACAA GCGTCTGCG CAGATTAGAT TGACCGCCAA AGACCTGACC 240  
 CAAATCGCAA CTGATGAAGA CATGAAATCT AAGGAGAATA GAGACATTCC AAAAGCAAAC 300  
 CCTGCTGTGA AGAGTAAGAA ATTCAGGTCT GGTACATTTC CTCGTAAGA AGACGCAGAA 360  
 40 TGTGTAGAT GAGAGGAAGT TGAGAGTACA GAAGCAGTTA GAAAAAGAAA AGGNNGCCN 420  
 CTGCGGAAG CANGANGCTG CTGAGNGAG CTANCAGNAG ATNCGANCTN CCTGNNGAN 480  
 GGTGACGNA GTCCACTGCG MNTNNCTCA CCNNNATTC TTCGTNNCN GANTTCACN 540  
 45 CANNNCNCT CCCGNNCTNN NNCTTNNCCN NCTTNNNTC ACCNNNNCN TCCNNNTCC 600  
 NANCCACNC CCCGNCNCC NNCCCNCCN CCNNNNNNAN NNNNNCCCC CTCTNCCCN 660  
 NCCCCCNCT NCC 673

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1017RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GATCAAGGTT	GAAACGAGC	AGCGTGATAA	AAAAGAGCAT	GACGCGGATG	TCCCTGAAGA	60
GGAAATTTAAG	ATTAAATATA	CCTCGACCTA	CTATAAGGTT	GAGAATATGA	CGCGTGTAGT	120
ACCACAGCAA	TTAAAATATA	TTGCATTTC	AAAGGATGAG	AGATTTACTC	CGCTCGCAA	180
GTTTAAGGGT	AGCAATGGCG	TTATAGTGCT	ATCGGACAAA	ACTCCTGACG	AGCCGGTGA	240
AGTAATCAAA	ACCGCTAGAC	AGGAAAAGA	GACGGATGCT	CCTCTGCTG	CTCCCTTCAA	300
GGTTCAGGAT	GACTTAGAAT	TCTGAACGA	TAATTAGGAA	GCGTCGATTA	TGTTTCATTAG	360
GAAAAAGGGT	ATTTTCTCTA	GAAACGAAAG	AACCTACTGA	TTGCAGCTCT	CTCTAAACAA	420
GTATATTATG	AGGTGATTTA	TTTCAACTGA	ATCTGGCTAA	CGCCCGGCAA	CTAGGTCTTA	480
TCTTCTGTGA	GTCACCTAG	AGGTGGTGGT	CCCCAANCG	CNC		523

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1017UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATCTCCATC	CAGTTTGG	CCTCGTTCCT	GAGCTCTCT	GTGACTTCAT	CCTTGATACG	60
CGCAATTAAG	CCAGGCGCTC	TGTATGCGTA	CGCAGTGTAG	AGTTGCACAA	AGTGGGCCCC	120
CGCTTTGGCA	AACTCGATGG	CATCCTGGCC	ACTACTGATA	CCACCACATC	CAACCAAAC	180
CAGGTTGCTG	TCCTTTGTGT	ATTGGTGTAT	CGTGGCGAAA	GCCTTTAGCG	CAAATGGTTT	240
CACGGGCTTG	GCGGACAAGC	CGCTGCTG	GTTTTTCAGC	TCCTCATOGA	CAGTGTACAG	300
CGAGTCTGGC	CTTTGGATAG	TAGTGTGG	AAACGATGAT	ACCCCCAATA	CTCGATTTC	360
TTGGGCGGCC	TCTGCGATOG	ATTGGAATCC	TGGCTGGTC	AAATCGGTG	CGATTTTAAC	420
AGGAAAGTTG	GTTATGGTTA	CTGGACCAAG	AAAATGCCNC	CGTGGNCAAA	GATTGGGTTA	480
GCANAACAAG	NIN					493

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

(A) LENGTH: 523 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1018RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GATCATCGTC	GAGGAGTACA	CGCACTCGCT	CTGCGCGTGC	GTGAACTTCG	CCGCGTGACA	60
CCCGTACTTC	TTCGACGCCA	CCGTGTTTCT	GAACCGGCAC	CCGGCCCGGT	CGTACAGGTG	120
CATGTTGTTC	CACGCCGTTG	CGCTCAGAAG	GTACTGTCCA	TGGTGTCTGA	ACGACAGCGA	180
CGTGATCGGG	CCCTGTTCTT	CTCGGCCAC	CTTGAAAGAC	TTGACCGCCC	GGAACCCCGC	240
CAATGTGTCT	TTGTTGATCC	CGATACTCAT	CCCGCTCGTC	TTGCAGCTTC	CGGTCTTTGG	300
CCCTCTCGCC	GCTGCTCTGC	ACTGCTGGCT	AGCAGAGCTC	ACCAAAATTT	TTATAGCCAT	360
GGCCAGGCCA	AACCTTCACTA	ACTGGGGAAC	CACACGACCA	CAGCAAGCAA	TGCCCTCAGT	420
ATGTCCGTCG	GTCGACCGT	CCTGGGATCG	CTACTAACC	GCACAGCTCA	AGCAGATGGT	480
GCACCTCAGC	GCCGACCTCG	CGCTGGTGGC	GATGGTGCTG	GCC		523

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 770 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1018UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GATCGCGTGT	ACGACTTCAT	GCGGATGCAC	TACGTTATCA	CCAGATGGT	GGTGGCGGCG	60
GACTTTCCGT	TCATGCGCGA	CTACCTGGAG	GTCTTGCGGC	GCGGCTCGA	GCAACACGAG	120
TTGTGCGATG	CCCGCATGTC	TGCCCTGTG	CAACGGGACC	ACATTGCCCG	ATACACCGAG	180
CTGCTGATGC	TGTATGCGCG	GAAGTCTGGG	GATGAGAAAA	TGCTGGCGGA	GCTCTTTGCC	240
TCCTTGGTCG	ATAGTCTGCC	TGCGGGGATG	GGCGGAGCCA	CTCTTCGTCA	GCCATTGCAT	300
GAAGTCATGA	CGTACCTGAT	CAGCGAAAAC	CAGCCGCAAC	AGGTGCTGAA	ACTGGTGGCG	360
GGCATGCGCA	AGGCGGAGCC	CAATCGCGCG	CCGGGCAAAT	CCTCCGTTCC	AGGCACCTTG	420
GCGCTGGTGT	TTTCGCGGTT	GCGACAGTTC	AACAATCCTA	ATCTGTGTGT	GAGCTTTATT	480

GTGCAGGCAT ACAGAAAGAC GCAAACGAGA GTGCTGCTGG GACAACTCGG GCTATGGTCT 540  
 CTGGCATTTT ATGGCCGGGC TGTTCGGCTC TCTCCCGAGG CGGCGAAGTC GCGCAGGAG 600  
 5 CTGGCGCAGA TATCGCCTGT GGACCTGCCG AAGGAGCTAA TACTGAAGTC CGTACCTGAC 660  
 AGCTGATAAT GTGGAGCTC TATCAGCGAA TCTATCCGAG AAGCGATGCG AGGTGCCCCG 720  
 GGAGGAGTAC CCGAGATTT AATCCAGCTA TTTCGGCTTT ACCAGGACTT 770

## (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 735 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1019RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GATCATGAC CCATGCTAGG TGAAGGAGC CCTTACCCGC TAACTGGAC TCCCTCTTCA 60  
 ATTGCTTAT CAGTTTGGTA TCCACAGCAC CCACGTGTA CAACAACCGC CCCATCAGG 120  
 TAGACTTCCC CCATCCACA TGGCTAGAA CAACAAACGA CATATGGGGC TTCTTCTCAC 180  
 30 GTACATATGC AGGGATGTCG AATGGGTTCC GCGGGTTAGT GGGCTGCACA ACCTTCTTGG 240  
 CCGACGGCTG TTGCCCCCCTC TTGCGCCCGG AATCTCTCTC CTGCTCTCG TAGTTCTTGG 300  
 GGGCCGGCTC CTGTGTGTG AATTTCAGAT CGGCCACCTT CTCGGCCACC TGCTTAATCT 360  
 35 CAAGGGCTCG CTCTCTGGAT TCCAACACCA CGTCATCCGG CGAGGGCTTC ATGAAATTGG 420  
 CACTGGCCTG CTCTTAGCT GCTTTATAGT TGTTAGGATA AAAAACTGAG AACACCTCT 480  
 CCACTGGCCT CTGAGCTGG GTTTTGGCTG GTTCTGCGCA TCTGTCTGT CTCGAGAGGA 540  
 GCACGCTCGA CAGCTGCAGT GCAGGGCGCG CTGCAGGCTT GAAGGACGGC TGACGCTGCA 600  
 40 GAAGAGCCCC CAGGGCCATC CACTGGTCTT GCGTGCCCTC CGTCTTGGG GGGGGGGCTG 660  
 CAACAGGCTT TGCTCAGCG TCGCCGGCGG ACTGCTTGGC AGAGACGACA GCGTCTGCAT 720  
 45 CAGCGACGCG CCGG 735

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 740 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1019UP



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

5 GATGCGAGAT TCATCATGCG TGTATACCA GGCTCTATCT TCCTCGAGGT CCTGGGGACC 60  
 AAACGGGGCG CTCTCTGTG TGCCAAGAGG TGCAGGACCC TGGCGGAT CCTGGGCCAG 120  
 CAGAGTGGCA ATCTGGTCTT CATCCGCTAT CGCTGTCAGC TTAGGCACAA AAGCCAGTTT 180  
 10 TTCCGTTTTG TGGCGTGAT CATCTGCTC GAGCGTCTC TTCTGATCTC TGGACCCCTC 240  
 TGCAAACCTCT TTGAGCTGCC TTGCTGCTGC CTTGTCAAGT CGCTTAAATC TCAGCGTTT 300  
 CTGTTTCTGG CCACCGCTCC CCAAGCTCTG GTCCGGCTCC AGTGCTGTTT CCAGTTCTGTC 360  
 15 GTCCGAATCT TCGAAGCTCA GGGGACCAA GTTCTTGAT GTGTTTCCCT TCAGGCGCTC 420  
 CCCGTCAAGG ACAGCCTTCA CCGTGGTGTG TGTGGCTCC TCCTGGGTAC TCCGAGGGA 480  
 TACTAGCAGC TCATGCAGGA ACTTCTCTC CCCTTAAACT TGCCAAGGC CATGCAGCTC 540  
 20 TTAGTGAAT TCACTGGATC GTATGCATGC ACGGCGCTA TATTCATAT CGGCTGCACA 600  
 AACTTTCTGT GACATTGGAT GCGGATGTTG GTGGATCACT CCTTCAGCG GGGTCATGTT 660  
 CTTAGCTCT ACCGTACTTG CTCTCTCAGA TGCATGATGT GTACCATCGC ATCTTCAGCT 720  
 25 TGACAGACTT CCATATAAGT 740

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1020RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

40 GATGTTCTCT GTTCTGCGG GCAAAGTTCA GAATTGACCT AGTGCCAGAC ATGACAGTAT 60  
 CGTTCAAACCT CCTGGGAGAG TTAGCCTTGG ATATCCACCA TGAAGACAAA AACCAGAGAC 120  
 45 CAACAGCGGA TCCTACCAA ATGGCCAGAA TACCGAAAAA CCAGTCAAT TCTCCGGTTG 180  
 CTTCACTCG GACAGTGACG TTCATCCAA ATAGACCCGT AACAAGATT CAAAGGAATA 240  
 ACATTGTTC AATCATAGTG ACCTTTCCCA ACATTTCAGT AACACGATT TTACACCGGA 300  
 50 AGGACTCAAC TTGCAATTGT GCCAAGTAGT TACCATGTGA ACGGGAGAAA ATCTTCTCAT 360  
 AGGACAGTAA ATTTTGAAAC ATGGGAGGA CATGGTCTG AATATCTCCC AAATAGAGCG 420  
 CTATATCAGC TCTTGGTTGA GTGGCTGGA CATGATGATG TTGTATGTTG GAGCCTAGCC 480  
 55 TGCCAGACAG AGGGTGTGT CCGCTAGCT GCAAGTTCCG AATGTTTATC TCGAGGT 537

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 563 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1020UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

GATCAGCACC GTGCOCTTCG TGTAOCCTCG CTGACATG GTGTGCGACG ACOGTGTGTC      60
GCATTTCTTA CACGTGAAAG CAATCATCAT CATCGGCTTG TOCACCTTTA TAGACCGGAT      120
ATGCCGAAAC TCATCTGCAA TAGGCGTTT CTGGCTGTTT TGCAGCTGCG GCGAACCGCT      180
GTGGAACCGA TGAGCTACCA AATGCCCCC AAACACCGGA CCCAGCACGT ACTGCATGCA      240
GTTACGGCTT GGGCGGAGTA AACCAGCAAT CCTGAGAGGC CCCATOGAAC GTCTAAGCAT      300
TTTAAACAGT TATACGTAGT CAGCGGTTT CCTAAAACAG GACATGAGAG TCGCTCGAAA      360
GAAGGGGTCA TCTCAAAATT TTCAACTTTA GAAGCGCTGC CCGAAAAGC ACCGTCACCA      420
TTTATCTATT ACAAGATGAA CAGTTAGTGG TCGCGGCAAT TGTGTCAGAT ATATGTCTCT      480
GGACATGGAT ACAAGACACT CTCGCCACAG AAGGAGCAGG AGATAGCATC GAAAATCTTG      540
CAGAAGGCTG AGCTGGCTCA GAT                                              563

```

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1021I1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

GATCTCACC TCAGCACCAT CGACAACCT GCATACGCG GCGGTGAGGT CATCGGCAAG      60
GCCCCGTGCC GCACACTCGA GATGCGCTC AATGCCCTGT CCGCTACCAA TGGCGGGCA      120
CGAACCTCG AAACCGTGC TATGAACATA CGCAAAGGCA TGGTTTCCAA GCACCGCAGT      180
CGCATCCGGG AGCACGAGCA GCTGGCCCG GACTCCGGCA CGTCTCTCG CAAGGTCGT      240
CGCGGAGAGT TCCGAAGAT AGACGCAACC TACAAAAAG ACATGAGCG TCGCATTGGC      300

```

ACGACCATCA AGGCTGCAGA CCGTGCCCGC AAGAAACACC GCGATC

346

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 562 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1021I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GATCTGCGCC	GGATGGCTGC	GAGTTGAGCG	CGCGAAGAT	GTGTGACTCC	TGCAGAAAAC	60
GCTGGAGCTC	GATGTCTGT	TCCAGCAGCT	GCTTCTCGTC	GCGGTGCGCC	GCGGCAGATT	120
TGGGCGCGGG	CTCGGTCTCT	AGGCCCGGCG	CCTTGCCGCT	GCGGATGCGG	CGCAGTTCTC	180
GTGGAGAAGG	CCCGCTGTAG	GCATCTGACG	GCGCGGGGAA	CGAGATCAGC	CGCGCGGTAT	240
GGGCGGCTTC	GTGTGGGAG	CTGGCTGAGG	CGCGGTCCAT	TTGGGACTGC	TGTTGGGATT	300
CAGACTGTCC	GGAGCGCGCG	TGCGCCCTGC	TCTCCGGGTC	ACTGTGCTTC	TGGAGGGGCG	360
TGGTGTCTGT	GTGCTGTCTT	TGTGAGCAC	GGTCTTGTTC	TACATATCCC	ATATCTCTTA	420
GGGAGCCAAA	CTGGGCTCG	AAGGCCCTCC	CCTGGGCCCC	GACGTGCTTG	NAITTTATCTT	480
CAATTGTGCG	TCATCCGGG	GGTTCTTTGG	GCCCCANGAA	GTNTNTNANC	AGGAANCCCT	540
AGNANNANGG	TTTTCAAATT	CC				562

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 611 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1021LRP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GATCTTGAG	TTTGTGCGCG	GCGGGTCCCG	CTCATTTACC	TAATCTGTTC	TATAGTAAAC	60
ACGTTGTGT	ATCTACATAG	CGACCTGTT	GTAACTTACG	CTGCACGCAT	GCGCGGGCGC	120
ACGTCCCCCA	CCAGCGCCCG	GTAGAAGGCC	TGGCCCGCGC	GCGCGCCGCC	CAGCATGCAC	180
AGGCGCAGCC	ACGGTTTCAT	CGTGATCAGC	AGGCCAGTCC	ACAGCGGGCC	CTGCACAGCC	240
GCGATCAGCA	GGACGTCCCG	CACCAACCAC	TTGGCGACGA	CCAGTGGGCT	GATCCCGCTC	300

TOGCGGTCCG CCGTCGGCTC GCGCTCCTTC TGTCGCCGCA GGTGTGCTG GCGCGCGCTT 360  
 TCCTTCGCCA GCGCTGCGCG GAACGTCCTT TTGGAACCTG ACGTGGGTA TCGTTATTC 420  
 5 TTGGGGTCCA TTGGAACGCG TGTCGGGGT CAGAGGGAGG ATTCTGCGC TGGTTTGGTT 480  
 TTTACGAAGA CGACCTCGG TGAGAATGTC AGTTTGGCCA CTNGGCAGCC CCAGGAAGGA 540  
 CCGNGAATTC AAACCACTG AGTNGGGCGN CGNGTAAAA ACGCTAAGTT AGTGCNNTGC 600  
 10 ANACCCNCT C 611

## (2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1021UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATCGGGTG TTTCTTCCG GCACGGTCTG CAGCCTTGAT GGTGTGCCA ATGCGACGCT 60  
 CGATGTCCTT TTTGTAGGTT GCGTCTATCT TCCGAATC TCCGCGACG ACCTTGGCGA 120  
 30 GGAAGGTGCC GGAGTCCCG GCGAGCTGCT CGTCTCCCG GATGCGACTG CCGTGCTTGG 180  
 AAACCATGCC TTTGGGTATG TTCATAGGCA CGGTTTCGAG GGTTCGTGCC GCGCCATTGG 240  
 TAGCGGACAG GGCATTGAGG CGCATCTCGA GTGTGCGGC ACGGCGCTTG CCGATGACCT 300  
 35 CACCGCCGGC GTATGCAGG TTGTGATGG TCGCAGGGT GAGATC 346

## (2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 438 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1022RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ANNNNNNNN NNNANGGTGG GCGGTGGTNG AATAGTGGT CTTTCTGCCG GGGTCTGTGC 60  
 AGAAAACGAG ATTCTGGGA GTATCTGAAA TTCTTTGTTG CCGCGAGCCG TCTGGGTCTG 120  
 55 CGTCAACCGA CAGCGAGTTT GCGACAGGAA CTGAAGCTAA TTTCGTTGCT GGAGGTGTTT 180

TGGGGCTTCG CGTTTTTCAGC CTTTCAGGAA ATCTAGAGGG GCTGTGTGCT TTGAGGCTGA 240  
 AATCAGGGGA ATAGCCTGAA TTTGCGAGCG TGAATTGAGC GGTATATATG AACTGTGGTA 300  
 CATCGNCACA CTGTACCAG AGGACAGCGA ATATCTGACA GTAGGGGGTC CTTCGTAAAG 360  
 ACACAGTGTA TCGCGTGAGA TAGGTGTGTA TTGAGTCTAG CGTGCTAGGT ACTCTTTAAC 420  
 TTTCACTCGG TGTTTTTT 438

## (2) INFORMATION FOR SEQ ID NO:73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1022UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GATCCAGCAG ACGTTTTAAT CACCGATTTT TTCGGTAACA TTCAAAATAT AATTCTCGAT 60  
 GACAGTGAGA TAGATGGTGA AACTCCAGCT GGACTTACGG AATCTGGCCG GACTCGCAAT 120  
 CTGCTAGAAT TCGCAAAAGC GAAATTTTTT GGCANIGTAG ACGCAGAGAC TAATGGCAGG 180  
 CATAAAAACG TGATTOCAAG CTATCCAGTG GTAAATGAGG ATTTACTAAG TGGGGNANCA 240  
 AATGCATCCA CAAACAAAAT GATAAAATTG TGGGGGATTA TCATCTTCTT GGCCTAAGG 300  
 TCATTAAATGA TGAAGTACGC CAACACTGAA AACATATCGG GTAGTCGAGC ACTATTATGT 360  
 TTCTCTTAGA AAAATGCTTC ATGCTTCATG GAATTAAGGC GGCAACAAGT GCAAGGTAA 420  
 GAACGGAATT TTAATATAGG CGGAAATTT GTATATATTA T 461

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1023I1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTCGAGAAAA CAGAGCTTGA GGTCCACTG TTCTTTTTC A CTGGGATGT CTCTGTCTGC 60  
 TCCACGACCC CCACTTTCAG ATTGTGGTGC ATCAAGCGCT GCAAGTGGAC TTCGAGACGG 120  
 GTGTCTGGGA TGGTGCACTA CGAAACTTC TTGTGCTTGT GATCAGCGGG GTCTGTCTCG 180

TGTACCGTAA GCTTGCCGGG CACCAGCTTG ATC

213

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 725 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1023I2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTCGAGGGAA GTAACCAATA TATTCAAGAG GGCTACCTAT GGCATCAATG AGACGTTTCG 60  
 AACCAAAGAT CGTCGGGTCC TGGGTGATAG CGCTTCTGTG TGGGGTCTTG TGTGCAAGCG 120  
 ACAACCTTCA TACACGGGAT ACTTCCTGGT TAGTGTTAAT CTCAACAGCG GTGAAGTTAT 180  
 CTTGATGAC TTCAAAGAGG AGCGTTTCT GACGGAGGCT TTGGAGACGC GAATAAAATA 240  
 CACAAACCCG AGTGAAGTTG TGGTCGGAGA TGGCCTTGGC TCAGAAATCG AAAAGGTGTT 300  
 TCATACTTCA GATTCCGATA TCACTCTAAA TAGGATCGAG CTCGTGGGGT TGTATGAAGA 360  
 AATCTTCAGT GAGCCGCACC CAGCCTTTAG GGGCAACGTT CCTCTGCAA CAGCGCTCAT 420  
 GCTGGTGCAT GGCTACCTAA CAACTTCAA AAATGAGAGT TTA CTCTTCT TCAAGGAAAA 480  
 CTTTAAACCA TTCTGCTCGA AGACGCACAT GATTCTTCCC TTCTAGGCT ATTGGAAGCT 540  
 TAGATATTTT GGGGACAGTA CAGATAGGAG CAGTAAAGGT CCGCTGTAT GGGTNTTAGG 600  
 TCAANCTAGA ANAACTAGGG TTAAGGACTT GGAGGACTGG NTTGAAAGGC CTNTTAATTT 660  
 GGTCAGTCA ANAGAGTTGN GGNNGCCAAN GATTACNAG GNGGNATIN TCATGGCTCG 720  
 GAATT 725

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 659 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1023RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TGCCCCGCAA GCTTACGGTA CACGAGACAG ACCCCGCTGA TCACAAGCAC AAGAAGTTTG 60

EP 0 866 129 A2

NGTACTGCAC CATCCAGAC ACCCGTCTCG AAGTCCACTT GCAGCGCTTG ATGCACCACA 120  
 ATCTGAAAGT GGGGGTCTGT GAGCAGACAG AGACATCCGC AGTGAAAAAG AACAGTGGGA 180  
 5 CCTCAAGCTC TGTTTTCTCG ACGCTAGGGA TAACAGGGTA ATACAGATAT CAGATCTAAG 240  
 CTTCCTCGT CCCCCCGGG TCACCCGGCC AGCGACATGG AGGCCAGAA TACCTCTCTT 300  
 GACAGTCTTG ACGTGCGCAG CTCAGGGGCA TGATGTGACT GTGCCCCGT ACATTTAGCC 360  
 10 CATACATCCC CATGTATAAT CATTTCATC CATACATTTT GGATGGNCGC ACGCGCGAA 420  
 GCAAAAATTA CGGTCTCTG CTGNAGACCT GCGAGCAGGG AAACGCTCCC CTCACAGAG 480  
 CGTTNGATTC TTCCCCACGG CNGCCCCNTG TNGAGAATNT AAAGGTTAGG ATTINGCAATG 540  
 15 AGGTNCTCTT TTCANTTNTT CCGTTTNTAA ATCNTTGTNG GTCAAGTCNT CANATCAAAT 600  
 TCCCAACATT AACACCNTGG TTAGGGAAGT TCANNTTTCN GGGGCCNNGA TTANTTCN 659

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 646 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1023UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATCTCAAAC CTGAGAATAT TCTACTTCAT CAATCTGGTC ACGTTATGCT TTCTGATTTT 60  
 35 GACCTGTCAG TACAGGCAAA AGGAACAGA AATCTCAGG TTAAGGGAAA TGCCAGTCT 120  
 TCGCTGTGCG ACACAAAAGT TTGTTCTGAT GGCTTCAGGA CTAATTCITT TGTGGAACG 180  
 GAAGAGTACA TTGCACCTGA GGTATCAGG GGAAATGGCC ATACAGCATC CGTGGATTGG 240  
 40 TGGACATTGG GTATACTTAC TTAAGAAATG CTCCTTGGGT TCACTCCTTT CAAGGGGAC 300  
 AACACAAATC AAACGTTCTC CAATATTTTG GAAGAATGAC GTTTATTTTC CAAACAATAA 360  
 CGATATATCT CGCACTTGCA AGGACTTGGA TTAAAAAGTT ATTGGGTCAA GAAAGAGAGT 420  
 45 AAGCGACTTG GTCAAAGTTT GGCGCAAGT GAGATTAAAA AAGCATCCCT TTCTTTAAG 480  
 ACCCGTCCAG TGGCGGTTA TTGGAGGGAA CCAGGAACCT CCGTTTATC CCGTATTA 540  
 CCGGAGATGG GTACGACTTT GGAAAGTAT CACATTAAAG GATGTTAAAA AGGCCGGGAA 600  
 50 TCCGGCCAC CCGGTTAGT CTCATATTCA AAGCGNGGT TCNNNN 646

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 557 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1024RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

10  ATNNNNNGNN CANNNGTGGG GCGGAGOGAN TAGTGGGTCA GCANGGTGCG CTCGGTGTGT      60
    GCGCAGCCGT TGGCATGCTC GCGGATCCTC GGTGCAATA TACCAGAATG CATCATGCTT      120
    CGCTGGCTCT ATATTGACCT GGTGGCCATA TATGAAAAGG CGGTCTTGA AGTTTGTGTAG      180
15  AAACCTGCTT GCTTGAGATG GGTAGCGAA CCCAAGGAAG CATTATATGC GGCATTACG      240
    AGCCCTGGAA ACACTAACTA CCGGTACTT CTCATCTAGC AGTGAAGGG GCACGTCTGC      300
    GGAAGGAAGC GGCTCTGGCA AGTTTTTCTC GCGGATAGA GCATATGGT TATCCTTGTT      360
20  GATGGACTTC AACAGTTGTC GAGCATATTC TATCTGGAG GCATTTGAG CTGGCAAATT      420
    TGACAGGTAG AACTGGATG GCGCGTTAG TATCGAATG ACAGCAGTAT AGTGACCAGC      480
    ATTACATAC GACCGGACGC ATGATATTAC TTCCTTGNEN ACTTAANNTN CCAATCTTN      540
25  NGCCAGATTN ATTTTGG      557

```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1024UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

40  GATCTAAATT CCCAGCCGC TGCGGGGTT TCTCTGCGAG TCTTTGCCGT GAAGCAGAC      60
    ATAATCGAGC CCAACACAG CAAGATCGCA GAGAATCAAG CTTATGTAAG TCTCAGTGA      120
45  CTCGANGCGT GCAGAACGGT ACGGTGTGC ACTGCAGGTG CCACGCCATG TCTCACATG      180
    TTGTAACAGC GCGCGACCGC GGTTCGGAAT ATCAACAAA CATATGTTTG CCGCAAAGG      240
    GACTGGTTCC CGCAGCTGCC ACCCGCAGGG GCACAGCGCG GCAATGCAGA GTCGGTTAG      300
50  GGTGCGGTG CCGGATGGG GCAGTGTGCG CCGC      334

```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1025RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATCAGCCCG TTGCGCCCGC CGCCGTTGTA CTTCTGGTTC TGGATGGACC CCGGCGTGAT	60
GGCGCTCTCG TTGCGGTACT CGTCGCTGCT GCGCAAGTCG CACTTCAGCG CCACTAGCAC	120
CAGCTTCAGC CCCTGGCAGT GGTCCGCAAT TTCGCTCACC CACTTGTCTT TGACGTTCTC	180
CAGCGAGTCC CGCGAGTCCA CCGAGAAACA CAGCATAATC GTGTGTGTGT CCGAGTACGA	240
CAGCGATCC AACCGGTCAA ACTCCTCTCG CCCAGCAGTG TCCACAGGC TCAGCGTGAT	300
GTGCTGGTTG TCCACGAAGA TGTCAATGAT GTAGTTTTCG AATACCGTGG GCTCGTACAC	360
CTTCGGAAAG TACCTCGGT GAACAGTTC AACAGCGAG TCTTCCCGCA AGCACCGTCT	420
CCGAGGATGA CGATCTTGCG CTCGATAGGA TGCTTCGAG ACGAGCTCGA CCACACAGAG	480
GCATCTTG TG TTTGTAGAGC TGGTGGTGGG AGCTCCTCTG ATGCCAGTCC ACGCTACAAA	540
TACAGCGTTT GAGACGAAAT ACTAGCTGCT ACTGTCTTT CTCTCTGAG AGGTGCACGG	600
CGCATCCCCG TTATAACTGT C	621

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 522 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1025UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GATCCCCATG AGAATGAGCG CATCTTGGAT ATGGCGGCGG CACCCGGTGG TAAAACCACC	60
TATATATCTG CCATGATGAA GAACACTGGT TGTGTCTTTG CAAATGAGCG CAACAAGGCA	120
AGAACGAAGT CCTTGATTGC GAATATTAC CGTCTCGGCT GCACGAATAC AATTGTCTGC	180
AACTACGAGC CCGCGAATT CCCTAAGGTT ATCGGTGGAT TTGACAGAAT TCTACTTGAT	240
GGCCCTTGCT CAGGTACAGG TGTATCGGC AAAGATCAAT CTGTGAAAGT AAATCGTACT	300
GAGAAGGACT TTATGCAAAT TCCACACCTG CAAAAGCAAC TGATATTATC TGCAATTGAC	360
TCTGTTGACA GCAACTCCAA GCACGGGGT GTCAATTGTCT ACTCTACTTG TTCCGTTGCG	420

GTTGAAGAAA ACGAGGCGGT GGTGGAATAC GCTACGGAA GAGACCTAAT GTCAGCTGTT 480  
 GAAACCGCT GGTATTGGT AAGGAAGGCT CACTAGCTAC GA 522

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1026RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GATCCAATTG CTGGTCATAC ATACGCATTA ACAGATTTTA TTACTATGTA TOCAACGTGA 60  
 ATTGCTATAT GTACCTTATT ATCGGTTTCA TAAAGATGCT TTAATTTCTT ATTCTGAATC 120  
 GGAGTCGTTT GACCGGCGCT TAGACTGGTT ATGCGCTCTG CCATCGTTT TCTOGAAAAT 180  
 GAAAATTCTA GCTTCACGCT CGGTCGACG CTTAGTCGTA TCCGCTCAT TGTAGTTCT 240  
 CCTATGACGG TATCTGGGA AGGTATCCCA CTGGAATTG TGCGACCTCT CAAGCTTTAA 300  
 ACCATGCTCC TTGGCAAGTA CCTTAGGCTG CCAAGAATCG TATGGATCAC CGGCAAATAG 360  
 GGACAAAATG ATCTCCCA TATCATCAGA TGATTGTTCT TTTCTACT TCATATCCGG 420  
 AAAGATGGGC AACAACCTAC TTCTTATTCG CCAGCTTGAT AGTTGTTTAC AGCTATCAA 480  
 AATATCCCGA TAGAGCTCTG AGCTCTCT 508

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1026UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GATCTAGCAG ACTAGACTCT CTATGCATC AAGTTTCTGT TTTCAAGTCT GGGTTTCTTG 60  
 AGCAACCTGG TGCCCTATA CTTGTGTCAG ACGCACAGG AAGCAGAGT CTATCGAOGA 120  
 TGTCGAAGTT ACAGACGAAA AAACAGGCGC CGCCAGCTAT TOCAGAGGCA GACGTATCAC 180  
 TCCAGGCTAT CAAGAAGCGG CGCATGTCG CCAGGCTTTC TACCTCCCGT AAGTCGGGTT 240  
 CTGCCACAGG TATTAGTGTT GTGCCACGG CGCAGCTTC AGAGTCATAT GTGGTTCCAC 300

CTGCTGGTGC TCCTCTGAAG AAAGAGTCTG CGGATGACTT ATTTCAAACG ACTGCTTCCT 360  
 5 TTTATGAACG TTACTACTATT TCCACACTGA AAGAAATACC GAAAAACATT GCAGATGAGG 420  
 ACTCTGCCCG ATATACCGTT AACGAGGATA GCATCACTAT GGCTGACCTT TGCAAACCTC 480  
 TATTCCCGAT AGGTGAAGTA TCTGATAATT TCACCGGGCG AAAGAAGCTG CAAAAGCCAA 540  
 10 GATGGAAGCT CGGAAGAAGC GCGCGAACT CGACAGATG GCTAAGGCTC AATC 594

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1027RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATATCGACG TACTCTGGCG TTGTCTCTTC TTGTCAGCA GGAACGCGT CCGGCATAGG 60  
 CTTACTGACT TTCACAGACA TGATTCTTTT GTCGCAAGTA AAGTATATTAT ATGGCGCTGT 120  
 30 CAAAAATGGT AATAGTACGG AAAGAGCAAC CTGAGAAGCG TCCAGGGCCT GCGATAAGCC 180  
 GTTTTFACT AGAGCAGTGG ATACAGCTAA TGTTGGAATC AATGCAATGG CTCGTGTCAG 240  
 AATTCTCGT TTCCATGGGG TTATAGTCCA GCGTATATGG CCTCCGCATA CTATTGTGCC 300  
 35 AGCTATGGTA CAGACAAATNC CTGCCGATG GCCCGAGATT AAGAGTGGGA GCATGAATAT 360  
 GGTACCTGCC GCTGGTGCCA AAGTGTGGA TAATAGGTGG TGTATCGTGT ATAGATCGCC 420  
 ATCGATGGCT TCCGGGGTAT CATACAGTGC GCTA 454

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1027UP

## (x) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GATCAACGAG TAAAAATGCC AGGTGTTTC GTTAGGTACG TGTATGAGT GCTAGTTTAT 60  
 55 GGTTTGGTAC GGCTGCTGGG GGGCGCTTTC TGGGAGGTTT CAGCGCTCAT ACGTTATGTG 120

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AAGATGCTTC GATCGNGAGG GTTGGGAGAA GGAATGGGAA TGIGCCAAGC AGGACTTGGT 180  
 GATTGGTTCC AGAAGCTGCG TGACTGTGTC AATATGAAA TCATTGGGCG AAACCTAGCT 240  
 5 TGCTACGGAG TCCAGCATGC AGAAGCTGCG GCGAAGCTA GCTGAGGCTC GATGAGACGG 300  
 TGGCGGAAAT CCTTCGATCC CAGGCCAAAG CAGAAGTACC TACCAGCTTT TAATGTGCCC 360  
 GCGTACTAAC ATGATATACA GAGAAGTTCC AGCTCAAGAG TTCATCAAGC CTTACGCTTC 420  
 10 TTTTCTTGCA AAGACAAGGT AAGTTG 446

## (2) INFORMATION FOR SEQ ID NO:86:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1028RP

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GATCATGCAA ACGGAGAGAA GGAGAAGAAG TCTAAGAAAG AGGGCACTAA AGAGAAGAAA 60  
 GCCAAAAAGC AGGAGAAAAA GGAAGTGAAG AACATCATTTG AGGAGTCCGT TGAGCAAAAT 120  
 AAGCTAGCAC TGATAGAAAA GGTGGAGGAA GAAAGAGGCC GCAAGAAGGA GAAAGACCTT 180  
 30 GACATCAAGT TCAGGTATCG GGAAGTTTCG CCAGAAAGTT TTGGCTTGAC CACCCGTGAG 240  
 ATATTTATCG CTGACGACGC TGCTTGAAT GAGTATATTG GCTCAAGAA ATTTGCACCA 300  
 TATAGAGCAA AGGAGTTGCG CAACAAAGAT AAAAGGAAGG TCATGAAGGC TAAGCGTCTA 360  
 35 AAAGAATGGA GGAAAAAGGT GTTCAATAAC GAAAATGGGT TGGCGGATGA GGATGAGGCC 420  
 CTTGATACCC AGGCGGCTCC TAAAAAGGAG AAAAGCCGTT CTAAGCACAA GACAAGTAAG 480  
 TAATATTACC GTCTTTATGT ACGTCTGCG GTAATTATAT TTGCTATAC ATATATATTA 540  
 40 ATTTAAACTT T 551

## (2) INFORMATION FOR SEQ ID NO:87:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1028UP

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATCCGCGCC CGGCACAGGC CTGGCAGCAC CCATGCGCGC ATGCTGTGCC TAAGATGTCT 60  
 CAGAATTACG CGGCGGCTCA GGGGGGCGCC AGCCCTCCA TGCTTTTGGG CCAGGAAGCC 120  
 TTCCACGAGC TGGGGGACTC GCGTGGCATG TCAATGTACA TGTCGCCCCA GACCCATAGG 180  
 CTCAAGGGCA ATGGGGGTA CCGTTTGCCG ACCGCTTCTA TCTCCGACCC TTGGGTGCTC 240  
 GGTGACACCG GCGCCCTCC GTCTTCTCAG TCATTGACAT CGCACCTTCT GCGTACCCCG 300  
 AACTTTAACA TGAATGACTA TGTGCATAAC CTTTTCAGCC CCTCACCAAG AATAGACCCG 360  
 CCAGGTAGCT CTGGGAATAT ATAGGGCCTC GCACACATTT AGCGCACAGT ATACTAGCTA 420  
 ATCCTACATT CTCTGTCATA GTAATGCCTA TGTGAGCACA CCTGCCGTAT AATTTCATTA 480  
 TTTCCTGITT CATAAATGCT GACATATGTC ACGTGGCTGG ATCAGCAAGT GATGGCAAAA 540  
 TTCTTATGAA TGAGCCTGTT CATCTCGTCA GACAATACAT TATACACGCA TCCATCTCTC 600  
 GGTATGATAC GGACTCTCTC ACACTGGA 628

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1029RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GATCGTAACA CTCTGGAGAA GTGGAAAGAG CTAGTCCCTC CGAGCTGTAA ACGATGCATG 60  
 GATGCGCTTC ATCACAACCG GTAAGACACC GCGAGTTTC CGGAGCACAC GCTOGAGGAT 120  
 GTGGGAAAAG GGGTTCCGCG CGATGCAGTG GTATAACATA TTGCGCCACT GTGGCAATTT 180  
 CCGATGGGAC TGGATCGGCG CGTGCTGCAG AGCTCAAAGA AGGTTTGIGT GCTATTCTCG 240  
 AAGATCGATA TGGTGGTGCA GAGACGTCG CACATGCGC AGGACGTAGG TGCATTTTTC 300  
 CAGAGCTTGC TTTATCATGA CCTGCATGTC AAGATCAGCA ACTTCGCTT CTTTCTGCG 360  
 CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT 420  
 GCGGGGCCAA ACGCGGGCAA GTGTCATTG ATCAATGCC TGATGAAGAC TGTGTGTTAC 480  
 GAAAGTCGCG GTCTGTTATC CTCAAAGCAG TCCTCTGGA CCGCTGCGA CCGGCTTCCA 540  
 AAAGCGCATT TGGACATCCA TTCTGCGGGT GTGAGCACA TACCGAACTT CACTCGCCAA 600  
 CCCAGCATTA CGATATAAAG GGCAAGATCT CCACGATTTC CAGGCTACCG CACAT 655

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1029UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GATCTCGTGG	TGTTTTCGAA	CTTGGTGCGT	GACGGGATAT	CTCAGGCTTT	GCGTCTGAG	60
CATGATTATG	AGGTGAACAA	GATGCGCCGC	GCGCTCTCCT	TACTCCAAAA	GCTGTATATT	120
AGGGATAGAA	GGACCAATTT	CCTCTCCGCG	GCCAAGGGGG	ACGACTTCTG	GGTCATTGCG	180
GATACCACGG	TGAAAACTG	CGACATTACA	TCTCTCCTTC	TTTACTTTGA	TGAGTTCTAC	240
AGAGAACAGT	TGGATTGTGT	CCTGGGCGAG	GGCGGTGCTC	GGCAGGAGGT	CCCCAGGGGC	300
GATCTCGTAG	CGTGGGAAAA	CGATATAAAA	GTAAGTTCT	TTAGCGAGAA	GTCATCGAAG	360
CACGCTTCGT	GGGGTTCCCT	TGCCCTGCGG	AAATTGGAAC	TGGTACTGCG	CGCTCCGTTT	420
CTGTTGCCCT	TTGCGGAGCG	GGTGGCCTAC	TTTGAAACGC	TGATACACCA	CGACCGACCG	480
CGGTTGCAGG	GACGCCACAC	AGGACCAGCC	TTGGGCTGCG	CGACCTGTA	CTTCCCGTGG	540
TCGGGGCGGC	AGCGTGGGAT	TATCTCCAGG	AACAACATCC	TGGAAGATGC	ATACSAGGCG	600
TATTATCCGC	TGGGCGAAGA	CTTTAAGGAC	CAGCTGGC			638

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1030RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GATCTGCTTG	TTGCGCAACG	CTTCCCAATC	GATGTGCTG	AGAAAGGGGT	GGGCGGGGAC	60
CTCTGGCGCG	TCGTTGACCG	CACCGAGGCG	GTGCTTGGGA	TTGCGGTTCA	AAAGGCCCTT	120
GACAAAGGAG	CGACCTTCCG	GCGATAGCAC	GTCCCTGGGG	AAATTGACCT	TGCCAAACGC	180
AATCTTCTGG	TACATCTTCT	GGTTGTCTTC	TGCAAAAAAA	GCGACCCAGC	CACAGCACAT	240
CTCGAATATC	AAGAGGCCCA	GCGACCAGAA	GTCAACCATT	TTGTTGTAGC	CGGTCTCATC	300
GAGCAGCAGC	TCGGGGCGTA	GATACTGGGT	GGTACCGCAG	AACGTATTGG	TGCGATCCTT	360

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TAGGTCCGCT TTTGAGAGGC CGAAGTCACA TAGTGCGATA TTGCCGTTGG CGTCTAAAAG 420  
 GATGTTTTCT GGCTTGAGGT CGCGGTACAC GATATCATTG TOGTGAAGGT ATTCCAACGC 480  
 5 AAGCACCAAC TCGCAATGT AGAACTTTGC CGCTCCTCC GCGAACGAC CTCTTTCTG 540  
 AAGGTGCCAG AAAAGCTCAC CACCGNCTAG GAAGTCAGTC ACCAAGTATA AGTCTGTGGG 600  
 CGTTTGAAAA GAAATTTTCA ACCAACATG AAGGACACG ACTTTGAGCA GTAOGAACA 660  
 10 GATGTTGCGC TCACCAATAG TATGTGCA 688

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 751 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1030UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GATCGATTCC CTGAGCATGT TTTTCCCTAT GCTGCAGGTT TTACATGGTG ACATTGCGGA 60  
 TGCCGAACCTA AAGAACCTTA TGCTTTTGAA ACTCTGGAAC ACTTACGGCG GAATTCCTGA 120  
 30 ACGCTGGCTA TTCACTACTC TCTACAAGAA ACAGCAAGTT ACGTAAATG ATACGCTGCA 180  
 GCTCGAGTGG TATCCTTTTAC GGCCAGAGTT TGTAGAATCA ACCTATTCCC TTTACAGGGC 240  
 CACTAAAGAC GCATTTTATC TGAATATCGG ACGAAGCATC CTCAGGCTC TATCAACGCG 300  
 35 CTTTAAAACG AAATGTGGGT TTGCGGGCAT ACAAACGTC ATAACGGGAG AGCCACATGA 360  
 TAGGATGGAA TCGTTGTTT TGGGCGAGAC CTTAAATAT CTCTATCTCC TCTTTGACGT 420  
 ATCCAATGAA TTGCATACAC AAAAAACGAC TAACCAATA TTTAGCACTG AGGCGCATCC 480  
 40 ACTGTGGTIG ACTGCTCGA TGAAGGCTCG CTACGAAAAG AACAAGTACT GTGAAAACGA 540  
 CGTGTATATA CAGAACTTGC GTGGCTACA GGAGCTTGAC CAGCTGAAAA GCGTGCCAA 600  
 TTCATTCACT GCAGAGGAAG CCATGATACC AGCTTCAGAT TTCAAAACAG AAGACTCGA 660  
 45 GGAGTCTTIG AAGGACCGG TTGCAGGCG ATACTAGAGG OCTACACGTA GATACGACAC 720  
 GTTCGTGGAA CATGCAGACC TTTCGGACA A 751

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 646 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1031RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GATCTTAGTA	ATGATCACGT	GATTGGATTA	CCGCTTGTGC	GTTTGTCTCT	COGCAAAGCG	60
ACATTTACAC	GGGAAAAGCG	GTGAACCTCC	GOOGAAACCC	AAATACTCGT	ACACTATGAC	120
TATAGACGAC	AATGTGATG	ACGTGAGCAC	AGTTTAACTC	TAGTGTACAA	TCACTGTCAC	180
ATACCTTCTC	TGCCACCCAC	ACATTAACCA	TTTATTTGTG	GTCACGTGAA	ATGAATOGAT	240
GCATTTTATA	ACTGCAGGTT	AGTTGAGCCA	TCTCGCCAAC	GATGTCTGTC	GACAGCATTG	300
GGGGCACGGC	GCGTCATGAG	TGATTGGAAG	GAGGCACAGG	ACTCCACGGG	GCGTGTTTAC	360
TACTATAATT	CGAAGGGGGA	AACGTCATGG	AATAAGCCCA	ACGACACGCC	AGTTGAGCTG	420
GAACCGCGAC	TGAAGAATG	TGGCTGGAAA	GTGGCAACGA	CGGAGGACGG	TAACGTGTAC	480
TATTACAACA	GGGAACTGG	CGAAAGCAGG	TGGGAGAAGC	CGGAGTTGGA	GCCAGCCGAG	540
GAAGTGCCCC	GGGAAGARGA	CGAAGCGCCG	CCGGAGGARG	AGAAGAAGCA	GOOGTCCGCT	600
GCTGARGAGC	CCGGGGTCCG	GATCGAACTG	CTGCTCAACT	CAAACC		646

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1031UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GATCANOGAN	CAGCACCGAC	AAATATAACA	GCAGCACGGG	CATTTGTCTA	GTCGGCTGGT	60
GYYTGTGTC	CACCGTGACG	CTGGCGCTGG	GCTGGAGTGC	AAAAACCGGA	GCCACAAGCG	120
TGCGGCTCCG	ACGGGGAAAG	CTGCGATCGT	GGCAGCAGCA	GAGAATGGGT	GCGGGAGTGC	180
YAGAGCGGTG	CTGGGAGCGC	GCGGACGCGC	GCAAGCTGCG	CGGGGCGCGG	CTGATGCTGG	240
GCGGGGCATA	CGAATCAAG	AAGGCACACG	CGCGGGGCGA	GCTGGCGATG	CAGGTGGCGC	300
GGCTGCSGCG	CCTGCGTGAC	GTGCGGCTGC	GCGCGGGGCG	CGTCCCGCTG	CTGGCKGTAC	360
ACCCCGGTCT	GGTGAACCTC	GCGTAC				386

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 base pairs  
(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1032RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GATCTTTAAC CTCTGGACTT CAATCTTCTG GGTAAAAGCA CAAGTTTAGA GATGTATGAT	60
CCAAGCACCA AACTACAGTC TCGAGACAGC AAAATAATCC TACTTATATA AACTGAACGT	120
TGCAATCTTT TAAAAAATTT ACTAACTTGG ATTAATGCGG CGCCGGTGAG CGCCTCTGTT	180
ATTAGCTGAG TCATGCTGAG GGTTTGGCTA GGAAGCATCC GCTCTTACTA CGTAITTTACC	240
AAGGCACAGG AAAATGTGGT GGTATTCTTG ATTTCGGCGG CGTTTGTGAC ATTACTCCAT	300
AGCTCATGGT CAGCAATCCC GTTCAATGGA CATTTGCTCA ATCGTGAGTC TTCCACTGGA	360
CTTGAAATCC CGCAGGGATT TTGGCTCCTT GGCTCAACCA GGTCGCGCGG ACACCTACAG	420
CCGAAAAAAT TGCTGCTTGG ACTAGGTCCG CTGACGTGGA CATGCGAGAT GACTTTAAAG	480
TGATACATTA AAACCAGGGC TGTATGAAGT CAGCAAAGGT CTCTTTTATA CAGTGTGCAT	540
ATAATATTTC GGGCGCTTGC AATTACCTCA TGCCAGGTAC TCGTAAGATT CGCCGTCCGC	600
GAGCGCTGTA GGTATTCCTT GCTAATTAAG TTGTGATGG CCTTCTTGAT AGAGATACT	660
TTGCATTGA CGGTGTGAG ATTGGCTAT GCATTGTCA CCAAAGTGGC ATGAGAGACG	720
ACCGTTTGC TTTCATAATT CTGACGATAC AAGCTTCAGA ACAATTGCTT TCTTG	775

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1032UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GATCCCGAAA ATAGACTACA TCTGCCGCAA GCAGCGCGCC CTATCTGCAT TTCTCTCTTT	60
GGTGGTTGTC ATGTGGGTCA TCACGTTTAC CATTAGCATT CTAAGGGTAG TGGAACGGGT	120
GAGTTCACCT TCACCCAGAT AAAAGTTAAC AGGACAAGTG AAAAAAACC GGGATAAAGG	180
CATCAGTTAT GTAATAAAGA GCTATACGGC AATAAACATT TAAGTAACTA CCATGGTATC	240
TCCAGGGTAT TACTAGGTTT CCTGAAGTT TCGAATGTGC CTTGGTTACC CGGTGTTTCA	300

# EP 0 866 129 A2

GCAGGCTAGC GGGACAAGAA AAATGCGGTC CCACCCATTC CACGATTAGC GGTGGCAAAA 360  
 GTCTTAAAAG TTAGGCAAAT AAACACATAA CCATCCCTCA AAAAGCGCTT GAGCAAGGCT 420  
 5 ATCGGGGGTC AGAGCAGGTG TAATATACAT TAGAAGTGAG CGATGAACGA TAAATTGCOG 480  
 AGAGCAGATG ACTTGAAGC CACTTGGAAAC TTTGTGGAGC CCGTATCGG GCAGATCCTG 540  
 GGGCGGGATG GGTGCGCCCA TGCAGGGGGA GTGCAGAAAC TGCTGTCAGC TGGATGTAC 600  
 10 ATGGATGTCT ACACGGCTAT CTACAACTAC TGGTCAACA AGTGGCGGTC CACGGGGCAT 660  
 TTTCACTCGG ACTCGGGCGA ACGGCAGTCG AACCACTCAT CGATCTGGT CCGAGGGAGA 720

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 602 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1033RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATCTGTGTC AACAGGTGCG CCCGTCGCG CAGTCCATC GCGATCCATA GGTACTCAG 60  
 30 TGACACATTG CAGTCCAGCA CCTCACCAC ATGTGCGTGC CCCGCGCACC GCGTCTGCAG 120  
 CACCACTCG CCGTTCAGAT CCTGTCGCT CATCCCTGCG GCTTTTCAGC GCTGACGTG 180  
 CACGAACCTC ACAGCCACTA TGTCTGCGG GTCTGCGCGC AGCGAGGCGG TTTTGAAGAA 240  
 35 CCGGAACGTG CCTGCGCCAA TGTCTGCGG GAGCTCTAGT TCCTTAATCT CCGGCAGGCA 300  
 TTCAGCTGCG GAGCACTCCA TAGTAGCCCA AAGTGGTTGG ACGGCGCTTC AGGTGGCGTC 360  
 TAAGTGCTGG TGATGGTTGG TTGAAAAGTG ATGCCCCAAC AATAGTGTA AAAACGGCAA 420  
 40 AGTGGGCGCTT ACGGGGGGAA CAAAACAAGT GCTAACTACA CGGAAGCAGG AATTAAATTTG 480  
 GGAAGTGGCG TTGGAGCAGG GTATAGGAGT ACCGGAGGTG GATATGAGTG TCGAACAGGT 540  
 GTCTGGTGGC CACGCGTGGC AAGAACAGGT GGCACGGTTT GAACGCAATG TGGAGGCGCG 600  
 45 GA 602

## (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 683 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1033UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

5 GATCCGCGTC GTGAAAACA GGTCCTTGGG GTGCGATACC GCCAGCACCT TGCACGAAGT 60  
 CCGCACCAGC TGGTCGTGCG TCTCCAGGCG CGTGATGATG TCCTCCACCG AAAACACCTC 120  
 10 CAGCACCGTC TCAAACGGCG CAAGCTTCAC CACTGTGTCC AGCAGCGACA GAAGCCCGCT 180  
 ATAGTCCAGC CCACTCATCT CCCCTGCCGT GAGCACCTTT TTCATGCGCG AGAGTAGTGG 240  
 CCGTGCCTCT GCGTCGAGAC GCACCATCAC CCCAGGTG AGCTGCAGCA TGTCACCAG 300  
 15 CCCGTTCAAC GACCCACGCG CGTGCTCCTC GGGCGCCTCC AGCACATCCG CCAGCTGGCT 360  
 CATTCGGTCC TGGATCCTCC ATTCTCCAT CGCGATATCG ACTCTTCCGA AGTAGCGTTT 420  
 TGGGGTTTGT AAAAGTAAAG GGCACCTTTC CAGCACTTCG CCACTTAATG TGTGAGGCA 480  
 20 CAGAACCAGG GCCCTATGTT GCGGAGTCA AGGCTTGCGT CGCTATATTC CGACTTCAGG 540  
 AAGCTGCAAG AGCTCAATCC AGATGGGTTC CAGGCTAACG TTCTAACATG GAAAGACCAC 600  
 CTGATGAACA CAGTGTGGCG GGACGAGCTT CTGATAGAAG GGGGCGACAA GCTGCTGGAG 660  
 25 CGATTGAGCA CCAAGGAGAC GGG 683

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1034RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

40 GATCATATTG GTCTTGGGCG CAGCATGCGC TCTTCTGGTT CTGAGCCAGT AGTATGATAG 60  
 CATGCCGCCG ATGAACCTGG CAATGGAGAA ACTAGGTGAG TTGTACATCC CGACGCCAAG 120  
 45 GGCAACGCCT GAGGGTAACC ACTGCGGCCA TCTGTACTTG TCCTTATCAA TACAATTCTT 180  
 TACGAGGGAT ATGACTGCAA AGATGCTTCC TAGGATGATC GAACATTCCA GTGCGTATGG 240  
 TGGGAGTGCC ATACCCATGA CCAGACGTGC GCAGTCTATC CATACGAACG CAGTTGGGAT 300  
 50 CCGGAATTGC TGGCTGGGGA TTTCGTAGAC CTGTGTGTAA AAAATGTACA TTACGCTAGA 360  
 CAACACGATC GACCAGCTGG CGCGATAAT CTGCGCGGTA AACTGAGCCC TAGGAGAAGC 420  
 ACGATTAAA TGCCCTGTCT TAAGATCTTG CATTAAATCG CCGCTTGCT GAGGCGCCGC 480  
 55 CTCAGCTATA CTTCGGCAA CCAAATTTAT TAATACAGCG GCCTTGTGAT CCCTGGGTAC 540

# EP 0 866 129 A2

ACAAGAGOGA AAATGATTTG AGCCAGCTTT CCGATGCCGC TGAACGGGTT GAGATCGGTT 600  
TCCCCAAGAC CCGGACGCCC AAAATCGATA GAAAGATGCT ATAAGGAGAG CCA 653

## (2) INFORMATION FOR SEQ ID NO:99:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1034UP

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATCAAGCAC AGCGGACACC ACCAAAGCAG AACCACGGTA CCATATCTCT CACACACGGC 60  
TCCCACTAGC ACAGGGCTC CACCTGGCCG CCTGGGCTC GGGCCCCCGT CGGCATAAGC 120  
ACGTGGGGGG ACCTATTTAG TTCCAAAAT ATTGTTGTAA CAGTAATAAT ATCCTCATTG 180  
AGGACATTTT AGTTGTACAC CTGAAAAGAA CAGATACTAC ACTTGATCTA AGCCAAAAGG 240  
CAAAGAGATT TGGTTTCTAA AAGAAAGAGA AACATGCCTG TAAGAGGGAG GGCCATGCA 300  
CATTTTTTCT CTCCTTATAT ACCAAGTAAA ATTTAGAAAA AGAAACGACG CGGCTGCTTG 360  
GTGGGGCCCG TCTGCCTGGG ACTCCAGAGG GGCTCAGCA GGAATCCTGC ATCCAGGGCG 420  
ATGCGATCAA GCTCTGAACG CCCATAGCTG CCGCCATACA CGCGCCATT CGCGAGCTTT 480  
CGTTGAGTTC GTAAGCCATG AAATCACAGT ATACGATTCT CGAGCGCAAG TTAAAGAGAG 540  
CCCACTGGGC ATACTGCTAG GCTTACAAT GCGCACCAGC TGCGAAAGCG GAACTCCAAT 600  
AGTTAAGGGC GGTGGCAAT AGTATCTGCT GCAAGCAGCT TCTAGAAATT GTAGATGAG 660  
TGGTTTCATG 670

## (2) INFORMATION FOR SEQ ID NO:100:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1035I1

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATCTTTTGT GGAACCAAGA TCACCACACA CGAATATGCG ACGCCAAGCG CCGGAACGAG 60  
CCACACATGG GCGCGGGCGG TAGCGGTGGG CCCAAGCAAG CGTATTTTGA GGACCTGACG 120

TGCTGTGGGT GAGCAATCCA GGGCATACTA GGOCCAGGTT GTCAGCTGAA AGTGTGTTAC 180  
 CCGGTATCGG TATTACCOGG CTCGTATAAA TGTTACCOGG ATATGGTGAA GCCAAAATTT 240  
 5 TCCACGGCGT AAACAACAGG AGAGTGTACG TGCATATGGC GGCAGCAGCT AGTGTAGCCT 300  
 AGTGAGAAGA AGGNCCTGTGA GCTAAGACTA GCGAGGAGAC GAGGATTGGG CACTGATTGC 360  
 GCGATGTGGA TATTCTCTAC GCGCTGAAG AGCAATGTNG NATATNNGGN CGGCTNGTN 420  
 10 GGCAACCNGN GGNCCNGNGG AGAGNACCGA GNTTGNNTNA NGGNGNGGCG CNCANAACCA 480  
 ANNNVINCNN CAATCNCCTA CNATCAANNC CAANTTNCN CNNNCANCCC CNNGNNNNAT 540  
 NNNNATTCNN NNNNNNN 558

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1035I2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

30 GATCCTTAAA AGCTGGCCTC CGCAGATAGA CCTTCTGCGC AGAGGCTGGA AACCTCAACT 60  
 AGCAAGTCGC CACCOGAATC AGATAAGCAC TAGAGTCGTT CCAGTAACAG AGGAAGCGAT 120  
 CAAGGAAGAT AGTAGAAGAG GACACTGCTG CCAGGCTTGA TGGACAGAG GGTTTAGCTT 180  
 35 TCTGTTGAAT TTCAGAGTTT CGCGCTTTG TTTACTTCGC TTCATTCCTT CGTGTAAGA 240  
 AGCTGTTTGC AGGATGTCAT CATTTGCCAG TCGCCAGGTA GGGTATTGCA GGGCOGACGG 300  
 AGTCGGTGAA ACAGAGTCAG GACCGAGAAC GCGATAGAC AGGCGTTTGG TTTGTAAGCG 360  
 40 GTGAGAGCTG AAGCAGCTCA AGAGGCCCCG CTTGCTCAGG TTGTGCGGTG GCGGTAGAGC 420  
 ACAGCAGGGC ATCCCTCGTC GGTTGAGCGT NCGGNCAGNA GCCCAGGCGC NTOGAACAGG 480  
 GGGTGTATTAT NANGANCNAC CGACCACAAA CACGCTNINA TTGNNACCGG CGGCCAGTTN 540  
 45 CCTCANCNTG GTTCCCGNGA CTGTGTTTNN GAGCCNATCC TTGGCNCCTC GGCNNAGNAA 600  
 AAAA 604

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1035RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GATCTTAAAT TGTTGCATTG TGACCTGAAA GTTGCCCCGT AGACGCTGCA TATTCAAGGT	60
TTCCATTTC ACGGGACGTA ACCTAATCCG CTGCACCTTC GACAAACGAC TAATGTATCT	120
GTTCTCGAC TCTGGGTCAT TCGCATCCCC ACTCCACTGT ACTTGTCCTG ACTGTAGTTG	180
TTGAAGCTTG AGGTTATCTG CCTCGAATGA CTGCAGTAGT AGTGATTTTC GTCTCCCAAT	240
CGTTTCTATG GACCGCCTGA ACACCGAAGG TGCTCCGCC TGAAGGACT CGAAAAGCCG	300
CCGCTCCTCT GCAGAAGGCG GGAAATAAGA CATAACTTGC TCATCGCGTA GGTAAATCTA	360
CGTCATTATC CGGCTCCACC ATGTTCCGCT GGGATAAAAT GGTGTTTCTT CCAGGGGGCG	420
GGGAATACCA CCCACTCTCC AATCCTGCC CCGTTANIGA ATNGNTTINT TNATGGGGNN	480

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1035UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GATCTGGCGT ACGGTACCGA TATATTCAA CTGAGGTATT CGTTAGAACA GCTACCTTCA	60
GTGGTCCAC GCTATATTGC GTTGCAAATA TGTTTGGTGA CCTTCTGGC TTATCAGTGG	120
CAITAAAGAG CGCGCTAATG GGGACTATCT CTTTACTGG GCCAGTGGTC TCCAAGAAGG	180
AAGCATTCCT AATATATTTT CGTGGTPTT TCAGGATGCC ATAATCTGGT ACACTCACAA	240
ACAATTTATG TTGCACTGGG TGAGATGCAG GGGTATTAGT ATTTGGAATC ATGTGGGTGA	300
TTGTCCCGGA TGGGGTGGC TTCAACAACG CAGAGGAAAA AATATCCCCA GGGGGATATT	360
ATTTGTCGAA GCAAGAATCG CTTCAGTAG GGATTGAAGA TTCTCTCTTG ATACTTAAAG	420
CTGAATTGGT TCANATGGGG TCCAACGAAN GANTAGNTG GATGNCCT TNGGGGGGGG	480
CC	482

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1036RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GATCATATTT CAATGCAAGA GCTCATTAA TAGGTATTGT CTTGAGACAT GCGCTCAAGT	60
CATTAATGTC ATGGGAAAAA TGCAACGTTT CACCTOCTAT CTCCAATGTA TATTTTAGCA	120
TTTCAAAATC ATGTTTTCTG TTTACTATAA AGTGCAACCC ATTCAAGTCT GCGGCTTTCT	180
TAGTAAAGOC TCTAAAGGCG TAATGCTGCT CTTGTATACT GCGTAGCTGT GGGTCAAAAT	240
CGGTACAGG CTGTGAAGA AGAGCGGTAA ATTGTTTCAG AAATTCGAGA TGCAATATTG	300
GTATGCTTTT AACAAGTGCA AAACAAATAC TTTTTOGGAA TCTTGGTCAT CTTTCATGGG	360
TCTTAATAAT ATGATGTGTA GTGGGCTTCC GAAAAAGAGG TCACCACTCG TATTCCTAAC	420
CCTTAATTAC CTCAGCAAA GCAGGGCTTC TTGTAACAAA GTTTCGGGAC CTGGACTCCC	480
CATGGGCCCC TCCAATNIGA TTGGNOGGAT NTGNNOCCCT TCNGATANA GGNCTOGATG	540
GCCANOGGAA NCCNTCTAG TGATNTCCCN CCCCTTCAGT GNNNCCNCTN GAGGTTTGA	600
NGGCNNNTTT TCCNIVINGG GGNVIVICTG GNAACCNCCC CCTINT	645

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1036UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GATCCCTTTT GGTAAAGAGA GGTGTGGGCT TGTATTCAAC GCACATCGTG GGCTATTTGT	60
CATTACTCTG GCGCCGTCC AGAGACCTAC AGGTATAAAT TCCCATCAA GTGCCACCAG	120
AAAGATATGC TATACTGGTT TTGAGCTTGA GCGACTGTTA ACTGCAACCA GCGGGACCGA	180
ACGGGGTAGC TTTTACTCAT TTATTGAGGC TAAATTGGAA CCAGACATCA CAATTCTGCT	240
TCAGTGGGAA ATGGACGCAT ACAATCCAAA AGCCAGAAG TATACTGAAA TAAAATCCTC	300
TGTGGACTTC AATGTACGAA ATGTCCGCA CCTGAGCAAA CTGCTTAAAA TATGGGAACA	360
AACAGGGGTG GTCCCATOCA CTGATATCTT GTAGGGGTCA GAGACCCATC AACCCATGTG	420

TTGAAACAGN CGGCOCTTAT GGGTGGTCAA ATCGNAGGAA AATCTTTTTA GGGTCGNOGN 480  
 NAGGCANCAC TTTTITANT TATCOGAGTG CAANATGGAA ATAANCATCG TNAATTTGGA 540  
 AGGTATTTCC CGGGGNGAAC CANGCNCNC AANNMTTITN NGGGGNGAA AGANTCAAAT 600  
 TAAATNGGCC NGT 613

## (2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 606 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1037RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCATCATT ATTTCTCGG TTCGTGCCA CGATTGAAG GGCGGGGTGG GTTCTTGAA 60  
 GGATTTGAGG CGTATGAATG TTGCTCTCAC CAGAGCAAAG GCCAGTCTCT GGATCTGGG 120  
 TCACCATAAA TCTTTATACA AGAACAAGCT ATGGATGCAT TTGATTTGAG ATGCGAAAGG 180  
 GGGTACTGC CTCGAAATGG CATGTCCGGG CTTCTTGAT CCACGGAACA GAGCGGCCA 240  
 GGATGCTCTT CATAGGTTC AAAATCACCA TAATTATATC GAGAAGCAG ATGATTATGG 300  
 GCGTGAACCG GTGATGACTA AATCAAGAGG ACGCAATAGA TCATCCAGAA AACGCAAACA 360  
 TATGGAAGAT AATCCAGATG ATAAGTACGA TCCGTTGCT GAATTCAAGA AGGAAAATCA 420  
 AAGAGAAAGC AACACAGGCA CCGTGGTTA CCGTGGGAT ACATCTAACC ACAGATTGGC 480  
 ACCTGCTAGG AACGATAGCA AGAAGGCCAA GAGTGTCTCC AATGCGCGCG GTATTTCCGA 540  
 GGCTACTTCA NARGATGGTG ATCGAAGTCA GAAAGGACAT GGAAGTAAGA AGATCTTCC 600  
 ATATTG 606

## (2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 653 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1038RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GATCAAAAAA AGAAATTACA ATTGACTGTT GCACCCACAC ATTCAACGGT TGCACCCACA 60



CATTATGAGA TGCTTGATTT GGGCGAACT GGGCTTTCCA ACTACAGTCC CGAGACTTTG 120  
 GGTGCCAACC GAAGCAGACT TCAACAGTGG TGATAACCAT AGTGTGGAAG TCTAGCGAAT 180  
 5 CTAAGGATAA TACCAAGAGA CAAAGCATAA TCGTATGTGC ACAGGATGGG GCGAAGTGTG 240  
 GTCTAGAGCT GTCGGTGCGA GCAGAATACG GTGCGGGCAA TGAGGACGCC GCAGACGCCG 300  
 AGCGTGTGGG CAGCTCACGA GGGCCGGAGC GCTTCCAAGC GGTCAGACAG AGTACTAAGC 360  
 10 CATTGCAGAC AAGATGGCTC ACGAAAAGT TTGGGGTCTC CCACCCNNAN AAATAACGGT 420  
 AAGGGGTCCC CCAGTGGGCG TGTCGGCTTC GCTCTTGTT GTTCANAAAG TACGGGTTCG 480  
 ACATCTTCCC CAATGGTICA NAGAGAAGGC CACGACATTG GTTCCCAAAT CCCCTAAGAG 540  
 15 GGGGGGGGCC CTTCCTCTCT TNCNAAATCC GGGGGGGGTT TGGTTTCNCG GAGGTTTNT 600  
 TATTTTTCNA NACCCCNVTT TTTANITINA NNCNCGGTNC CCAGNNGTTT GGN 653

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1038UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GATCGGTTCT CGGGCTTCTT TAGCTGCCCG TTATTCAACG AGTCATCGAC TGAGAAAGAG 60  
 35 ATAAAAGCGG TCGATAGCGA AAATAAGAAA AATCTCCAAA ATGATATGTG GGGCTTTTAC 120  
 CAGCTGGGTA AGTCGCTGAC CAACCCATT CACCCGTACC ACAAATCTC TACTGGAAAC 180  
 TTTGAGACTT TATGGAGCAT TCCGAGATCG AAAGGGTICA ACGTCCGTGA TGAGCTGCTG 240  
 40 AAGTTCTACA AACGGTCATA TTCTGCAAAT CTCATGAAAT TAGTGATCTT GGGCCGCGAA 300  
 GATCTAGATA CCTTGGGTCA GTGGGCATAT GAGCTGTTCA AAGACGTCCC TAAOCATGGG 360  
 ACCAAGTGG CTGAGTATCA CGGCCAGGGA TTCACGGCCG AGACCTGATG AAGGTAATTA 420  
 45 AAGTGAAGCG GNTAAAATCT TAAGAGTGTG GAATTCATNC GNGGGGCAGA TTGGTTAGN 480  
 ATGGAGGCAG CAGTCGTATG NGGATTATC GOCAGAGGAA GGTCTCCCG NTCTGGAGAA 540  
 AAAGTGAAN CGNCNCCGT NGGNNTCCCC TTNAAGGAA AATNCCCNC AANNGGCTTN 600  
 50 ANNAAGGNT 609

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1039RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GATCATTTCT	CTTCAATCCC	ATTGACGTGA	ATGATGAACC	GCAITATCTT	TTTAACAGCG	60
ACAACATGCC	ACGGTATATA	ATTGTCTCTA	CCTCGTGATA	TGCAGAACCA	GGTGTTTAGA	120
CTGGCAATAT	COCTAAACTG	GTGTAATATG	GTCTTCAAAA	GTITTTGTGCT	GTCCGAATGA	180
GGGCAATTTA	GTAATTTAAC	CTCGAATTTG	TCTAAAGTAT	CGCCACCGGC	ACATCTTTTA	240
AACCGCACCA	GCGCGCGCT	TTTTATTGCG	CATCGGCGCT	GTGAATTAGC	AAGTTGTAAA	300
GGGCTACTGA	ATAAGACGCC	ATGCAGCTCT	TCATCGATAT	TCACAACCTC	GTAATCATCC	360
AATTGGTTAG	CTTGGATTTT	GGNGGCATA	TCTCTTATCC	CTAAAAAGTG	GGTTGGATGA	420
TGGATAAAAC	TGATCTTCAT	CATATAGAGA	AATTITGGGCT	CGCCCCAAGC	CAGACACAGN	480
CAATGTAGTT	TCTGTGGCA	NAGTTTNGCTN	CGCAGGNATT	ACTCGCANCC	GGGGAGGTNT	540
CACCCCGGAG	ACAAAAATTC	CCCTTTTCT	NTGGAAATCG	TNGTAGNNCC	TANCAAGGAT	600
GGGTCAAGGA	CCTGGTTGCC	ATTCCANITTT	ACCATTTTTIN	CCC		643

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 635 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1039UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GATCCTTCCA	ATAACGGCTA	AACATCCATG	TGCTGGTTTT	AACTATGAGG	GAGTITGGAGT	60
AATTTGCGGG	TCTCGCAAAG	TAAATTGACA	GAAAACCTC	AGATCGGTAA	CGAACAGCT	120
GAACGACGGA	GATTAAAAGG	AAGAGGCAAA	TAAGCTATAG	ATAAGATCGA	TAAATATTGA	180
GGGGGGGATG	GATATATTAG	AACTAGCTT	TAGACTTGAA	GATGTGCTTT	CACGCTATTA	240
TAGAGTTGAA	AAGGTGGTGC	GAGTCAATTA	TCAACAGTTC	GTACCGAGGA	CTCCAGATGA	300
TCAATGGTGT	ATCCAATCCG	AGCTTCTTAA	TCCGCAAGAA	GGATCCGAAA	GCGCTGGTGG	360
CGCTTTTTC	GCGGGAATC	TGGTGCTTTT	AGCATCAATG	ACCAGGACTT	ACCCATTCOC	420

GGGGTTGGAA GGGATAGGCG AACCCCCCNC CTCGAGAAG AAGGGCCACT TTACGGCAGG 480  
 GTTTTCCAAG GCNAACCTGC AACGCCNNITG GATCTTTTTA AAGCNITGGG GGATGNTCAA 540  
 5 TAANAATTCTN GAGGCGNAGA ACCTTTGGCA ATTGGAAAAN NNNTTTCOC C GNAAGAAAGC 600  
 NNAGGGANCC CCCCCGGNCN NATTTTGGGA ATGNC 635

## (2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 648 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1040RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GATCCAGTGT ACCAGGTAGC GTCAGGCACT TCTAGCGCAA GGGCCGCCGT AAACCTTGGC 60  
 25 CTCTCACAGC ATTTGGGATG AGTATGGGCC ATCTTETAGG CAGTGAGTG ATCATGATGG 120  
 GTACAAAAAG AAATGATTTC GCCCAGGATC GAACTGGGGA CGTTCTGGGT GTTAAGCAGA 180  
 TGCCATAACC GACTAGACCA CGAAACCACT TTCTGCAGGC TCTTATTGGA CAGGTGATGT 240  
 30 TAGCGCAGAA GAACATGAAC GTGATAATAA TTCAGAAACC TCTTATGCTA AAGTGAATT A 300  
 CTATTGCTTA ATAACCTGAA GGAATAGGC ATTGCCAGTA TTGAAAATCG GGCTTTGGGT 360  
 TTATTTGGCTA ATTATATTAT TNNCANTATA TATATATAAC AACAGGTGA AGAATGNTG 420  
 35 TCGNTGGTTT GGGGGCGATA CCNAGAACC AAAGTAGAAG TTGACAAGTT GGTGGNAGNG 480  
 GTTCAATTCA GNACTTCATG GCAACNTTTA CNATNNTTIN NINAGAACC CCNATTANTC 540  
 TTTNNCTTCG GGGGGTCTCN NNAACCGGA AACAATNTIN CNGAAGTGA TTTGGGGGAN 600  
 40 GTTCNCGGT NTTTTCNCC TTGGGTCCA AATTGGGCGG GAANCCCT 648

## (2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 613 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1040UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GATCAGCAAC CTCTCCGCC GTCTGTGTCC TGCTTTTACC GAGGATACGA AAATAGCCGC 60

GGCTCTGTTT CAAATGGCGA TGCTGACGAG CAAACCACGT CTTCTGATGC AAGCAGTACT 120  
 AGTTACATTA TTCTAGAGAT GGAGCAATG OGGACAGCTC TGCGTCAGTA TTTGAGGGCA 180  
 5 ATCTGCCAAG ATGCAGAGGT ATCCGCCAGT CTGTCCCTAA CGAAATTCCT ATTCAAGAGG 240  
 ACGATAGACA AGCGTGCTTT TACGCCAGAA ATCCTGGAAG ATATTGAATC TCGGGAGCTT 300  
 ATGGATGTAT ACAACCTCGA AAATCAAGTT AAATTCCAAA AAATGGGGT TTGGATAGAA 360  
 10 CTGTGAAGCT ACAAGTCTC GCTAAAGTCC CTAAAAGAAA AAATCTTGCA AGATATGACT 420  
 ACAATTATGAG GTTTTCNCC AATTTAAGGA GAGGAGGATC CCAGNGACNA TTTAGCTCTC 480  
 AGAGATTCTT GGNITGGGAA AATTTTTTAG GTACCNATNC AGGTTCCCGG AATNAATGIN 540  
 15 NATINTTTAC ANTCGGCNG AAATATGCTC ANAGNNAAG TTTGGGCACC CCCCCNCT 600  
 ATGANGTTTT GTC 613

## (2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 649 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1041RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GATCCTCCAC CAGAGCGTGG GCGTCCATA CCTCTGTTC ACGCAGTGGC GCGTCTTGT 60  
 35 AGAAAACGCC CAACAGTTGT TTGTAGGTGA ACTGTCGGG GAATTTCTGG GCGCGAATTC 120  
 GCTCCAGCTC CTCTTGGAA AGCTTTTCAC GGCGCACCA GCTTCTCATC CGGTTC AACC 180  
 AGCGCTTTTC GTGAGTGGC CGCTGTCCG CCGCTCTGC CGCAGCAATA TCTGGGCGCA 240  
 40 GATGCGGTAC GCGCTCGCC ACTTCATGAC GGATGACGCC CTGCGGCTCT TCTGTGAAGA 300  
 ACTCGTAGTC CAACCCAGCT TGAACAAAC AACTGCTTCA CGTATGCGG CCATACTTTC 360  
 ATCGACGTCT CGAGATAGTC GCGCGGAGGA GGGCAACAA ACAACGCGAG CCGCGGGGT 420  
 45 TTGGGCGATG TGTGANGTG GCTGCGCTG GGCCTTACC AACGACGAAT AATGTTGGAT 480  
 TTNGCCCTNG TCCNTGGG GVNCAATCA GAATGCCGN TCAACCNAN CAAAAGGGAC 540  
 AATNGCCGG AACCAAGCG GTTCCANGCC GAAAGTGTAT ATTNCCNAC TTTCCGGTA 600  
 50 NAATTTTTNT TTNCTG GNVGTGNT NACCNCACC CCNAAATAA 649

## (2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 645 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1041UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GATCTGCTTC	CTGAAAATG	GCGTCTCTGT	CTTACTGGTA	CTCTCAAATA	GCTACGTCTA	60
GGTACAGGGC	CATTTCOGGA	TCCAGGCAC	GGTCCACTG	CAGGAGGTAC	AACAGGATAT	120
CGCACGTCTC	GCCCTGOGCA	CGTCACTTGG	AGCCTCCCGT	TCTCGTCTTG	ACGTCTCAAT	180
AAGGTACGCC	GTTTCTCTTC	GCCGATGGAC	TGCCCTAACT	GTATGGCCTG	GCTACAAGTC	240
TGTTGGTTTC	GAGCAGCCCA	CTTCTTTATC	CACCTCAAG	GTTTACCGCA	ATCCAGCAAT	300
TTTGGTCTCT	GGCAGACCG	GATATCATGT	GACTTAATT	CGTCAACGTT	CAAGAGTTGG	360
GGGCGGGGCG	AGCAAATTTA	ACGGGGGCGN	CGGTGCTCC	CCCCGATCGG	GGGGGGGGGA	420
GGGATATTAC	ANTCCANTGC	CGGCCAAATC	TTNGTTTACA	NAAAGCAAGC	ANANTCATAG	480
TGATTTGGGG	GAANANCCCA	AGGTINNGGC	CNCCANGGNT	CAAANTCNCC	CNTTNNTTTT	540
TGGGTTCCTG	NOGGAAAANN	CCATTTCNCG	AGGGGCCNAG	GNCGGGAAT	TTTCCCGNGT	600
TNNAGGGGAG	TCNNTTNGGG	GGGGANNNG	CCANAGGAAG	GNGGT		645

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 682 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1042RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GATCCGTGCT	GCGACAACC	GCCAGAGCTC	GCCTACAGCC	CGTATATATA	CGCCGGCTGC	60
CGGCTGCGG	CATGCGATT	GTCCACCTC	GCTCTGCTTC	GTCCCGCTG	CCGTGCTCC	120
ATGGGACCTT	TCATTTAGTG	TCTCGGAAC	GTTTGAATG	TACCTATOG	TGGTACCAOG	180
TTGCTGCGG	TGCGTTACT	ACAICTTCTA	GCGGGACTG	AGTCACATGT	CTGCGCGGC	240
ACTCCTTTTC	TGTAGATAGT	CAGACGACAG	ATAGTCGATA	GTTGGAGATT	TGGGCAACAA	300
TAGCGGTGGC	CATTACGGCT	GCCATTGTT	CCCATGTCAT	TGGGAGGCTG	GGNCCACCC	360
ACGGGAATC	TTCCTGTTT	AANCTNANA	GNCCNGGGA	ATGNAAAACN	CTTCTTTTNG	420

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NCNGCNGCAA ACGGGCCTNN AGGNGATTTC TTGNGGATT NGGGANGCAC TGAGAATCCA 480  
 AGTNGGAAGG GGGCTNNAAA AATNGCTCCG GGCCANNCT NCCCAAAGGT TINAAAANCN 540  
 GCNTAAATINA GGCNCAGAAG AACNCGGGA GGAANCANAC ANAAANINGG CCCCNOCTGA 600  
 AGGAAAGGGG CNGNNNITGGG GNGAANCCC CNGNAACGNT NTTTCTTAAA GGANAACAAA 660  
 NGGTNCAAAA AAAATGGGGG NC 682

## (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 649 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PAG1042UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCGCGTCC TCGAGCGACT TGTGAGGGTG AAGCTGATA CGGTGATGGT GGTGGTGATG 60  
 GTGGTGGTGA TGGTGGTGTG CTCTGCCCTG CGGTATGACC TGGGCTGTTG GCGTGGGCT 120  
 GTTGCTGCCG ACAGCAGCAC CTGTATCCGC AATGCCCGAT ATGCTAGAAT GGAGCAAATT 180  
 AATGGACTGG TCTGCATTCT TGCAGAGCGG AGCCTGCAC ATGCTGGATA TGCTTACGAG 240  
 ATCGCCGGAG GATCTTTATG TCTGTTTCGC TATTCACCAC GTGGTGTGG CAGTGTGTT 300  
 GTTTCATGAC CAGCCCGTAT CTTCANAGGA GTCGTAGTTC ACGCATGTGT GGCCAAAGCC 360  
 AGTCGAAGGA GGCCATCCTC CAGGTCGGG GAGTCCCGG GGGACGTTT CACAAGCCAA 420  
 GGTACCTAGA AGATGAATCT TTTTGTGANT ANCGTGGG CCGCTNGGCA ATTTNAAGTC 480  
 GNAANTGNIG AACTTCGGAA AGTTGGAAAT TGGNCCNAGG NCTTCTTCCC CCGNCCNCT 540  
 TNGGNAAGCA AAAANAANA ATTAATTGNN CCCCCCCCCG CAAATTTGNG GTGNGAGAAA 600  
 TTCCAAACC TTGGGTTAAT AGTAAGGNC CCGTGNCTG GGCCCNCCC 649

## (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 648 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PAG1043RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGATCGGCGA TGGGATATAA AGAATTGCTC CCTGATTGAT TGTTGTTGGA AGGAGATGCA 60  
 GATGGATTGT CCAGAAAAAC CGTTTTTAAG ACTCGTTCAT CAAACTTGTT AAACCATTTG 120  
 5 CCATCGGCTT GCAGTATATT GCGCAAGGTT TCGCGGATAT TTCTTCTGTC TAATGATAAT 180  
 CGCCCCACAG GCTGGTCAGC GCGTGATGCA GAGGCGAAG AGGGTGGGTC TATCATAGGA 240  
 GGAAAGCTTT CTTGATCCGG GGAGCCGGTC GGGCTGTGCG TTAAAAATGG AGGTGCGTCT 300  
 10 AATGAAGACA TTAGCTGGAC AGGTCTAGGG GCTTCAATAT CAAATTCATC ATCCGTTTCC 360  
 TCCTGTCTTT CTACGCACCC TGTCCTTATG TTTAAGATCT CAAGCATAAC CGCAGGAGTA 420  
 CCTCCAAATA TGATAACGGT GAGAACCACA ACTACCAGCA CAGTGGCCAG AAGAGGGGAA 480  
 15 CTTGGANCTC GCGCNNGGA CCCTAGCCA GNGNCACTCC AANAGNAACC CCNANCCCG 540  
 NCCNNNNGG NAACNNCCTN NNTTTNGNNT TGGATNTCCC CNANNANINN AAAACCCCCC 600  
 CCGCGGGIN TTNNGGGNC CCNNNNNCCC MNNAANGGN AAAANNNC 648  
 20

## (2) INFORMATION FOR SEQ ID NO:118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: 1043UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GATCAGATTG TCTTGATGAT GAGAAGCTGG CGCATCAGTA GAGTGAGAG AAGACCCATG 60  
 CGGAACAACT GTACCACCCA GGGACTGCCG TCTTCCCGGA ATGTTGGGAA AAACAACAGC 120  
 ACGGCTGAG TCACTTACAG TCGAGTGGG TTGGAGGCG GACAGATTAA AAGAAAAGCG 180  
 40 CTCGGGTTT GTGAACAGNT CAGACCAAAA CCCAGGTCTT GCTGGCGGA ATTCTTGCT 240  
 TACCTTCACA TNCAACTTAG TGTGTTGCT GTCCNAAATA TACTCCAAAA TCTTGATCGG 300  
 CGCACTCTG TGGTTCATGT CTTGCACAAG TTGACCACTG TATTCCAGTT TGACATCAGA 360  
 45 GGGCGAAATC ATCAGTGTGT GCGTTCACA GAGCAAATAA ACTCCTTTAC TTCTGCAC 419

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1044I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

5 GATCTCCGAC TCCGCGCGTC TGTACCCGTC ATGCGCCCTCT GTAGTCGCGG TCATGCTCAT 60  
 OCTACCCAGC CGCACCAACC AATGCTCGAT GCAAGCTCAA TGCTCGCAGC CGGCGACTGC 120  
 10 TGTATACGTG CTGGCTTAGG GTGGGGACGT CCTTTCACGG CCGGGCGGCC AITGGAGTCC 180  
 AGCAAGCGGG GAATGCTGTT GTGACTGTAA CACCCATACA TTGCAGGCGG TACATTTCAA 240  
 CGATGGGACG CGAGTGGGTG GGGAGCTGGA CGGAGACCGA ACCGGGGGAG CCAGGGCGGC 300  
 15 GGGCGGCAAT CCGCAGGCGG ACCCAGCGGC CGACCAAGCG GCGCTAGGC CGAGGGCAGC 360  
 AGGCCAGAGC CGCGGGCGCG GTTTTTCATG AAAAATATAG TGGCTACAAG AGGGATAGGT 420  
 TGGATATACC AGAACTCACT CGTAAGAGAT AATTAAGCAG ACGAAATGGT TGTTTGAGG 480  
 20 ACGTTGSTAT CGCGAATCAC AATAATTGA CAAAAGGTTT TTGANTCGGG GAGGTGNTG 540  
 TTGTTGNGGG NCGNAGACCG CCNTATTANA NGAAGNGAG GNAACNCAAG ANNGGGGCAN 600  
 GGGGTC 606

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1044I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

40 GATCTACAGA ATGCAGGAGA CGCTGCTTGA CACAACACAA ACGGCTGAGA CGGCAGGCGC 60  
 GGCCGAGCGC GTGCAGGAGG CGGACCCGGA CGGACAGGGG GCGGGGCTCG ACTGGGGCGA 120  
 GCTGCTGGAG GTTGTGGAGC GCCACTACGG GCGCGGGCGG TCGCGGCTGG GGACGATACG 180  
 45 GTACGAGGCC GCGCGCGCGG GCGGGCTGAC GGGCGGGCGG GCGCGGGCCC TGCGTTTTC 240  
 GTACGAGGTG GGGCAGCAGA CCGTGCCGCT GCGGCTTGCT GCGCGGCATG GGCACGGCAG 300  
 CGATCCAACA GGCTCGTGAC GGTGGAGCTG AGCGCGGAGG ACCTTGAGAG CGCGCTCGCG 360  
 50 ACGGGCGAGA ACGCAGCGGT TGCGCAACCC GGAGCTTTTG TGGGTAGNCG TGTTCAACTN 420  
 AGANTCGGGA CCCNVTINCT NNTGCTNNG NACTNNGNG TGNTNNAOEN NGAGCTGAGN 480  
 TGCAGGNCAN GNNAGNNNC CNNNCNNOEN ACGCCCNCCA ACCCNNGAN CCCNVTITTT 540  
 55 TAGNNNGNTT TAANNCCNVC CCCNNNTINN GNGNGGNTT CCCCCTTGT NTNNNNNNNN 600



ANTTNTTCATT TTCCCCCCTT CGNAGGNITN NT

632

## (2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 626 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1044RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GATCGGGTGC CTAGTGGGAC CTCATGCACC GCTTGGAACT GCGGCCCCAC CCATGTCAGC	60
ATCTTTATCT TGCTCGAACC TGTCACCGAG TAAACAAGCA CGTCATCCA CGTCTCAGCC	120
TTCCACATG GATGTTCAAA CAGCCAGGCA TGGTCAATGC CTCGTTTGTG AACTATCTTG	180
TGTAATGTT GTAAGTTGCT CGAATGAAGT AGCAGTAAGC ACTTGGTGTG GCGGACGAAT	240
ATTGTCCGA GCGGTTCCGA GTACAGCAGC TCTTCTACAC CATAATTGGG GCCAAGCAAT	300
TCTGTATATG TCTGAAGTAG ACCCAGGCCT CTCTCGTCCA TACTGGAGTA CACCAAGAAG	360
TCCCTATTAT TTCGGACCAC CACAAGTTGT CGAACGGCAT CAACCACAGG GACACACTGA	420
GCACCTTGGG ACGGAATGGG ATTTACTAGC TCAGCCCTAA GCATCTTATG ATGAGGGCTG	480
CCCTTAGCTT GCTGAGTGCT TCGGGCTGCC TGCTTGTTGGT TGGTGGGTCC TTTCTTAGAA	540
CGATTGTTCA AAACCATGAT GATGGGGTTT GGTCCGGCCN GGTGATTTGA AGATTTAAAC	600
CGGTCACAAG GAATTGACCN TGGGGG	626

## (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 545 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1044UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GATCTCCTTG ACCGGGGGTG GCGCTCTCTT CTGAAGGTG ACACGGTGCA ACTGCTACTG	60
TTAGTATGGG TCCGGTCTGC GGCTCCGCTC CAGCAGCAG GGAGCCCTGC TCCGCACTCA	120
ACATACCCTC TTGTGCAAGT TAATGGTGTA CTGGGAGTA ACAACGTCTT TCAAACCAGC	180
CATTTGGGCT GCTTAATTAT CTCTTACGAG TGAGTTCTGG TATATCCAAC CTATCCCTCT	240

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TGTAGCCACT ATATTTTTC A TGAAAAACCG CGCCCCGGGC TCTGGCCTGC TGCCCTGGGC 300  
 CTAGCGCCCG CGTGGGTGGC CGCTGGGTGC GGCTGGGGAT TGCCCGCGCC CGCCTGGNTC 360  
 5 CCCCCNNOGG CTCNNCCAG NTCGCCACGA NTCGNGCCA TNGNNGAAAT GTACGGNTTG 420  
 AANGNTGNT GTNAAAGGCA NAAAAGAATC CCCNNTNGT GNTTNNAAAN NNNGGCNNNN 480  
 10 NNNNAGGGAN GNCOCACCN ANNNAGAANT TTAANAAGNG NNNNNNANA TNNNTGATN 540  
 NANAA 545

## (2) INFORMATION FOR SEQ ID NO:123:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1045RP

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GTGGATCCGT AATGTGGGTT TGTAGGCAG AGGGGATTCG ACGGTGGCTG GGGGCCATTC 60  
 TGCCCGTTAA TTAGATGCCA CCAATGTGT TTCACATCCC AGGCGAAGGT TOGCATACCG 120  
 30 CCCACATACT TGGGTAATTC ATAATGCGC CACATGACGG GATACTAAAC AAAGCAAAGT 180  
 GTCACATCTT TATTTTCTGT TGTGGTCAA AATCGGGGG TAGGCGATCA ATTTGCATAT 240  
 ACAACACGAA AGGGGATCGG AGATTTCTAG GTCACAGGAC AGTTTGGGGT TTTTATTTGG 300  
 35 TGTCTTTGTG AAACCATAGG CACTTGACAT AGGAGCCCTC TTTAGAGTAC AATAAGCAAC 360  
 TGSCAGCAGC CCTACAGCTT GGCTAAACT TCTCATTAT GTGAAACGGG AAAGACGACA 420  
 ATGCTCTGA AGCTTTTCAC GCACTTTTG GTGGCCCAAT TGCATNGNTT CGNAANTAN 480  
 40 NNITTININN TNGGNTTTT TTGNNNAAA AAAACNNNA AAAAAGGGG GGGGGGNTA 540  
 AAACCANGA TNNITTTTTT NGGGNGGGG GGGGCCCCCT TTTNINAAAN CCNNCCCCC 600  
 CNNNAAANN GGNNTTNNN GGNNAAAAA TTNNTNNN NTTTTINGEN NNCCNNNTT 660  
 45 NCCCCCCCNA NNGNCCNNC CCNNNTTTT TTTTNNNA NNAAANCNC CNGGGNGG 720  
 CCC 723

## (2) INFORMATION FOR SEQ ID NO:124:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1045UP

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATCTAATAA CCACCGTTG TATATTGGG CGGTAACTA TATATGGGA TCATATAAGT 60  
 10 GCTTAAAAAC ACCTCACCCG CAAGGGGGTC ATCTATAAAC AAGCCATAGT GTGTGTATCT 120  
 TTGCTACAT AGCATCATGA CTATGTTGG CACGCGTCAT TTGCACTGTT TTAGCATGTA 180  
 ACTGGCAGAG CCAGCAACGA ACAGAGCTAA TTTTGGAGGC TTACCATACT GTTGTGCTG 240  
 15 GATGTTGAAG CACGGCTGTT GTGGATAAGT TTAGAACCOG TCGCCAGCAC ATTCTATACC 300  
 TGAAACTACC AGTTCAGGG GACATGTTCT TGTGGCTTT GACAGAAITA TTATTGTAGT 360  
 CCAGTTAGAT GTACTACCAT TGTGCGCTA ACATAATCAC CATTTGTCATC TCTGGAATCA 420  
 20 CGTGTGCCA AGCATATTAA TGTGTGTACT TAACTCGGT ACTCCCTTTA TCGAAAGGCA 480  
 TCACGGAATC GCCCTTCACT AT 502

## (2) INFORMATION FOR SEQ ID NO:125:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1046RP

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATCGCGCGC GCAAGCCCGT GCGCGAGCTC GAGCAGGTTT TCGAGGTGCG GGGGCAGCGC 60  
 40 GTCACACGAG TAGGCGTAGG GATAGAGGAT CTCCTCCGAG TACGAGTGCA GGTCCAGGTA 120  
 GCGGTAGATG TCCAGCTCGG CCTTGTGCTT GTTCACTAG TCGTTCCAGC TGCGGCGCTC 180  
 CACGGCCTCG AACGGCTGCT GGCGCTATA GTCGCCCGAG CAGGGGTAGG CGTGCTGGCC 240  
 45 GGTCCAGTGG TAGTGAACG AGTGGTCAAT GTCGACGCA TCGCAGCCG GCATGTACGT 300  
 GGGCTGCCCG TTCTTGGCGC ACAGGCGGTC GTGCGTCCAC GTGTACGGT AGCGGTCTGG 360  
 GTTGAACACA GGGATCACCA GGAAGTGGAG CGCGTCCAGG TAGCGGTCTT CCTTGGGCGC 420  
 50 CCGCCATAC CGCGAGAGCA GACGCTCCAC GACAAAGCAC GCCGTGCTCA CGCCAATCCA 480  
 CTCGCGAGCA TGCAAGCCGT CCGTAATTAC CACCG 515

## (2) INFORMATION FOR SEQ ID NO:126:

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1046UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GATCCGGGAG CTGCATCATT AGAGGGTCTG GACTTCGGGA AGACACGCAG TGGTATGTCT	60
GTAACCTTTC AATTTCAAAT TAATTCCTCT TTCATCGTAG TTCGGGCTGC TGGGCGATCT	120
CCGACACAAA CGGCTGAGTC GCTGACACAA ACAAAAATC GACTACGGAA AACGACTAAG	180
CGTCGCAGAT GCTATATATA TACAACCTGG TTCCTAATTA GGGTTAGATC CTTGCCGAGAA	240
ACAGACGTTG AGCTTGTGCA CTTTCAAAAT TTAGTCCCGT CTCGGAAGTT TCCAGGCAAC	300
ACGAATAACA ACACATATIG CCATGGCATC GGTAACGTTT AAAGACAATG CGGAAGTGAT	360
AATGATAGGT GAGCAGGATC GGAGAAGAGA GCAAGGTATG GCCAGGCCCT GGATAACGGG	420
ATTTCATCGAC GCGGATATCA TGTTGGCAAAA GGACGGTCCG TAACTCATAG TAGACATCGC	480
CAAAGAGAAC TTCGACAGCT TATATTGACA TTCGTCTCTT TGCTCTACAT TGTGAGGCA	540
AAGATATAAG AGAGTATGGT G	561

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 685 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1047RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GATCGAGTAG ATGTTCCGCA GCGCTGGCAT CTTACGGTCC CGGTACGTCA GGATGAACTC	60
GCCAATGCTG GTATCCAGCG TGAACCCGTT GAGCCCTGTC CCGTCTGTTA GCATGACGTG	120
CGTGGACGGG CCGTACATCG CGTAACAAGC TGCCACGATC TCCCGGCCCG ACCGCAGCAC	180
ATCCTTGATT GTCCCGCTCG AGTCCGGAGT CAGCTTGAAA ATCGAAACGA TCGTGCCAC	240
CGACACACCG GGTCCAGGT TCGACGACC GTCAATCGGG TCGCAGCACA CCGCATACGT	300
CCCACCGGTC TCCGGGAACA CGATCAGGTC CTCCTGCTCC TCCGACACCA GCACCTTGAC	360
GTTCCCGCTG GCCTTCATCG CATTGATGAA GATTCATCG CCCAGCACAT CCAACTTTT	420
CTGCTGGTCC CCAGTCGGT TAGACCGGCC GGAGAGCCCA ATCAGGTTCA CCAGCTCCGC	480

GCGTCTGATC GTCTGCGAGA TGAACITGAA CGCAAACGAC AGTGAGTTGA GCAGCAGGTT 540  
 5 GAACTCGCCC GTGCGGTTTT TGGCCGAGCT GCGCTGCGAC TCCAGGATGA AACGGCCAG 600  
 CGTAATGATA TCCGTGTGGA TAGCCTCTGC GGAGTCGCGT CTCTGTGGGT TCACGGTAGC 660  
 CATTTCTGCT TGAGTGGGCT GTGGT 685

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1047UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GATCACTCCC CTCGCTTGAA ACAATGCGT ATAGCGGAAT CTGGCCGAGC ACCAAGAAGA 60  
 25 TCAGCAGCGA GACGGCTGTC CAGATCAACT TCTGGTTGTA TGGCACTTTG CGCTCGGGCG 120  
 CGATCACCTC GGGCAAAAAA GCTCGAAGG GTTTGAATAG ATCCAACAGA CGCCCACTCA 180  
 30 TTTCAGGCTC ACAATGTTTG TAGGTAGCTT GCTGGGCTTG GATTGGCTAC ACAGTTGGAA 240  
 CCACACAAAG TCACTATTGG GCGAGATGGT ACTCTAAATG ACTGCAAGGA GAACTGGTCG 300  
 GTTTOGTTTC CTGAACAGCT TAATTGGACT GAGTTGCAGT AGCTGTACTG AAAGGAACAC 360  
 35 GTATCTTGAA AAAATTATAA ATCTCAGTAC CACGTGACCG GATACGAGGT GCTATTCCAT 420  
 CTOGCTAGAG GAGCTATATG CCTAGTCGGC GTACCTTGG TGAGTAAGAA TAGCTCTCTT 480  
 GGACAATAAT CCGTGATGAC CTTATTATGC TATAAAGCTA TTTTACATAG CAATGGATCT 540  
 40 CCGTGTTTAG ACCTTTGCGC CGCCAAAAGA CCAAGTACAT CAGCACCGAG AACAGCAGGC 600  
 AATCGCCAGG CGCTTGTGGA GCTOCAGAAG ACATGCTGGA TGCAAACCGG AAGAACGCGG 660  
 NTCGGAGTAC AGTTGGCG 678

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1048RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

5 GATCGTCATA GTCCGCTCG TGTATTTGGT TCCTTCTGG CCGGCGCTGC ACCGGCATA 60  
 CCATCGCGTC CACCTGCATC TTGTCATCCG CGTCCATCTC GTCGTCCAGA AACACCTGGC 120  
 TATCGTGGAG CATCCTGTCC CGGCATTGA GCTGGGGGTC GATCGGTCCG CCGTCCGCCA 180  
 ACGACAGCTC CTGTGCTCC GGTGTGTCCA CGCCCTCATT TTCATAGAAG TCCTTGTTCG 240  
 10 GATTGGGGGT ATAGTCCCGG TACATGTCTG CGCCACCAG GTCGAECTCG TCTATGGCGT 300  
 CTCTGTGCTC ATCCAGGTCC TCTTGCAAAC TCGATGGCGT CGTCGGGTC GGTAATCGGG 360  
 GTTCTCGAAG TCGATCTTCG TCCCGGGGAC CCCAGGGGG ATTATTCCCC CATACGGGAA 420  
 15 GCGGGGCCCC CTCCCAACTT GTGGGAAGAT AGTGGGTGCT CCGAGGTCTT TTGACCTGC 480  
 TGTAAATANTC CNCTGTCTTT TTCGGTTCAA CINTAGCCCT CNGGGCCNGG TINACCCCC 540  
 ATCCCGTATG GAAGCANCA ATAACAAATG CCTCCGAAAA NTTTGTNTT TTCNATTTT 600  
 20 GGAANAAGNA AGTTCTNANA ANGAATTTIN NANTTNNN 638

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 621 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: PAG1048UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

35 GATCCGCTC CTCAGCCATG GCTTCTCTA ATAGTAACAC ACGCCCTGCT TCGTAGTCT 60  
 CGAGGTGCAC ACCTACCCGC GCAAATAATG CCTCATCTGA CAGCTGCACC TGGTAGAACT 120  
 40 GTGAGCACCG GAAGTGCAGC TTGCTGCAGA AGCTTGTGAG ATATTGTAG GGGTGTCTT 180  
 GTGTGAGAAA GTTGCTCACC CGTGGATTCT CGTAGGGATC ACGGATACGA CCTTGGCTCT 240  
 GCGCGCACAG CCGGTACCCG CATAGCTTGT TTAGATTGCG CTCATCTATC AAGTCTGAAT 300  
 45 ATGTGGGCTT GGGGAAAGAA CCTTCCACG TATTTTAGTG TCTCGGGTGT GCATTCTTGT 360  
 CTTGCGAAGA GCAGTTCGGA GCAATTGAC CGTCAGAAG TCCCCCTCT TTAGTGAAAG 420  
 NNGCGATGTT GGTGATAGGA ACTTAAACCC CGTTTGGNT TNCNCAATA GNAGCCANNA 480  
 50 CCTTANGTAC GGTNINCCGT TCTTAACCCC GCGGGTCCC NGGGGGTTT CAAGTCTTG 540  
 GNGGGANAAG GTNCCGVINC CCGGGGGTNC GCTACTTAA GNGANGCAN AAGGNAAAAG 600  
 NCCCCNGAA AAGTGGNTTT T 621

## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG149RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

15 GATCTTTTCAG CTTTGGCGTG CTATGGCAGG CAGCCTGCGC CTTTATGGCC TCAATGCCTC 60  
 GCTGACGACT CTCATGTGCC TGTGGGCAAT CTGGTCAAGT GGGTACTATC CAGCGAAGGG 120  
 ACTCCCTATG GCTGTGTGAG ACAAAGOGAA ACTCAGCATG CTCTACGTGC CCTACTTCCT 180  
 20 GATTCTCTCT CGCCTCGTCT TGTGTGTGAGG TCTGGAGCAA TCAGAAAGTG CAACACTCTA 240  
 TATATAATCA CCTGACTATG TACCTATTTC TGCATAGCA CGTTACGTTT TGTACGATT 300  
 CCAGTCAGTT AGCTGCTCG AGCAACCGT GAGCTCCGAA AAGGGAATTC GCTACAAGGT 360  
 25 CTTAGCGCAT AGNCTGCAA CTGGCTTTGG CTAGGTCAAT TGGTTTTCTT GGAACCAATC 420  
 TTGGTATAGA CTCPTGGTA TTGATGGGC TGAGGAGTGT TTNGNGGNA GNCAAACACC 480

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1049UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

45 GATGCTCTCC TGGGCGACAG CGCTTCTAG ACCCTGACG GCGACACCT TGATGCTGCT 60  
 CTGCTCTCA AACGTACCA GACCTTGTA GTAGTGACG CGTTTTTCT TGAAGAGCAT 120  
 CTCAATACCG CCAGTCAATT GCTTCACAAC GGTGCTCTG GCCTTTTGA ACTGGGGCAT 180  
 GTTCACAGTG ACCTCGCCT TGACGTGAT ACCGCGCTG TTGGCATGA GTTGCACTG 240  
 50 GTGCAGCAGG TGCGAGTTGT TTAGCAGCGC CTGGATGGG ATACACCCA CGTTCAAACA 300  
 GGTTCACTT AGACGGGGG GCTTCTCCAC ACAACGGGG TCGAAAACA GTTTGTGCA 360  
 GCTTGGATG GCGCCACNN TTAACCAAC GGGACNCCA CCCATCAACC ACAACGTGG 420  
 55 GGTTTTCTTT TGTGGGAAT TCAACCAGG CCNCTTTNNT GGGACGACN CTTANNC 477

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1050RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

NNNTTNTTGG TGGGGGGTGT AGANTAGTGG TCGGGGNGCC GCTCCACATT CTCCATGCTC      60
ACCACCACGA CAGACTGGAA GTACAGGAAA AGCGACATTG TCGTCCGAGA GATGTGGGAC      120
GGGGGGTTTG AGTTCCAAAA AGCAGACAGC GTTGOGGAGC CCAGCAGTCC AAGCCCCGCA      180
ATTGTGGCCG TCGCCCACTT CACAGGTGTT TGGGCCACGG TGGGGCGGTT CGTGAAGTGC      240
GTCTGGATGC ACGACACCTG GTCGTTCGAC TGGGTTTGGT GTACCATCAC CTTGAGGTAG      300
GGTCATTGT CCGGCACCTG GTACGTCACG CCGGGAATCT TTTTGTGTT CTCGGGCTC      360
ACATACTGCA CGGCTGGAT CTGAATGCA CCGGGTGTC CAGGACAAA CTGCTTCTAG      420
CGATCCCAT ACATGTCCTT CGC                                          443

```

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1050UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GATCCTTTTG TATGAAGTAT GCAGCTGTGG ATATGCTTAG TTAACITCTG CCCAGCTATT      60
TAAGCTGCAA TTGAATCGG GGTGACTCAG CTTGCAAAGG GTAGCAGAGA GGACGGGATG      120
GGTTTATTCG GAAAGGATAG AGGTGAACGG ATAGCTGAGT TTCCGTGTTA CCTGCTAGAG      180
ACCGAAGCC ATCTGGTGCC GATGNCAGG GATTCTATAC AACCTTGTA TCGAGGGGAC      240
ATATNGGAG CCGATACTAG GGCAGNTCC TGGGATAGGT GAGGCINTAG ACCGGGGGCT      300
GACGGGGGCT TTTGAGGCG CAGAGGTACC CCGCGGGTT GCGGAGGTGA TGAAGGGGTT      360
CCAGGAGCG TACGACTCCC GGGGACAAA ACCGAGGCCC                                400

```

## (2) INFORMATION FOR SEQ ID NO:135:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 713 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1051RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

15	GATCAAATTT GACATGTAAT TAATATATTG AGGTAAAATC TAGATAATAA ATACTGCCAG	60
	CAGTGTCTGAC CAACTTCCAT TAGCAAGCAT ATAAGAGGTC TTAAATCAGC CGAAGGTATA	120
	TGCGAGGGAA GATAGATCCC CCGGGCTGCA GGAATTCGAT ATCAAGCTTA TCGATACCGT	180
20	CGACCTCGAG GGGGGGCCCC GTACCCAATT CGCCTATAG TGAGTCGTAT TACGCGCGCT	240
	CACTGGCCGT CGTTTACAA CGTCGTGACT GGGAAAACCC TGGCGTTACC CAACTTAATC	300
	GCCTTGCAGC ACATCCCCCT TTCGCCAGCT GCGTAATAG CGAAGAGGCC CGCACCGATC	360
25	GCCCTTCCCA ACAGTTGCGC AGCCTGAATG GCGAATGGAC GCGCCTGTA GCGGCGCATT	420
	AAGCGGGCG GGTGTGGTGG TTACGCGCAG CGTGACCGCT ACACTTGCCA GCGCCTAGC	480
	GCCGCTCCT TTCGCTTCT TCCCTTCTT TCTCGCCAG TTGCGCGCT TTTCGGTCA	540
30	AGCTCTAAAT CGGGGGCTCC CTTTAGGGTT CCGATTAGT GCTTTACGGC ACCTCGACCC	600
	CAAAAACCTTG ATTAGGGTGA TGGTCACGTA GTGGGCATC GCCCTGATAG ACGGTTTTCG	660
	CCCTTTGACG TTGAGTCAC GTTCTTTAAT AGTGGACTCT TGTTCCAAAC TGG	713

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1051UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

50	GATCTATCTT CCTCGCATA TACCTTCGGC TGATTTAAGA CCTCTTATAT GCTTGCTAAT	60
	GGAAGTTGGT CAGCACTGCT GGCAGTATTT ATTATCTAGA TTTTACCTCA ATATATTAAT	120
	TACATGTCAA ATTTGATCCA CTAGTCTAG AGCGGCGCC ACGGGGTGG AGCTCCAGCT	180
55	TTTGTTCCCT TTAGTGAGGG TTAATTGCGC GCTTGGCGTA ATCATGGTCA TAGCTGTTTC	240

CTGTGTGAAA TTGTTATCCG CTCACAATTC CACACAACAT ACGAGCCGGA AGCATAAAGT 300  
 GTAAAGCCTG GGGTGCCCTAA TGAGTGAGCT AACTCACATT AATTGCGTTG CGCTCACTGC 360  
 5 CCGCTTTTCCA GTGCGGAAAC CTGTCTGTCC AGCTGCATTA ATGAATCGGC CAACGGCGCG 420  
 GGAGAGGCGG TTTGGGTATT GGGGCTCTT CCGCTTCTCG CTCACTGACT CGCTGGGCTC 480  
 GGTCTTTCCG CTGCGGCGAG CCGTATCAGC TCACTCAAAG GCGGTAATAC CCGTATCCAC 540  
 10 AGAATCAGGG GATAACGCAG GAAAGAACAT GTGACCAAAA GGCCAGCAAA AGGCCAGGAA 600  
 CCGTAAAAAG GCGCGTTGC TCGTTTTC ATAGGCTCCG CCGCTGACGA GCATTACAAA 660  
 AATCGACGCT CAAGTCAGAA GTGGCGAAAC CCGACAGGAC TAT 703

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1052I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GATCTCCGCT TCAAACCAGC TAGGGACGAC CCGAGGTCGT TCCAGAGAAA GTCAACAATC 60  
 AATATCCTGG GTAAAGCTAG CACCGCCGAA CTACTTGCTC TTGGCACCAC CGCAAAGGCA 120  
 CACAAAGAAA ACTGGGAAGA TGAAGTGAAG AAACAACAAA CCGTCACCGT TGATGACCAG 180  
 35 GTTGTTCGCG CAGAAGATTC GCGCTTTGCA GAGCCAGTGC AGGAACCAAA GACCTCAGTG 240  
 TCCGGCTACA TCAAGAGGAA ACTATCCCTC AAGCGTGATA AATCCACAAG ATCCAATCGT 300  
 TCGCAATATG ATAGGTTACA GGACTAGATA TGGATGTTAA GTATAGAAAA ACTGTATATT 360  
 40 ATTTGACGTG CTGGGCGTTA CGGAAACATA TAAAGATTTA ATTACTCATG GGCGGATGGT 420  
 ATTTTTCAT GGGCCCCACT GGACTCCATT TGGCAGTTG GAGGACGAAG TAGGAACCCA 480  
 ATTGCTGGTT ACAAGCGCTC GGTTCATGT ACCTATACA CAAGTATCCA TTATTNGGGC 540  
 45 TTATTGATTT GTGTCTNIGG GCGGACTTT TANTTTCTC ACTGGGGGAN GTCTT 595

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1052I2

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

5	GATCTGGGTT GCGGTGAAG ACCACCAATG CGATGCACAC GAGTATCATG ATCAGCAAGA	60
	TTAAAGAAAA GACAGCGTTC AAAATAAAAA ATACCCATGC CATAATGGAG CTGACGCTTG	120
	CAGGCTGTCC AAAGAGCCCT GAGAAAAATA AGAAGAGGAA CGAATTAACA AGAGTAACAC	180
10	TGGATATCAT AATGTTGAGG ATGTTAGTCG CGCGGTGAG GTACGGCTG CATTTAGCCA	240
	GAGCTGCGAG GTATATTATT TCAATGACAA ATAGAGCGAC GGCTGGGTT TTACCGGAAT	300
	TGTGGGCAAA TGCAATAAAT ACGCTTTCA ACAAATATG CGCGAGGATC ATGCAGGACC	360
15	ACCAAGTAGT TGTCGCACTG TACATTGTTG AGAAGAAGCC GTATTGTGT AGCACATTTT	420
	CATTGCCGCA TAGAATGGCA GCTGGGTTG AGTGACACAC AATGGAAGCC CTTCACNGT	480
	AGATAGTGGC GCAGGCAGCC CACCCATAA TTGACAAGAT AAANGTNGAG CTAAGNCTGC	540
20	CAGAACGACC NCGCCGGGG ATCANGTTC ANTGATTOCC CACCAGCAGA GATCGCNATT	600
	GANTGACCCC GGCAGTNTIN CGCAA	625

(2) INFORMATION FOR SEQ ID NO:139:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 486 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
30	(ii) MOLECULE TYPE: DNA (genomic)
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1052RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

	GATCGCGAC GCGTGGGCG AGAACCTGGC GTGGAGCATG GGGCTGATCC GAGTGAATT	60
40	CATGCAACGC ATCTTCGGT GGTACGTCCA GCGAGCGGC GCGAGCCGT CGCTGCATTT	120
	GACGTCAACG ACCACGTCG TGCTTGCCCA ACGTCACTG GATGCGCTAG TGGGCGGGCC	180
	CGTGAGCAAG GCGACACAGT CGCTATTTGC CAGCACACAC ACGATGATCT TCAGAGGGAT	240
45	CCGTAGACTG GCCTACCGTG CGAACATAGA GAGCTCATCG GTTGTGTGTA CCGGGCTAAC	300
	GTTCCTCCTT CTGTTCGGCT ATTTGGATTG GCGTGGCGT TTACATTTGT TCAAGCGGG	360
	CTACTCGGAG CTGCTTATCC CGCATGAAG TCAATGAACC CAGGTCCGG TCCCTAGACT	420
50	TCCAAGAAAA ACGTGGGTGA TTNGCTCAA AGGTGTTCTT TTGGGGTANA TCTTCCCCG	480
	NGTTCA	486

(2) INFORMATION FOR SEQ ID NO:140:

55	(i) SEQUENCE CHARACTERISTICS:
----	-------------------------------

(A) LENGTH: 468 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1052UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GATCCAGCTC TTGCGCGGTA TGAACCTTTC CGCCCGCACC GGCGCCTCGC ACACCGAAAT	60
CGACCGCACC TCCGTCTGGG TCTGTAGTTC CCAATTTTCC GCGCGCCCG AGTACAGCGT	120
GATCAGCACC CACGGCTCGC TCGGGTGAAA GTCAATGCCC TTCACCCCTGT CTGTCTCGA	180
GACAAACGTT TTCTACTCAC GTTAGTACTT GCTCCGCGCC CTGGATAGCA TGGTCGAGCT	240
CTGCGGGTCC GCCCCCTCCG TGGGTGGCAA AGATGGTCTT CAAACACACC GTAATAGGCC	300
GTGCGGACCC ATGCAGGCC CATTCGTCTT CGGACACACA CATACTTCG TTTCAAACT	360
TCATTGGTCC CCACTTGGGA TTCTAGTAG CTGTTCAACT CGGCTTTTGT GGTCTGTGTG	420
GAAAANTAAT ATTCCCTGG ATTATTTAAA TAGGGGTCCN TTTTNTTT	468

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1053RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GATCATAGTG ATTGATATCG GGAGAGGGTT TGGTATGIGA CAGCCTGTAT TCACGTATCT	60
GGTCTTCAC TTCATATATT TCTTGTGGGA GCTGTGAATA TATCTCCATG CGTTCTCTGT	120
TOCATTTTTC GTGCAITTTG TGAATGCAG CCCACTTCTC GTACGTTGAA GTAGGCTTGG	180
GTACTAACGA TCCTGAACA GCGAGGAGGC ATGTTGCGAG GGAGAATATT AAGGAATCAT	240
ATCTCAITTT TACGTCTGAG ATAACCTAGTA CTAACCTGCA TCGGGCGTCC AAATACCGT	300
CGTAGTAATC GTATAGGAGC AAAGCTTCAT CTCTTATAG ATGTGGAGTT GATTCACTCC	360
ACTGCAGCCC TTGGTATTTA GCCAGCATTC CATCATATTT GGACTGATAA TATTGGAAGT	420
TCTTCCACGC GTCTTATAC GGATCAATTA CTGATTTTAC AACATCGAGT AATATGGAAA	480
GATATAACTC TGGATTGCCC TGTATGACTT CCAGCACGCC ATGGAACATA TCCCGAATGC	540

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CGTCGCGGCA CTTCGAGACT AACTTTGGCG TGTATATCTG CTCTTCGACT GTCCCATGGT 600  
 TGAGGTAGGT ATCTTCAGGT AGAATGAAGT CAATGAGCGA TAAACTGACT TGCTTGAATC 660  
 5 GTCCCAAGA GT 672

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1053UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GATCTCGGCT CGCTGCTGCG GCTGAGGCC TACTGGGCAG AGCGCTACCC AATAAACAAC 60  
 GCCCTAATCG GCGGTGCAGA TAAATTGCAC AAGCTCTACT CAACCGATT TCGGCCCATC 120  
 GTGCGCGCCA GGACTTTTCGG CTGTGAACCTC GTGACAAGC TTGGACCGCT GAAAGACCTC 180  
 25 ATAATGGCAA AGGTCAGCGG CCCAAATTAA TAGTCACGTG TACATAAAGG TTTTCCTAAT 240  
 AGCTATACAG CTTCGCGCGG TCTTCAGCTT GCAGCGCGCA ACCGCGGTGC AGCATGAGC 300  
 GTCTACTTGG AAATAACCAT TGGGACCTT GTAGTAGACC TGGACTACAA GACATGCAGC 360  
 30 GCGAGAGCT ACAACTTCCT CAACTCTGC AAACTCGCT TCTACGACTG TCAGTGCATC 420  
 TACCGACCTC CATCTGAAG GCTCAGCAG CCTCGGCGA TCCACAGGTG GGCCTTGCAT 480  
 TCGCACGGA TTTCGCTGTA CACAATACTT CGATGGAAG CCTGCGCGAC ACACGGGCGG 540  
 35 TCACCCCGAA GCTCATTGAA GCTCCGTTG CCGTCAACC CGCAGAGCGC TTGGACAGG 600  
 TGCCTTTG 609

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1054RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATCGTGC CGGTCCGCCA ACGACAGCTC CTCGTGCTCC GCGTGTCCA CGCCCTCATT 60  
 55 TTCATAGAAG TCCTTGTTGC GATTGGCGGT ATAGTCCGCG TACATGTGCT CGCCACACAG 120

# EP 0 866 129 A2

GTCGACCTCG TCTATGCGCT CTTCTGGGTC ATCCAGGTG TCTGCAAACT CGATGCGCTC 180  
 GTCGCCGTG TTATCGGGGT TCTCGAAGTC GATCTGTCC GCGGACCCCA GCGGCGAATT 240  
 5 ATTCCCATA CGCGAGCCGC GCGCGCTCCC AACTTGTGGC GACGATGGTG GGTGCTCGTA 300  
 GCTCTGTGAC CTGCTGTAC TACTCGCTG CTCTGTATCG TTTTCATCTC TAGCCCTTCT 360  
 GCGCCGTTGT GAACCTCCA TTCCGTTATG CGAAGCCATA CCCAAATTAC CAAATTGCCC 420  
 10 TTCTGAGAT CTTGAATACT ATCTCCAGA TGTITGACAG ACGCGCAGCT TCTCAGATA 480  
 CGAAATATCG TGATTTTACG TGACTTTCAA TACCTCATTT GGATTGGATT GGTAAGCAT 540  
 AGATTTTCAG TCATATTGAA AAATTATTTT CAAACAGGC AATTGGATGA GCTG 594

## (2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 545 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PAG1054UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATCGTCGCG TTGCGCAGGG CTGCCAACG AAGCCTTGAC ATGTCAAAC GCTTGAAAGA 60  
 AGAGGTGATA TGGGCCACCC ACGAGGCCAA GTGGGAGCAA CTGCTCGCTA CTGGGACCT 120  
 TCCCCAGAT GGGGCCAAAA GCGACTGGAA GCGTGCCGA GCATGCGTGG AACCATATGA 180  
 35 GCGCGGTTT CGGAACCAGC TTGCAAATCG CAAGCGCAG AGCCAGAAGC TCAAGCGTA 240  
 TAGTGCCAA ATCAGCAAGG TACACCTCC GTATTACATT AAGTGCAGTG CTGCTATGCA 300  
 TACCGTCCG GCCAAACGCT TCGAGTGTIT CCAGAAAGAG CTCCACACCG TTAATCCATT 360  
 40 CGTTCCAGG AGAGATCTCG GTTCCCTACT CTCCAAGTG CGAATGGTGA ACGGAAAAA 420  
 CTACTATCG TGAATGTATA TAGTTTATAG TCCTATTCTT TCATCAGGT TCCAGCAGA 480  
 GCGCGCGCT CGGTCTCAAC TATGCGCACC TCGCTCAGC ATTGCTGAG GTCCTTCTGA 540  
 45 GTTCG 545

## (2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 532 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:

# EP 0 866 129 A2

(A) ORGANISM: PAG1055RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

5      GATCCGTCGC CGGTCCGCCA ACCACAGCTC CTCGTGCTCC GCGTCGTCCA CGCCCTCATT      60
      TTCATAGAAG TCCTTGTTGC GATTGGCGGT ATAGTCCGCG TACATGTGCT CGCCACCAG      120
10     GTGACCTCG TCTATGCGCT CTTCTGGGTC ATCCAGGTG TCTGCAAACT CGATGCGCTC      180
      GTGCGCGTGG TTATCGGGGT TCTCGAAGTC GATCTGCTCC GGCGACCCA GCGGCGAATT      240
      ATTCCCCATA CGCGAGCCGC GCCCCTCCC AACTTGTCGC GACGATGGTG GGTGCTCGTA      300
15     GCTCTGTGAC CTGCTGTGAC TACTCCGCTG CTCGTGTATG TTTTCATCTC TAGCCCTTCT      360
      GCGCCCGTGT GAACCTCCA TTCCGTTATG CGAAGCCATA CCCAAATTAC CAAATTGCCC      420
      TTCTGAGAT CTTGAATACT ATCTCCAGA TGTGTGACAG ACCGCGAGCT TCTCAOGATA      480
20     CGAAATATCG TGATTTTACG TGACTTTCAA TACCTCATTT TGGATTGGAT TG      532

```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1055UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

35     GATCGTCGCG TTGCGCAGGG CTGCCCCAAG AAGCCTTGAC ATGTCAAACC GCTTGAAAGA      60
      AGAGGTGATA TGGGCCACCC ACGAGGCCAA GTGGGAGCAA CTGCTCGCTA CTGGGACCTT      120
40     TCCCCAGAT GGGGCCAAAA GCGACTGGAA GCTGGCGGA GCATGGCTGG AACCATATGA      180
      GGCCGCGTTT CGGAACCAGC TTGCAAATCG CAAGCGCAGC AGCCAGAAGC TCAAGCGCTA      240
      TAGTGCCCAA ATCAGCAAGG TACACCTCCC GTATTACATT AAGTGAGTG CTGCTATGCA      300
45     TACCCGTGCG GCCAAACGCT TCGAGTGTTT CCAGAAAGAG CTCCACACCG TTAATCCATT      360
      CGTTCAGGC AGAGATCTCG GTTCCCTACT CTCCAAGTGG CGAATGGTGA ACGGTAAAAA      420
      CTACTATGCG TGAATGTATA TAGGTTATAG TCCTATTCTT TCATCAGGTC TCCAGCAGA      480
50     GCGGCGCGCT CGTCTCAAC TATGCGCACC TCGCTCAGCC ATTGCGTGAG GTCTTCTGT      540
      AGTGTGTCAC CCG      553

```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1056RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GATCATCAGC GCGAGCTTCC AATTGTGGG CTTTCTGTG ACATACATCC TCACACCTC	60
GCAATGCGCG CGCCAGGGCT CGGCTTTTG CCTCGGCTG ACCCTCAGG GATACGGTA	120
CAGCATGATT CCTAGGAGC TGACGAGCAA GGTCGCAAG GACCGGACA TCGCGCGGT	180
GSAGCTGGAC GACCCCAACG AATTGGAAGA TTGCACTG TACTGCGCG TGGGCGAGC	240
GGCGCAGGAC CGCTTGAAT CACAGCTCTC GCACGGGCTG ATGGAAAAAC GGCGCAGAAT	300
TCCGCGGCTC GCGATCGTC TAGAGATTTT GGGGCTTGA ATTATGTGA AAAGGTGTA	360
CGACTACATT GTGGTCAAGC GCATGGAGCG CGCATCTTT ACTGCGAGCG ACAGCGAGAG	420
CCCCGCATAG ATGTTTATAT AACTTATATA TCCTCATG ATCTTGGCTT GGGCCCCGTC	480
TAGGGAGCAG ACCAGCAGTT TCCTCGTTG CCTTAAAGTC GATGCCGCCA GAGAGACCAG	540
ACGCCCCAGC GGGTA	556

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 550 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1056UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GATCCAACCC AGGACTTCTC GAAAGATAGA ACTCGAACA CAGCCACCG CAGGAATTC	60
TCATCAGCTA GCAGCAATAC TAAGCAGACC TTCAGCGAAA ATGAAGAAGA ATCTGATGCT	120
GAGTTCGAAG ATGTATAGTT GTACCCGTAT ATTGCATTTT TTTTTTTTTT TTTTTTTTTT	180
TTTTTTTGA GATGTCAAAA GCTCATCTCA ACTCCATGAC CAGCCAGTAG TGAATAAGC	240
AGTGTGTCTA GTTCTTCTAA GTGATTTTAA GGACTATGAG CTTTAATGAG AAGGTGAAGT	300
GGTACTAGG CACTGCTGTT GCGACTCTAG TTAAGATAAA GTCTGTGAA GCCGTATATC	360
GCTCTATGC AGCTAAGCAG AACACTAGCA GGAGCATTTT TGGGGAGGAG AAGGACGTAA	420
GACTGGCCAA ACGGATTCGT GAGTCTAGG CGTACGATGA GGAATTATAT CCGGAGCAGT	480



TAGCTCGGAA CTACGCATTT TGGGGAAGA CGGTATGGCA CGACTACAGG AACAGTACTC 540  
 ATATGGTGGG 550

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 653 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1057RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GATCAGGGCC AAATCACTGC TAAGTACAAA CACAAAGGGC CAAGTATTAA GGTGAGAGAG 60  
 CGTTACAGGT GCATTGATAA TACCGCAGGT ATATATCAAG GCGCACAGTG AACACATTCT 120  
 GCAGACGATA GATATGTCTG AGACGAAGTA GGTGAGATA TTTACGCACA AGCCTCATTT 180  
 GTAAGATAAA TGGTCATTAC TAACGTTTTT GGGTTTAGCA GCAGCAGGCG GAGCAACAAC 240  
 GAGGGGCAGG AGCACGGTGG TGGTGGACAG GGTCCAGGAG TCGAGGATGG CGGGGAGCCA 300  
 CCGGCCAGGG CGAACACGCG CAATGTGACT GTGGCAATCC AGTACTCGTG GCTCCACGAC 360  
 ATGAGGAATG TCGGGGGAGA GGGCGAGGAA CCGGACAGGG CCGGGGGGAG AACGGAGATA 420  
 CGTTCTGTGAT GAGCTTCACG GACGTGCCGG ACTCGACGTC GAACGATCGG TTTCAGGAAG 480  
 TGATCGGCAT TCGGGGCAG TTTCATTTGA GCGCGTGGC GCGGCGGATC AGCCTCCTGC 540  
 GGGGGCTCTC GAAGGAGTCC TTGAAACT CCTCTCAGG AAGCTCAGCG AGCTGGACAG 600  
 CGAGCTGTGC AGTATATGCT ACGACGACTT TGAAGACGAC ACGTCGATCG GGT 653

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 668 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1057UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GATCTAGGGG TTCTTCTTGC CCGCTACGG GCGCCCTCG CAGCCTCGG CTGGCTCCCG 60  
 CCGGAGAGGG GATCGGCAAG GCTCCTCGCA GCGCACACT GGTCTATGC CTGGACCGTC 120

CGGCGAGCCG GACAGCCGAG GAGCAGCCCC GCGATGTCCTG TCTCCCCGGC GGCGCTTACT 180  
 CTGGGGCTGG TGTGTAATTT TCTAAAACT GGTGAAATG TACGGGCTCG CTGGAGCCCC 240  
 5 CGCCTGTGCA TTGTACAAGG GAATAGCGGA TCAATTGGAT GGGGACGCA GTGTTACCCC 300  
 CGAAACCGTG CGCAGCGGCT GGCGGGCGA GGGCTGAGGT GCGCTGCGG CGCAAGGCGC 360  
 ATTTGCTGTC GACTGCAGAG CTGCAGGAGC TGTGGAAGC GCAGGACAAG TTGCAGCTGT 420  
 10 ACGTGGCGGG GTTGTGCGAG AGCGAGGAGA CGCAGAAGCG GTTGAGCAG CAAAGAAAAC 480  
 AGCTGGCTGA AATACGGGAA ACGTTTGGG GCTTGAAGG GGAACGACAG CGCGTCAGG 540  
 AGCGGCTGGA CGGGTATCAG AGGCTAATGT TCCGTACCA TGAAGCGTGG CAGGCGGTAR 600  
 15 ACGGGCGTGC CGGGCCCGTT ACAACGACGG GTTCTGCGCG CGCGGCTGCA CAAGAAATGC 660  
 GCGCTGGG 668

## (2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 614 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG105811

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GATCTTCACA TTGCAATGCA GGTCTCTCTT GTTTTATAGTA GCACCCCTCG GGCGCTTGT 60  
 GGCGTTCAAC TTGAGTTTAT CGCACTTGG CTTGATAAGA CCAGCTTTCA AGTACACCAT 120  
 35 GATGTGCTCG TCATCACCGT GCTTAAAGCA ACAGCGCTTG CCATAGCGGC AGTAGCCTGT 180  
 CTTACTCCAA TTGATACATG GCTTGTGCG GAATTGTGTC GACCGCTCCT TGAACCTTAA 240  
 CTGTGAGAGA CCATGGGCAA ATTGGCACTT GTTATGTTAC TTGCAGGCC CCGTAGTGC 300  
 40 AAATGATTCG CATAACTCTG TCTTGTAAG CATCTGTGTT ACCTTCTCCT GCGATGGCTG 360  
 TGGCTGCTGC TGTGGGTGG CGGGGGGGG GACTGAACCC GCAAAAGTT CGGCTCCGGC 420  
 TGTGCGGCTG CTGCGGCTGG GCGCTGGGT CTTCCGACG GATGCTGCAG GAGCGCAGGT 480  
 45 TTTGGGGCGT CAGGGTAGTA TCCATTTGT AGGCCGNTAA TGAGAGTTTA TGGCCACCTC 540  
 NAAGGTAGGT TCCCGTTCC GAGGGGCAA GGGVAATCAN TNGCCGCCA AACCGTNAAC 600  
 CCCCCCNCC CNGC 614

## (2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 634 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1058I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

AAGCTTGCAT GCCTGCAGGT CGACTCTAGA GGATCTTGCA AAGTATGGCT TGGTAGTGTG	60
GTGATGGTTA TCTGCAGTTT CAATTGCTTT GTTAGTTAGT GTATCACATT CTCTGGCTT	120
TGGCCGATTA GAGTGTCTGG CCTCATGGAT GGGGATCTCC GGTGTATACA CGTATATTTA	180
TTCTCTTCGC CCAAGTGGCG GAGTACAATT TTCTCTAGC TGGACCTATT TCGTTGTAT	240
TTCASTAGTG AAATAAACT ATCAATTAAG TACAGCTTTC GTATGACTCT GCCACAGGAT	300
GAGAGCAGAC ACTCTGCAAA GTACCGGATT TCAAATAAAT GTTTAGGAAT AAAATCAAAG	360
GCGTACAATT ACATAATTAT AAAATGCTCT CGTAGCTATG TCTTTCGGGT CTTTTTTTTA	420
TCCTAAAGTG AACATCGAGT CTGTGCTTTC TTAGGTGTTT AGATGACAAG CTTACATGCC	480
TCCNGNNGNN AAACAGTTNG TCGAATCCCT CGGATCCTCN CCANGTAGNA AGGNANTACG	540
NNCAGCAGAG TCATTACCN C NACCCACCGG CTTGCCANCC NANTTNCCTN GGNGNAGNG	600
GGNGGNGNT TGNACCNANN TTGNGNCCNT NGCC	634

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1058RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GATCATTTCT GAGAATGCTC ATAGTTATGG TTTAACGGTT CTTCAAACGG AAGAGTATCT	60
TCAATTACAG AGTAGTTTGG AGAGAGAACA GGTAACTGCC TACAACATTG CCGAGAAAGC	120
AACTACAATT GGCTACGTTG CACTTCCAAG AACCGAGTAC GATGAACCTG TAGCTTCGCA	180
AGCTTCTACG AAAGAACAGA ATTTTGAGGT ATACGGCGCG GAAATGGCA AGGTCATAGT	240
GGATAAATCT GAGTATCAGC ATTTGAAGAT CAAAGCTATC CCAGTGATTT CACCATTGCC	300
TCAAATGAGC AAAGAGCAGA TGGTTGAAAA GGCCAAGGAA CTTGGAATGG TAGCTTTGCT	360
CCATTGACGA GTATGAGAAG TTAAAGAGCC CTATTTCCCG ATAACGCTTT GGATTGCAAC	420
AGCGAAGGAC CCGGAAAGG TTGGTCTCCT AAAGGAGGAG TACAACCCCT TATTG	475

## (2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1058UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GATCTGGGCG CCGACAGCC TGCCAGGTG CGCTGCATC CGCCGCTCCT GGTCGGGCTC 60  
 GTCGAGCCCC AGCTCCTGCC GGAAGCTAGC CCTCCAGCTC ATGTACGACT CATGCGTTAC 120  
 CTTCGTTCCG CGGAATTCTT TCTGCTCTTC GAGCTCGGT TOGCGTAGCT GCCGCTGGTG 180  
 CTCCTTCTCT CGGCGCTCAA GTCCTTCTG AAACCACGAC TCCGCTCCT CCTTTATGA 240  
 CGAGATCAGC GCAAAACACA TCTGTATTCC CAGCAGGATG TCTCTCTCA CCTGTGGCAT 300  
 GGACTGGCTT GGAAAGACCG TCCACCTCGC CGGTCAAAAT GAAATGCTTG TCCGGAATAT 360  
 TCTCCAGTTT CGCAACACAA GGGTCCCCC GTGCTGTGTC GGACTTCCIN GTTCTCAAT 420  
 CCNCTCTCAA CTGCTCGGN TTTCGGCGG GAAGGINCCA NCGGCTTAA TGTCAC 476

## (2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 644 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1059RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GATCTGTTAC GCTGCAGGC GAAACCTCCA ATGCTCTGGG CCAAGGTTGG CGGCTGGGAT 60  
 TCTTGGGCTC ACTGCATGCT TCGGTTTTCA AGGAACGACT GGAGAATGAA TACGGCTCGA 120  
 AACTCATTAT CACACAACCC ACTGTTCCAT ATGTCTGTGA GTAATCGAT GGGACCCAGA 180  
 TAACAGTAAC AAATCCAGAT GACTTTCTCT ACCTGACACT TCGGCGAACC AAGATAAAGA 240  
 ATTTCCAGGA GCCATATGTA GAAGCTATAA TGACTCTTCC ACAGGATTAT CTCGGAAGGG 300  
 TTATCACTCT CTGCGACGAC AACCGTGGCA TACAGAAAGA GATAACGTAC ATTAACACCA 360  
 CGGGGCAAGT GATGCTGAAA TATGATATCC CATTCGCACA TCTAGTAGAC GACTTTTTTG 420

GTAAGCTCAA GTCGTGTCAG CATGGTATG CTCCCTAGA CTACGANGAT GCAGGCTATA 480  
 AGCCGTCTGA CATGTGCAAG ATGGAGTGC TTGTAAATGG AAAAGGTGTG GATGCACTTG 540  
 CACAAGTGAT GCATCGCTCC CAAACCGAAC GARTGGCCAA AGAATGGGTT ANGAAGITCA 600  
 AGCAATATGT CAAATCCAG TTATACGAAG TGGTTATCCA GGCC 644

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 649 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1059UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GATCGTGGCG GACGTGTTTG TGCGCACCGC GGACGTGCTG CTGAAGATGT CGCGGTACGA 60  
 RGAAGCCAAG GCGGCGGCGG ARCGCGGCCT GAGCTGGAG CCGGACCACA TGAAGCTGAA 120  
 GCGCGTGCAC CTGGAGTCTG TGCGCAAGTT GCGCGACTAT AACGGGACA TCTAGTCCGC 180  
 GCGCGCGGCC CGCGCGGCA CCACGGGTAT ATATACACAG CCGGTCTCCG CGCGCCATGC 240  
 CGCCCGCGCG GACCGCAGAC ACAGGCCCCG ATCTTGGGCG GCGGCGGCG ATGAGCTGGT 300  
 GCAACCTCT TGGCCCGTAC CCTGCTAAGG AGGTAATCT CCCAOTCAG TACTATAAAA 360  
 AATTTTAAAG TTAGCCACTT TCGAGTTACA ACTCCCGCC TGTCGGGTAA CGGATCTCAA 420  
 CTGTGAAGC CCTAACGCT GCTCTACTCC TTTTGGCTA AGGCAATATC CCGCATGTC 480  
 TTGTCGGAT ATCAATGTC CCGTTGATTC GTTTATGAT AGGTTGAAGC GGAAGCAGAT 540  
 TACTGGCAG TACAATGTGT CGCTGGAGAC GTTACAAATT CTGATCGGTT ACGTATCTGC 600  
 CATCCGGTGG TGACGAAGG ACGARCTCAT TGAACAGATC CGTCTACTC 649

## (2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 641 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1060RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GATCTGCTCA TACTGAGCG CCAACTGGTC GTACTCCGTA TGCAAAACAT CTGTGGTTTC 60

CTGGAAGTGC GCCACCTTGA GCGATATCTC ATTAAACTTG GTAACCAGCT CTCCCAACTG 120  
 ATGATTGACT GCACTGGTIT CCGTCAGCAG GTCCCTCCAGT TCGCCAGTTC TGGTGTCCAC 180  
 5 TTCCGCCACG TATCCGCTGT ACAATGTATA CTGTCGTTC GCAGACCCCA GARCAGAAGC 240  
 TCGCCGCCAC TCTGGCGCCA GCAGCTCAAT TACCTGAGGT TCAATCTCTG TTTCACCGT 300  
 TGCCAACAGA GTGTCTACTT TTTGGCGTAA CGAACTATCC CCAAAAAGCG GAGGCAGCTC 360  
 10 ATCGTGAGAR GARGCACCGG GATTTGCCGC TACATCCTGT ATGACTGART TCTTCCGGCT 420  
 CCTAAGCATG GTGCAGTTGC TGCTCAACG GCTTTCTTCC TGGTGARGT CTGCAGTGGT 480  
 TOGTGCTTAT GCGCAAGCAG AATACCATGT TGAGCCGGCG AAATCTCATC ACGTGATCAT 540  
 15 CATCTTGCAA CCGCTCGGAR GACRGTGATG CACTGTTCCA TAGGCTTAGG GCGCAATTAT 600  
 ACGCTAGCTA GTTATATTGA TAATATGTAC ATGATGCCTT C 641

## (2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 649 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1060UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GATCTTGCCG TCCTTCTTGT CCAGCTGTAG GTCCGGATGA GGGTACGCCT CGCTCAGGTA 60  
 35 CTCCAGCCGC AGCTGCGCGC TCTCCATGGA CGCCTCCAGG ATCGAAGGCG CCGGCACAGC 120  
 CTCGGAGGGG AGGGGCGGCT GCAGGAGGGG CATCTCCTGT CGCTCCTGGT GCATCTGCAG 180  
 CGCCGCAGCG CTCGGCTCCA GCGCCGGGTC GAAGTACTTC ACAITGTGCA GCGCCGACTT 240  
 40 GTACAGATTC AGGATGCAGC CCTTGAGCTG CGCACGGTGC AACCGGTACG CAGTCGGGAC 300  
 ATACTGGTAC CCGCTCGTCC CCCCTCCCGT GAAGTGGCGC CGCTCCGATC CGATCGAAGA 360  
 CAGTGACGCT GTTGGCTGGT GGCTGTATCG CCCCTCGCGC GCGGCGGCTG CGCCCTGCGC 420  
 45 CTGTGTCACC CACCCGAGCC GAAACACAGT CCCGTGTGAC GTCTCCCGGT TCAGCCCGCC 480  
 TCCAGTGC AC CGGCGGARC CCGCCGGCTG CGARCAAGC GACACCTGCT CCTCGCAGCG 540  
 CGACCCCGCC TTCATGTCTT CACATGTCAG CGTCCGCTTG TGCGCTTGCC CCGTNGCAC 600  
 50 CTGTTAACTG CATCCGCGTC TGTTGGCTGC TGCTGCTTGC TGCTTGCTT 649

## (2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 570 base pairs  
 (B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1061RP

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GATCTGCTTT TGTAAGTATT CATCAGCTAA ATACCGTAAA GCTGGTTTGA ACGGAGGTCC	60
TGCTTTGTGC TCATATATTA TAGAAGTATC AATGACGAGG GGATGCCGCA TTITCAAGAC	120
15 GTTCAAGTCG GCTGCAATG AATGGCGGAT AAGCACATCT GTTGGGCTTA TCATCCGCAA	180
GAGATCCTGT TGGACGCTT GCAAAGTGT GTTACCCCG ACCAACTTCT CCTCTGTAAT	240
ACCGCTGTAC TTGCTCAAGT AGTCCACAAT GGGCTCATCT GGCTTGACAA ACTTGTGATA	300
20 AACTAAGTTA CAATCAAAAT CGACGACGCT CACACGGGTC AACACGTATC CGT'TTTTAGA	360
AAGGCACATC TCACAGTCGA TGGCAAACGT GTGAGAACCG TCGTGTGGA AACTGACAGT	420
GTCACCCAC CCACTGCACT TCTCCTTATT CTGATACTTT AGCAACAAAG CCTTTTGGGT	480
25 ACTCCTCGA TAAGCCAGGT GTGTTTAGAT GGATGGGGTA CTCATTATGC AATAAGTCAA	540
CAACGGGCAT AGCAAATCAA GCAAGTGATT	570

(2) INFORMATION FOR SEQ ID NO:160:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 522 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1062RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GATCTCGGTG ACGTGGCGCT GGTATGGCTT CATCCAGTCG CCGTTCAACA AGAAGTTTCT	60
GTTAACGTCG AAGTTACAGC TGGTGAAGGA ATCAACCTCT GGGCCACGG CCTTGATCAC	120
45 CTCTGGTGTG TTCAAATACT CCTCACTGTA CTTCATGTCA TCGTAGCAGA GCTGGCCCTC	180
ACACTCCTTG CGAACGTCGT AGACGTTCTT ACCAGTTCTC TGGAAACGGG TCAACTGGTT	240
GCCATTACAG TACAGAGAGG CTGGAACACA CGACCACAG TTCTGCAGGG TGTAGCATGT	300
50 GCGGATCAAA CGCAAGCACC GTGGCAAGGT CTCGTTTCATT GCGGAGCATT GCTCTGGGCC	360
AAGAATGGCG GGTTCGCGC CACCACGCA GGCCATACGC TCGTAGTAGG GGTACTGTGT	420
CAATGGGTCT GTCAACCGGT TOCCAATTAG CACAGAGCTC AACTTAAACG AGCGCTCCTC	480

55

GCCTGGGTGC GACAAGATCT CGGCAGCAAT AGCAGGAATG TG

522

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1062UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GATCCTGGIT GTATCATAGA GAATGAACAT ATTGATAAAA AAATGCTACT GTGTACAGTA	60
ATGTCTGAAC ACCAACATGC TCITTTCTTG TATTAAATGA TGGGATAACG AAGTCTTGGA	120
AGAATCCTGG GCGGAAATAG TAGACATGTT TAGAGAGATT TTTGTAATGG CTAGAGTCGG	180
TTTTGATGCC CGAAAAAGAA GTGCCAACAT TTAATTTTGA AGGTTTATCA GGTAGGTCAG	240
GGAATATACT ATCCTCGTAT AAACCTTGA TTGTACTTGC AAGGAGCTCC AAGTCGTCTG	300
AGTTAGGCGA TGGTTCATCT TTAGTGTCAG CATCGACGAG GACCTCACAT GTGATTCCTG	360
AGTCAATTGC ATCTATGACC TCTCCATTCA CAATCAAGCC CATGGGTCCA ACCTCCTTGA	420
GAGCCGCTTT GATAAGCTCA GTACGCAGCT CGACCGAAGT ATCCAAGTA AGTGACTCCT	480
TTATTTTGAA TTGCAGATAT TCGGCGCGCA CTGCATGTAT AGATCCCCCA TGAATAAAGG	540
AGAATTGCTG CACAGTAGTA AACGCAAATC CCGGTAATT AGTTGGTTGG CTTCCTTAGGA	600
AGTCAGTGAA CCGATTATTT GGTCTCTGAT CCT	633

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1063RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GATGACTTGG ACCGTCAACC GGTACTGGTC GTACTTGTGC ATGAACTGGT CCTGTAGTTC	60
CCCCAGTTGC TAGATGAGCA CGCCAGTTT GTGGTCAAG TCGACACAT CGTGTGCTGT	120
GTCCATGCCC CACATGACA GCTGCCGCGC AGCGCGCGC CGCTCATTGG CCACCACTTC	180
CAGGCGACGT AGCACCCCCCT TTTCCGTCTT CAGGAACGAA GACAGCTTCC GTGCCAACTC	240



# EP 0 866 129 A2

GGGGCCAAAG TTTCCCGCTG CATTCTTGCG GAACGAGGAA GCAATCCCGG CACGCCCAAA 300  
 GAACTTGGAA CGTGTGGAAG AGGGTGGGGG AGGGGGTGAC TGGAGGTCTG ACGCAGTAGG 360  
 CGCCTTCTGG TTTCTCAAAG AGTATGTICT GTGCATATTC TCGTGCTTAG ACTGGTCTGG 420  
 CAGTCGGTAT TTGTAGGTCC GATAAGATTC TCAGACGACA GCAAGTAAAG TACAACGGTG 480  
 GTCGGTGCCC CTCCAACGTC TTTT 505

## (2) INFORMATION FOR SEQ ID NO:163:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1063UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATCTTAATA GCAATAGTCG ACTACAGGAA ACACAAGCTT TCATAATGTC GAAATCTTTA 60  
 TCATGGGATA CACTAGACTA TACTCTACAA CCATGGATTC GTACTGCTGT TGATGCCATG 120  
 GGTATGAGA CCATGACACC TGTACAGGCA TCGACGATCC CGCTATTTGC CAGAAACAAA 180  
 GATGTGGTTG TAGAATCTGT GACCGGTTTC GGAAGACCG TGGCATTGT CATACCTGTA 240  
 TTGAGAGAG TGATACAGGA TGATGCCAAT AGTTCAAAGC TCAAAAAGG CCACTTCCAC 300  
 ACCATAATAA TCTCCCTAC GCGGAGCTT GCATCACAGA TACAGGGCGT GATTGAAGCG 360  
 TTTCTGACAT ACTATCCAGA TGGAGAATAT CCTATAAAT CACAGTTGCT TATCGGTAGC 420  
 AATACCAGTA GTGTCAGAGA TGATGTTGCA GCGTTTTTGG AACATAGACC GCAAATTTTA 480  
 GTTGGTACGC CTGGAAGGCT ATTAGACTTT CTTAAGATGC CAAACATCAA GACGTCTTCA 540  
 TGTGGCGCAG CTATTCTTGA TGAGGCCGAC AAGTATTTGA TATGAATTTG AGAAGGATGT 600  
 CCAGACAATA CTGGAGATGC TACCAAGCCA A 631

## (2) INFORMATION FOR SEQ ID NO:164:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG0164I1

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

	GCAGGAANTG GGTAGCCAAG AACCCGGCAA GACCTTCCCG AGCTACAACC GCGTCATCTC	60
5	GCAGGTGTTT GGCATCTGCG TCAGCATGGC CGGCTGTATC GGGTACGGCT GGGGAATTCA	120
	ATTTCACTAT CACATCGCTA TCGTGCTATT CTTTTCTTTC CTAATGGCGT TGGGTATGAC	180
	CTGGTGCTCT AACTCCACCA TGACCTTCCT TACGGAGTCC AACCCAAAAA GAGCTGCCCG	240
10	TACCATTTGCC GTAAGCAACA GCTTCCGCAA TATCGCTGCC GCCATCAGCT CCGCCATTAT	300
	TTTCAAACTA TGCAACGCCA TGGCGGTGG ATGGTGINTT ACAGGCTTGG GTCTAATCGA	360
	CTTGCTATCC ATGTTGAGCG TCTATTACTT GATCCGTAAT GGGGCGGAGA TTACAAGGAT	420
15	AGCTGCTGAG CTATGATATC ATAACACATC CGCATTTTITA CGGATTTAGA TAACCAAAAC	480
	AGCATANTTA GCATGTTTAG AATCTATCAG AAGAACCTCC CTGTTCCTT TAATGATTAA	540
	TTTGAACAGT CATTGATTCC GTCTTTGAC CAAGAAGITA GCACGTGATA TCCGCTGACG	600
20	CCGAAACGGC GTGCCCTTGT TTTTAC	626

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG106412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

	AAAAATCATT TTTATCACCA CTCAAGATGC AGTCTGATTG AAGTGTAAG CTGCAGTAGA	60
	AGAGACAAGT AAGCCATCAT GAAGGTATGT TATAGGTGCT AAGTTCCCGA TACNAGCACA	120
40	GTGGGCATGC TAGGGCTGCA GAGACAGGGC ATGGGCGTGT TACGATAGCC GGAGACTCCG	180
	ATTTGGCGGC TAGCGGGAGG TTAGCGGGC GTTGAAACGA TAATGGGTGC CAGGACGCGG	240
	GCCACGGCGG CACTGATGCT TGTATTGTTT GGCATGAATC TGATACTAAC ATTCTGTAG	300
45	TTGAACATTT CTTACCCAGT TAATGGTACG CNAAGACCA TTGAGGTGCA TGACGAACAC	360
	CGTGTCGGTG TCTTCTACGA CAAGAGAATT GGCC	394

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 559 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

# EP 0 866 129 A2

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1064RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

	TAGTGGATCC AGCATCCCGT CTCGACCACT CCTGAGTTCC GCGGCTCTA TCCTAGACCG	60
10	CCAAAGCCCA GCTTGAAGAC GTACTGGGAG ATCGTGAAG AACCAAACCT CACTATATGT	120
	TCCTGAGCA CAGCGCTAAT GTTCGCCACC TACTATGGGT TCAGCGTCAC GTTCGCCAC	180
	TACTTGAAC TTGACTATGG CTTCACTAAC CTTGCGATCG GCGGTGCTA TGCTGTCCA	240
15	GCGGTGGCC TAATGATGG CTCCTCTTG GCGGTGACA TTTCGACCG CTTCCGACG	300
	AAGTGGGTAG CCAAGAACCC CGGNAAGACC TTCCCGAGCT ACAACCGCCT CATCTGCAG	360
	GTGTTTGGCA TCTGCGTCAG CATGCCCGC TGTATCGGT ACGGCTGGG AATTCAATTT	420
20	CACTATCACA TGCTATCGC GCTATCTTT TCTTTCTAA TGGGTGTTG TATGACCTGG	480
	TGCTCTAACT CCAACATGAC CTTCTTACG GAGTCCAACC CAAAAGAGC TGCCGGTACC	540
	ATTGCGTAAG CAACAGCTT	559

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 611 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1064UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

	GATCTGTCT CGCCCGCTTA TGGGCGCTG CTGCGGCGAG AGGGAGATCG TCCTGGTGG	60
40	CCTAGGCTAG GCACGGCCCT AGGCGGAGCT TGTCTGCGG AGGCGCGGCC GCCTGAGCCC	120
	CGCTGCGCAG GCGCGCAGC CGTGAGACGG TAGCGGCGCG CCTAATGCTT CTAACGCAG	180
	GACCGCGCAG CGGACCTGCA CGTTAGTAAA AAATCATTTT TATCACTACT CAAGATGCAG	240
45	TCTGATTGAA GTGTAAAGCT GCAGTAGAAG AGACAAGTAA GGCATCATGA AGGTATTTTA	300
	TAGGTGCTAA GTTCCGATA CAAAGCACAG GTGGGCATTC TAGGGCTGCA GAGACAGGC	360
	ATGGGGGTTT TACGGATAGC CCGGAGACTC CCATTTGGG GGGCTTAGCG GGAGGGTTAG	420
50	CGCGGNGTTT GGAAACGAAT AATGGGNTGC CAGACGCGG GCCACGGNG GACTGATGCT	480
	TGTTTTTGT TGGGAATNAA TCTTACTACT AACCAATCCN GINGGNGGA CAATCTTAC	540
	CCNGTTAAT NGGTACGCAA AAGACCATGN AGGTGGGNTG ANGACAACCN NNTCCNNNT	600
55	TTCTTNCAN A	611

## (2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 615 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1065RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GATCTGTAGT TTCGCAGTCC CTGATGCGGT CCGCCAGAGC AGGCAGCGCG GGCCAGGGTC 60  
 TGCGCAAGGC AGGCGTTGTG TCACCGGGA GCCACTCTCT GGCAGGCAG TTCCACGCT 120  
 CCTGAACGAG CGCGGCGCATG ATGGGGCCCA GAATCTGCG ATAGGCATCC AGAATGTGGA 180  
 ACAGGGTGGT CTTTATGGCC AGACGCTCT TATTATGTGG GGGTTCCATG TAAAGCGTGT 240  
 CCTTCGAAGC ATCAAAGTAG AGGGACAGGT CGTTGCTCAT GTGTACAGA ACAAGACTG 300  
 ATGACATGG AGTAGGTCTG GGATTCGCA CAGACCTGA CACTTGGGG GCAAAATTCT 360  
 TTGTCTTGTG GAGGGNTTTT CCCNTCANTC CCCNGGCAGG TGGGGGCAGN CTTCCCCNGG 420  
 GCAAAAAAGG CTNITCCCCA CCNAGATNAA CCCCTGGGAA ANCCCGAAGG TGNCANNAAT 480  
 TNAGNGGAAG TNNCCTNACC NCTCCACCNA ATCGGAAAAA TTGGGGANNA ANGCCCCANC 540  
 CCAACNCCA AANTTTTCTT GGAATAAAAA AGGGGNGCC CCCCCGNG GANTNANTTT 600  
 TTTCCCCCCC NATCC 615

## (2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 604 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1065UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GATCTCTTCC CTTCGATCAT CCTCAGTTG GGTCTGAGT CCATCGATGC GTTGACGCAG 60  
 TTGGCCACAC AGTTGCAGAA CGCACAGGCT GCAGCTCCAG CAACCGAGG CCATGAGGCA 120  
 GCGGAGAAGA AGGACAACGA CATCCAGAG TTGATGAGG GCCAGTCTTT CGACGGGAT 180  
 GTTGAATAAG TGGCTGTGC GAGGACTGTG TTCTGCGGC CCATCTCAGA ATTTGTCTAT 240

EP 0 866 129 A2

TTCCTGCAGGG AATATACATA TATTGAGTGC ACATATGGAT ATTAIGTATA TATATGTACA 300  
TAACTATAC CGCCCCCGTC TTAGTGGGAC CACATAAACC TACGGGTGG CGCCCTATA 360  
5 TCGTTTTACA ATAAACGGCG CGNCTTGGG GGNVINCTTC GANAATCTCN TTGGGGGGCC 420  
CNCNNCNC TANNAGGTNC TTCNCCGGG TNGGAAGTNA AAAAGCNNNN GTTCNGTTGN 480  
NAGNGTCCC GGGGAAANC CNCCCCGNG GNGGATTTTC NCCCAAACCG NAGAAACNN 540  
10 CMTTGCNCCA AGTTGCCCGT GGGAGAAAAA AANCCNATGN NGAAGNAAAA TTGCCCCCTG 600  
CCCN 604

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 653 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1066RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GATCCTGAGG CCTCACTAAG CCATTCAATC GGTACTAGCG ACGGGCGGTG TGTACAAAGG 60  
GCAGGGAGCT AATCAACGCA AGCTGATGAC TTGGGCTTAC TAGGAATTCC TCGTTGAAGA 120  
30 GCAATAATTG CAATGCTCTA TCCCAGCAC GACGGAGTTT CACAAGATTA CCCAGACCTC 180  
TGGCCAAGG TTATACTCGC TGGCTCCGTC AGTGTAGCGC GGTGCGGCC CAGAAGTCT 240  
AAGGCGATCA CAGACCTGTT ATTGCCTCAA ACTTCCATCG GCTTGAAACC GATAGTCCCT 300  
35 CTAAGAAGTG CGCAACCAGC AAATGCTAGC AGCACTATTT AGTAGGTAA GGTCTCGTTC 360  
GTTATCGCAA TTAAGCAGAC AAATCACTCC ACCAACTAAG AACGGCCATG CACCACCACC 420  
CACAAATCA AGAAAGAGCT CTCAATCTGT CAATCCTTAT TGIGTCTGGA CCGGTGAGT 480  
TTCCCGTGT TGAGTCAAAT TAAGCCGAG GCTCCACTCC TGGTGGTGCC CTTCGCTCAA 540  
TTCTTTAAG TTTCAGCCTT GCGAACATAC TCCCCCAGA ACCCAAAGAC TTTGATTTCT 600  
45 CGTAAGGTGC CGAGTGGGTC ATAAGAAAAC ACCACCCGAT CCTAATCGG CAT 653

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 669 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1066UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

5 GATCTGGAGG ACCTATATAT ACCATTTCGC TGCACCTTTC TTTTGTGGCC TGATGTTTTA 60  
 TAAGTAGACG ATCTCTGATT ATTATGCGA GGTGCTTAAA GTCCCATGCG AGCACACTGT 120  
 TTGCAATGAT GGCCATCGCC CACCAGACCA GTCAGAAGTA GATATCTGAA TTGCATGTGA 180  
 10 GCCATACTAG GGTGACCTGT GTTGGCGGCC AGCTTGCCAG AGGAGGAAAA AAAAAAGATT 240  
 GCAGCACCTG AGTTTCGGT ATGGTCACCC ACTACACTAC TCGGTCAGGC TCCTACCAGC 300  
 TTAAGTACAG TTGATCGGAC GGGAAACGGT GCTTCTGGT AGATATGGCC GCAACCGAAA 360  
 15 TATATAGCCT AGAGCAGACA TGATATCAGA TGGTGGATGC ACGTGAGGGC GTAGACATGT 420  
 AATAACGATA TCGAGTACAT TTGGTGGCAG ATGGCTGGGG CTATGGCGCA GATGTGTGGT 480  
 AATTGGCACA TCGGGGTAAG TCACGGGGTA AGAAGAGTTT GTCGGCATTG GAGTGCCATT 540  
 20 CCGTACCGAA TGTACGCTAG TGATCTGAAA AGTGATATGC TATGTGAAGT GCAAAGTATG 600  
 GGAAGTCTGG CTGGGGTTAR GAAGAAGATG TCRACCTCAA GSCAACGGAA CGTCCGARCA 660  
 ATGCTTTGA 669

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 652 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1067RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

40 GATCCCTTAA CTTCGTTCT TGAATTAATGA AAACGTCCTT GGCAAATGCT TTCGCAGTAG 60  
 TTAGTCTTCA ATAAATCCAA GAATTTCACC TCTGACAATT GAATACTGAT GCGCCCGACC 120  
 GTCCCTATTA ATCATTAACGA TGGTCCTAGA AACCAACAAA ATAGAACCAA ACGTCCTATT 180  
 45 CCATTATTCC ATGCTAATAT ATTGAGCTT GCGCCTGCTT TGAACACTCT AATTFTTTCA 240  
 AAGTAAAAGT CCTGGTTGCG CTAGAGTACA AGTACCCTAG GTTAGCCAGA AGGAAAGGTT 300  
 CCGTTGGATC CCGTACACGA AGAAAATCGG ACGGGCCAAC CAAACCCAAA GTTCAACTAC 360  
 50 GAGCTTTTTA ACTGCAACAA CTTTAATATA CGCTATTGGA GCTGGAATTG CCGCGGCTGC 420  
 TGGCACCAGA CTGCGCCTCC AATTGTTTCT CGTTAAGGTA TTTACATTGT ACTCATTTCA 480  
 ATTACAAGAC CCGTATGGGC CCGTATCGT TATTTATGT CACTACCTCC CTGAATTAGG 540  
 55 ATTTGGTAAT TTGCGCGCCT GCTGCTTCC TTGGATGTGG TAGCGTTTC TCAGGCTCCC 600

TCTCCGGAAT CGAACCTTAT TCCCGGTAC CGGTGAAAC CATGGTAGGC CA

652

## (2) INFORMATION FOR SEQ ID NO:173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1067UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GATCGGGTAG TGAGGGCCTT GGTGAGACGC GGCAAGTGTG CTTGTGGTCT GTCCGCGGG	60
GCTTGCTCCT GGGACGGAC TGCTTGCGTG CTCTGTGTA GACGGCCTTG GTAGACCATC	120
TCTGGTCGTC GCTTGCTACA ATTAACGATC AACTTAGAAC TGGTACGGAC AAGGGGAATC	180
TGACTGTCTA ATTAAAACAT AGCATGCGA TGGTCAGAAA GTGATGTTGA CGCAATGTGA	240
TTTCTGCCCA GTGCTCTGAA TGTCAAAGTG AAGAAATCA ACCAAGCGCG GGTAAACGGC	300
GGGAGTAACT ATGACTCTCT TAAGGTAGCC AAATGCCTCG TCATCTAATT AGTGACGGCG	360
ATGAATGGAT TAACGAGATT CCCACTGTCC CTATCTACTA TCTAGCGAAA CCACAGCCAA	420
GGGAACGGGC TTGGCAGAAT CAGCGGGGAA AGAAGACCTG TTGAGCTTGA CTCTAGTTTG	480
ACATTGTGAA GAGACATAGA AGGTGTAGAA TAAGTGGGAG CTTGGCGGCC AGTGAAATAC	540
CACTACCTTT ATAGTTTCTT TACTTATTCA ATTAAGCGGA GCTGGAATTC ATTTTCACC	600
TTCTAGCATT TAAAGTCCTA TACGGGCTGA TCGGGTTGA ARACATTGTC AGGTGGGGAG	660
TTTGGCTGG	669

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1068RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCCACCNC TNNCCATTG AATCGGTACN ACTCGACGGG CGNNMTGTNN AANCGGNCCG	60
GACCTAATCA ACGANAGCTG ATGACTAGAC GCTTACTAGG AATNCGTCCT TCAAGANCAA	120

TGATTGCTC TGINTCTATC CCGAGTCATT ACNGNCTANC AGACATGATC CTCCATGATC 180  
 TGTCGGTGCT GTGTGGTATN CCGCAGGACN CCGNCNCTGT ACCGCGGCTG CGGCCAGAA 240  
 5 NNICTPANGGG CCTCCAGAC NTGTTATNGC CTCTAACTTN CATCGGNTCN ANACCGANAN 300  
 TCCTNCTAAG ANGTGGGCNA CCAGCANNTG CNCCNGCNC TATTTACTAG GTTAAGGTCT 360  
 CGTTGGTTAT CNCCNITANT CAGACAAATC ACTCCANCN CTAANAACGG CNNTGCCCCN 420  
 10 NCNNOCNGAA NNINNGAAA CANCTCTCAT CTGTCAATCC TTATCGTGTC TGGACCCGCT 480  
 GAGTTTCCCG TGTGAATCT AANTAAACCG CAGGCTCNAC TCCTNNTGGT GCCTTCGGTC 540  
 NATTCCTTTA AGTTTCAACC CTGCGACATA NTCCCCAGA ACTCANAGAC TNIGAT 596

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 641 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1068UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

30 GATCTGGAGG ACCTATATAT ACCATTTCG TCACCTTTC TTTTGTGCC TGATGTITTA 60  
 TAAGTAGACG ATCTCTGATT ATTATCGGA GGTGTTTAA GTCCCATGG AGCACTGT 120  
 TTGCAATGAT GGCCATGGC CACCAGACCA GTCAGAAGTA GATATCTGAA TTGCATGTGA 180  
 35 GGCATACTAG GGTGACCTGT GTTGGGGCC AGCTTCAGG AGGAGGAAA AAAAAAGATT 240  
 GCAGCACCTG AGTTTGGGT ATGGTCACCC ACTACACTAC TGGTCAGGC TCTTACCAGC 300  
 TTAACCTACG TTGATGGAC GGGAAACGGT GCTTCTGGT AGATATGGC GCAACOGAA 360  
 40 TATATAGCCT AGAGCAGACA TGATATCAGA TGGTGGATC ACGTGAGGC GTAGACATGT 420  
 AATAACGATA TCGAGTACAT TTGGTGCCAG ATGGCTGGG CTATGGGCA GATGTGTGGT 480  
 AGTTGGCACA TCGGGTAAG TCACGGGTA RGAAGARGTT TGTGGCATT GGAGTGCCAT 540  
 45 TCGTACCGA ATGTACGTA GTGATCTGAA AAGTGATATG CTATGTGAAG TGCAAAGTAT 600  
 GGAAGTCTG GCTGGGGTA AGAAGARGAT GTCAGTCAA G 641

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 654 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1069RP

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GATGACCCC GGTCCCGCTC GCATCAGCGA GCTGCCCGTG CCGATCAGCA GCCCGGTCCC 60  
 TAGCGACCCG CCGATGGCTA TCATCGACAC ATGACGTGCC TGCAGGTCTT TCTTGAGCCG 120  
 GATGCCCTCG TGCTTGCCAT CGTAGTTCCA GTCTACGGAC TGGGCTCTCT GGTCTGTGCT 180  
 GCTGTGGGTA TGCCGCAGAC CGCGGCCCTC ACCAGCGGCG GCCAGCTTGG GGCTTTTCAA 240  
 CTCGTCCAGC GTGGAAGCCT CTGATGCTG TGCGAACTTC TCTTCGGCCA TAAGTGGGA 300  
 GCTGTATCT ATGCTACTCA AGTCCCGCC GTATAGCCTT GCTATATATA CTTACGCTGC 360  
 GACGCCCTAT TCCGACACA GCTATATATT GGCCCGCGGT CTGGCGGCT GCTTGGGGAG 420  
 CCGACTGACC CCACCTGAT AGTGCCGTG CACTTCTGCT GGGCCGCTC AGCCCGTTCA 480  
 GGTCCGACT GTGACATGG GCTGCGGAG CGCGATTAA CACCGACTG GCCTGCATGC 540  
 CGCACTAAAC CTCCCTGCG GCGCAGGCG GCCCTTATCG CCTCGTGAT GACGTACGTA 600  
 TGTTTATCAA AGATCCGGAG AMCTGTTCCA GGCTCTACG TTGCGATAAG AGGC 654

## (2) INFORMATION FOR SEQ ID NO:177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1069UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GATCTTTCTG CCCTTATCAG GGATGGCACC ACCGGTCTTC ACCTCGTTTG ACTTGTAGCC 60  
 ACAGTGCTCG CAGACCGTGG ACATGATGAT GACCTCTTTG AAGTGTGGGA TGTGACCGG 120  
 CTTCATATGC GTGTACATG GGTGAACACA TGATGGGCAC GTGGCAGTGA AGGCTGCAC 180  
 CTCGTGTGCG AAGTCTCGA TATCCGTAGC GTCAGATAAG AGACCGGCTT GTGCGCTTG 240  
 CGATTGTGTT CGCTCGGCT GCGACAGCTC CGCGCGCTTC TCTGACGOC GTTGCTCCAA 300  
 TTGGTCGCGC GTAATGATGC CCACCTGGAC GTTTTGCTCA TCTGAACGCA GGTACTCGGT 360  
 TTTGGACCAT TTTGGCGCAG CTTGCGCTGG CTTGTATTG ATCCAGGAAT TGCCAGCAGG 420  
 GTCGTCCAGC GTAAAAGTCA GCGGTAGAGT GCGCGCTCG CACGACAGCG CAGCGCGGAC 480  
 CTTGGCAATG AACTGGGCAA TCTGATCGTA CAGGTCTCG TCCACTTCTT TCCGCGCGC 540  
 CTGGTCGGCG TCCAAGTCTT CGATCATCTC GGTCAGCAGG CCTCCACAG TCGTCAGCTG 600

GCCGCGCTTG GGAAGAATCT CCAGGTCCAA TTCAACGAAG CGGGAAGCOG CAGTTTGGC 660  
 CTTGATGACT GCGTGICAAA ATCGGCGCTTC TCCCAACCT TCAGCTGA 708

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1070RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GATCCCGTAC ACGAAGAAAA TCGGACGGGC CAACCAAACC CAAAGTTCAA CTACGAGCTT 60  
 TTTAAGTACA ACAACTTTAA TATACGCTAT TGGAGCTGGA ATTACCGCGG CTGCTGGCAC 120  
 CAGACTTGCC CTCGAATTGT TCCTCGTAA GGTATTTACA TTGTACTCAT TCCAATTACA 180  
 AGACCCGTAT GGGCCCTGTA TCGTTATTTA TTGTACTTAC CTCCTGAAT TAGGWTGGG 240  
 TAATTTGGGC GCGTGTGGC TTCCTTGGAT GGGGTAGCGG TTTCTCAGGC TCCCTCTCCG 300  
 GAATCGAACC CTTATTCCCC GTTACCGGTT GAAACCATGG TAGGCCACTA TCCTACCATC 360  
 GAAAGTTGAT AGGCGAGAAA TTGAATGAA CCATCGCCAG CACAAGGCCA TGCGATTGGA 420  
 AAAGTTATTA TGAATCATCA AAGAGTCCGA AGACATTGAT TTTTATCTA ATAAATACAT 480  
 CTCTTCCAAA AGGTGAGAT TTTAAGCATG TATTAGCTCT AGAATTACCA CAGATATCCA 540  
 TGTAAGTAAAG GAACTATCAA ATAAACGATA ACTGATTTAA TGAGCCATTC GCAGTTTCAC 600  
 TGTATAAATT GCTTATCTT AGACATGCAT GCGTTAATCT TTGAGACAAG CATATGACTA 660  
 CTGGCAGGAT CAACCAGATA ACTATCTTAA AGAACAACCC GAA 703

## (2) INFORMATION FOR SEQ ID NO:179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1070UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GATCCTTTAG TTCTCGGAG TTTGAGGCTA GAGGTGCCAG AAAAGTTACC ACAGGGATAA 60

EP 0 866 129 A2

CTGGCTTGTG GCAGTCAAGC GTTCATAGCG ACATTGCTTT TTGATTCTTC GATGTGGCT 120  
 CTTCCTATCA TACCGAAGCA GAATTCGGTA AGCGTTGGAT TGTTCACCCA CTAATAGGGA 180  
 5 ACGTGAGCTG GGTTTAGACC GTCGTAGAC AGGTTAGTTT TACCTACTG ATGAATGTTA 240  
 TCGCAATAGT AATTGAACTT AGTACGAGAG GAACAGTTCA TTCGGATAAT TGGTTTTTGC 300  
 GGCTGTCCGA CCGGGCATTG CCGCGAAGCT ACCATCCGCT GGATTATGGC TGAACGGCTC 360  
 10 TAAGTCAGAA TOCATGCTAG AACGCGATGA TTCTTTTTCT CGCACATTAT AGATGGATAC 420  
 GAATAAGGTG CTTTTAGCAT CGCTGAACCA TAGCAGGCCG GCAACTGGTG TTCANACGGA 480  
 AAGGTCTGGG CCGGTGCGG CGGATTGCAA TGTCATACTG CGCGAGAGTA AATCATTTGT 540  
 15 ACACGACTTA RATGTACAAC AGGTATTTGT AAGCAGTARA GTAGCCTTGT TGTTACGATC 600  
 TGCTGAGATT AAGCCTTGGT TGCTGATTT GTTTCTATT TGAAGTCTG CAGGACCAGG 660  
 CTTTGAAATA RAGTT 675

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 498 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1071RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GATCTGNGGG GGAAACNCAG CATTACCGT TGTGCAAAAA GATTTGACTG GTAACATCAC 60  
 CAAGCTTGGC AACAGACAAT TGTOGCACCC CGGTGAGTCT GCAACCCGTC AGGAGCTTGT 120  
 GATTGCAGAG CGTGACAGG GCAGCAAGAC TGCTTCGGAA GGGCTGCTGT GGCTCACCAG 180  
 40 AGGCTTGCAA TTCACCGCGC AAGCTCTTAG AGAAACGCTA GACCATCCAG AGCTCGAATT 240  
 GTCTAAGACA TTCACAGATG CGTATTGGAA GACGTTGACG AAGCACCATG GTATGCTTGT 300  
 ACGTCCGGTT TTCAAAGCTG GCCATGAAAG CTGCCCCCTA CAGGAAGGAC TTTTTTGACG 360  
 45 AAAGTAGGCA GCGACCAAGA GAAGGTGAC ACGCAACTTT AAGCAGTGGC TGGCTGCACT 420  
 TGAAAAGATC GTAGAGATTG TGCTTCAAAT CCTTGGGGG AAACGTGCAA AGGATTTATG 480  
 AGTATTATTA TAGAAGCC 498

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 625 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1071UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

10	GATCGACAGC CTCGAAGAAG TAGCCTCCAC AGCTTCAAAC ACAGCGCACA GGTCTGCATA	60
	CATCACGCTG GTGCTTGCTG CAGGCTTAAC CGGAGAACTT TGTGGCGGTG GCACGGCGCT	120
	GGCAGACTGT GGCAGCACCC CCCCCGGGCG GGGCTTATCT GCAAGCTCGG GGAGGATGTT	180
15	CTTCACCTCG GGTCTCTGTT CATGGGCTGC CGGTGCGGCT AGGCACTCGG GAGACTCTAC	240
	CTTCGATTTC TTGACCTCG CTGTTGACGT CGCTOCATCT TGAGGCTCTT TCAGCGCAGC	300
	GAAGAATCGG ACCAATGTGG CCTGCTTCTT TGGAGTAGAC ATTGGGCTGA AGTAAAACCC	360
20	TACTGACCTG CCAAATAGCT CCACCTTGGT CTGGGACAG GAGCTTCNA AGANTGACAT	420
	TNNNTGTNGN NAAGGCCNNN NNNNNCAAA GACGAANCTN NTATCAAGGN CCTNNNTNCC	480
	CCAGNCNNA NAAGNAANAA NNNNATTNNN GGNATTNNNN AAATTANGGT TNNNNNATNN	540
25	NCTTNGNAAA TTNNNNNGNN TTNNNATTC CCNNNGGNTT TCNNNTNCC NNCNCCCTNN	600
	GGVTTTTTTN NANNVNANAN NNCC	625

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1072RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

40	GAGCAACTAT TATTAGGCGC CCCCCACCC AGTCTGCAGC ATTGAAAGC CTTCCTAGCC	60
	TTTGTGGGAT GTCCCAAGGT ACAATTTTCT CGCAGNTGAA AATACGAAAG AAGCGCCAAG	120
45	AAGTGGGCTT CTTTGAATCC AAGCGCGACG CCAATGATGT CGAGGCGGGC GAACATTTTA	180
	TAACAGAGCT CGATAAGGC GATAAGCGC TCGGCTGTGT TTCTTGGATC GGCTTGATAT	240
	GCAATAGAAT GCTGGGACA GGTATCTTTG TGGTCCCGC GAAGATCTTC CAGTCCGACT	300
50	GGCTCAGTAT ACTTTGGGCT AGGGTTATGG GTACTAGGAG CTTTAATTGC TCTAGCAGGT	360
	CTTTATGTTT ACATGGAATT TGGTAACTGC AATACCGCGC AACGGTGGCG AGAAGAACTA	420
	CCTTGAGTGC ATCTCCAATG AAACCGAACT TCTTCACTTA CAGTCAAGTG TACTCAGCAT	480
55	ATGATCATCT T	491

## (2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1072UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GATCGCAGC TTCGGCAAGC GCGCTTCTC CTCGTTGTAC TCCTCGTGGT CGTGTACTC	60
CGGCACCATC GACGCTCCG GCTCTCTCTC ATCCGCGTC GGTCTCTCT CCTGTCCAC	120
CGTCTCCGC AGAAGAGAGT CGGCTTCTC CCCGCTCTG TGTGTGTGC GCTCCAGCAG	180
AGGCCCCGA AGCGCTGCT CGTCCGGAG CGGCCGAGG TACGGTACT TCACCGGACC	240
CATCTCCGC TCAATCCCG GGATCAACAC CTCGCGACG TACCGGTCCA TGATCTGGC	300
ATAGTGTAA GATTACCTAA TTCATACGTG TAGATCATCC CATGCTTACC ATGTTGAACC	360
GTCACCATGT AAATTTCCAA TAATCTCTA GTCTCTCATT TGPAGANATT AGNANCTTTC	420
CTTTATATTA ATNCTTTTAC TNAATAATTN ATNNANNITT TNNITTGANC ANTTCTCCAT	480
ATTGTATTAA ANINATATAT AATATTATTN TCTACTAATC TAACAAATTA NNNCTNTAT	540
TATATATTTA NNNANCATAT NATNATATTA AATTATTIAT AATNATNCTN TCCTCTTNTA	600
ATNTTTAAAT NNNANNVIT TNNCNLANN CTAATNNATT TTINGATATT TTNNTNNIA	660
NNNNNTAAA AAATATNNNN TTTATCNANT ATCTTCCATT TATNAATCN NTTTTATCA	720
AACCCC	726

## (2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 641 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1073RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120

5  
 10  
 15

ATTGAGITTA TATTAAATTC ACCAOCCTCTT ATTCATTCAT TTAATACTOC TCTAATTCAA 180  
 TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG 240  
 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT 300  
 ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360  
 GGTGTGTACC TTAGCTCTCT AATTAAAGTT ATAAATTTAT CTTAACTAAT AAAAATAATT 420  
 AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480  
 GTTATATTTA AATAGATCAA AATTTCAACA ATTTCATTT CATTAGTAC TACCATCACC 540  
 ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTTACTAT 600  
 ACATGGTATT ATGGGTAATA TTTATCCTTT ATTATTATCT T 641

## (2) INFORMATION FOR SEQ ID NO:185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1073UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

30  
 35  
 40  
 45  
 50

GATCTTAATT TAAATTTTA ATTAACATTT TATAATTTAG AATATATATA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTC TGGCATCTTA 180  
 ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAANTAGTA TTTAATTTAA TTTTAATATT 300  
 AAATATACCA TTTTATTATA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
 TTTTATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480  
 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540  
 TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCN TTTTATTATA TTATTTAAAT 600  
 TATTATTAAT TAGTAAATTA TATTTATTTA TTTTATTAAC ATAATTTTIT GNATAATAAT 660  
 AT 662

## (2) INFORMATION FOR SEQ ID NO:186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1074RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GATCTAAATA TATATAATTT AATTTATAAA GATTAATATA AACTTTTTTA TTATAATATT	60
TAAGTATTAA ATTATTTAAA CTATTATTAT CATTATTTAA TAAATTAATT ATTTGATTAT	120
TAATACTTAT TATATAATTA TTATATAATT TACTTAATTC ATCATTATTA ATATTTATAT	180
AATTATAAAA ATAATATTTA ATATGAATAC TATTTAGTCT ATGTTCAAAT TTAAATTAG	240
TTATTAAAAT ATTATTAGAT ATTATTATTT TCTTTAATAA ATTATTAAAT AGATTATCAA	300
TAATTAATAT ATTATTTATT AATTGTTTAT TAAAATAATA TATTTTATTA TTATAAAGAT	360
TTAATTTATT TAAATATTGT AAATTATTAT TTTTATTATA ATATCTATTT TTATAAATAT	420
TATGTTGATT TATATTATTT AACTTTTTAT AAGAATTATT ATTAAAATTA ATTTTAACTT	480
TAACTTCTTA TTATTAATTT TTATATTATT TAATAAATTA TATTCATTTT ATTTATTTAT	540
TTATTTAATT AAATTAATTA TTAAATTAAT ATTTTATCAT TATTTAATTA ATTAATAAAA	600
TATTATAAAG AATGT	615

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1C74UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GATCTTGATA CTAGAGCTTA TTTTACTTCA GCTACTATAA TTATCTTAT TCCTACTAGT	60
ATTAAAGTAT TTAGTTGATT ACTAACTATT TATGGTGGTT CATTAAGATT ACTAACACCA	120
ATATTATATC TATTATCATT TTTATTTTFA TTTACTGTAG GTGGTTTAACT TGGTGTAGTA	180
TTAGCTAATC TATCATTAGA TGTAGCAATC CATGATACTT ATTATGTAGT ACTACATTTT	240
CATTATGTAT TAAGTTTAGG TGCTGTATTC TCTATGTTTG CTGGTTATTA TTATTGAAGT	300
CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATTCATT CTGATTAAAT	360
TTCTTAGGTC TTAATATTAT TTTCTTCCCT ATGCATTTCT TAGGTATTAA TGGTATACCA	420
AGAAGAATTC CTGATTATCC TGATCTATTC CTAGGTGAA ATTTAGTATC TTCATTTGGT	480

TCTATAATAA CTATTATATC ATTAATGTTA TTCCTTTATA TTATTTATGA TCAATTAATA 540  
 AATGGTTTAA CTAATAAAGT TAATAATAAA TCTATTAAAT ATATAAACT ACCTGATTTT 600  
 ATTGAATCAA ATAATATTTT CTTAATGAAT ACTACTAAAT CATCATCTAT TGAGTTTATA 660  
 TTA 663

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 639 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1075RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GATCTATCTA ATTACAGTAA AGCTGCAAAG GGTCTTTTCG TCTTCTTACA AATACTTAGC 60  
 ATCTTCACTA AGATTTCAT TCACTTAGA TTAAAGGAGA GACAGTTGTT GTATCATTAC 120  
 GTCATTCATG CAGGACCATA ATTAGTGGAC AATGAATTTT GCTACATTAT AACCTCATA 180  
 ATAAGGCTGC TATTTAATAA AATTTATTAT TATTATCTTT ATTAAATAT TAATTTTAT 240  
 ATTTTATCAT GGAGCAGAGT TCACACTTTA TACTTTAACT TACGTTTCTG CAAAGTGTG 300  
 TGTTTTTAGT AAACAGTTGT ACAACTTTGT TCTTATTATT AATTATTATT TTAATTAATA 360  
 TCTCTTTATT GACTAACGTC AGAGCTATTT TTGCCAGATT CCTTTCCTTT AATTATCTAA 420  
 TTCACCTTCA TATACTCTAC TAACATACTT GAGTGGTCT ACATTACGGT ATTTTATACA 480  
 TAAATATTTT TTGAACCTAA TAAATTTATA AAGACATTAT TTAAGTTAAT TTATATATTA 540  
 GATTATTTCT ATCATATTAT ATTTTTAAT ATATTACTTA AGAACCGCTT TTATTGTTAA 600  
 ACCTTATGCT TTAGGTGATA AGGATTATAC CTTATTTTC 639

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1075UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:



EP 0 866 129 A2

GATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGTTAA 60  
 CAATAAAATT CAATAATTTA TTAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA 120  
 5 TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTTG 180  
 TGCCAGCAGC TGCGGTAAGA CAANGGGGGT TAGCGTTAAT CGTAATGGCT TANAGGGTTC 240  
 GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA 300  
 10 GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA 360  
 TTAATTGACA TTGAGGAAAG AAGGCTAAAG TAGCAAATCG GATTGATAC CCGAGTAGTT 420  
 TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA 480  
 15 AATTAAAGTA TTCCGCTGA TGACTACGTT AGCAATAATA AAAATCAAAA CAATAGACGG 540  
 TTACAGACTT AAGCAGTGGG ACATGTTATT TAATTCOGAT AATCCTCCGA TAAATCTTAC 600  
 CATTTTTTGA ATATTTAATT ATAATAATTT ATAATTAATT ACAGGGGTGA CATAGTTGTC 660  
 20 TTC 663

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 650 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1076RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT 60  
 ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT 120  
 40 ACAATAATG AAAAGAAAAT TATAAATACA AATACTGTGA CTAAATCTTT AAAAATAAAA 180  
 TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240  
 TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA 300  
 45 TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TOCTCATAAT 360  
 CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420  
 GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480  
 50 GTTAAATAAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TTTATAAGAA 540  
 CCATAATATA AACCTTTACC AATATGAATA TACATACCAA TAAAGAAGAA TGAAGCACCA 600  
 TTAAGATGCA TATATCTAAT TAATCAACCT AGTTGTTCAT CTCTCATAAT 650

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 663 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1076UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GATCTAGAAT TATTAAGTCA ACTATTAAC T AATACTATA ATAATAATGG TTTATCATTA	60
AAATCATTAAGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA	120
AATTATGTTA ATAAAATAAA TAAATATAAT TTTACTAATTA ATAATAATTT AAATAATAAT	180
AAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATTCTT	240
ATAATATAT TATTAGGTAA ATATTTACTA GGTAGTAATA TCCAATTARR GGTAGACTA	300
TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAGGTAC ATTTAATAAT	360
TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT	420
ATTAATAAAC TTAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAATTAATA	480
TTAAATACTA TTTAATAAAT ATTCTATAAG TAATTTCTTA TTTATTTTAT AACATTTTAA	540
AATGTTTTAT GTTAAATAGA TAATAATCAA TTAAATAATA AAAATTAAGA TGCCACAAAT	600
AATCCATTTT CCTTTATGAA TCAATTAACT TATGGTTTNC TATTTATTTT ACTAATTTTA	660
TCT	663

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 642 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1077RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GATCCAGTTA CTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTGGTTAA	60
CAATAAAATT CAATAATTTA TTAAATAAT GATTAAATAA TCICAATATA AAATTATTAA	120
TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTTG	180
TGCCAGCAGC TGCGTAAGA CAAAGGGGGT TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240
GTAGAATGAT TATTTAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300

GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA 360  
 5 TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTGATAC CCGAGTAGTT 420  
 TTAGCAGTAA ACAATGAATA OCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA 480  
 AATTAAAGTA TTCCGCCTGA TGACTACGTT AGCAATAATA AAAATCAAAA CAATAGACGG 540  
 10 TTACAGACTT AAGCAGTGGG ACATGTTATT TAATTCGATA ATCCTCGATA AATCTTACCA 600  
 TTTTGTGAAT ATTAAATTAT AATAATTAT AATTAATTAC AG 642

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1077UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GATCCGIGTA TTTTITATTT ACATTATTIA ATTAAAAATA ATGATTTAAA TAAATATTTT 60  
 30 TTATAAAAAA TAATTAGTGC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAAACC 120  
 ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTTAC TTAATTAAGA ATTAGGAACT 180  
 TTATCTATTA GTCTGGGCTG TTCCCTTTT GATTATTAAC CTTATCGCTA ATAATCTGAA 240  
 35 ATATTTTAAT TTAGATTAAAT AATATATTCT GAGATTTAAT ATTTTAAATA AAATAAATAA 300  
 TTATTCCTTA AATAATATTIA ATAACTATAC CATATATATC TAATATTAA ATAATCATAC 360  
 TAACATATGT TTCGTAGAAA ACCAGCTATT TGCAAATCAG ATTTGACTTT CTCTACTTAC 420  
 40 CATTATTCAT CAGATAATAT TGCTACATTA ACCTGTTCAA TCGTTTTTAT ATTTTATTAT 480  
 ATTTTAAATA TAATAAATAT ATATTTTAAT CATTGATAA TAGTAAGATC ATCTGCTTTC 540  
 GGGTTAATTA ATATTAACTA AATTAAATT ATTTTAATTA ATTTTAACAT TGTTAAATAT 600  
 45 TTATATTATT TTTAATATCA TTTTITATTT TAATATTATG CTAATATTAA TTAATTGC 658

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1078I1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

	GATCTAGTTC GTTAACTTCC GCAAACACC TGTCAGGCG TTCAACAAAC GTCTGGATCA	60
5	GATCCAAGAT GGCCAGTTCT GACTCCTGGT CGTCGACAAT GAAAGTAAAA TAGAGTGTTC	120
	CATAGTTCTT GTAGATTATT TGGATATCTT CGTTAATGGT TTCACTACCA CTCGATAGTA	180
	GCGAGGGCGG CGTAATTAAG AATGAAGACT GAATTGAAGT GTTGGGCTGG CTGATCAGCT	240
10	CGTAAACCTG CTCAGTAGT AGCTTCTGCT TGGGAGATC GACAGGAGTA TAGTACTTTA	300
	CAAGCCTAGG TTGGCACTTC TTGTTAACTT CATGTGTTAG TAGGATAATT TAAGTACTGC	360
	GGCTGCGCGG TGGCAAAGGG GTTCACCCAT ATCAGGACGG CGNCGNNTCA TCNCGTCC	420
15	CCACCACGGN TACNCGCCNC NOCCA	445

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1078I2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

	GATCTAATAT TCAATTGGCA AACTCTTGAG AGTGTCTTGG AGGAAATTAT TCAAGGGGGT	60
	ATGGTAATTG AAACGAACGT GAAGAAAATT GTGGAGACG TCGACGAGCT CAATAGAACT	120
35	TCTAACCAGG AAGCCAGGTT TGGGAATGGA CTAGGAAACG CTTTTCAGGC CATCACCATG	180
	GGTGGCTTTT CAAATTGGGG TCGCGGCGAG TGAATATTAG CACACACTGT CTTGAAACCC	240
	CATAATAAAT GAAATAAATA CTCCTTGCTA GTGTCTAAGT ACGAAACAAC GCCAAGGCTT	300
40	TTGGATCATC TATGTACGCA TTCAGTTGG CAGCACTCAC CATGGGCACC AACTCTTCTT	360
	ACTTGCTATT TCCTGTGCTT TCATTGCGC TTCGGCTGCC TGATGTCTC AAAGCTCCTC	420
	CCTAATCCTC TGTAACTCTC CTG	443

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1078RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

5	GATCAGGATG GCGATGAGAT ACTACCTTGA AGCAGCAGCC TTGACCTCAG CTAACCTCCGC	60
	AAATTCCTTT CATTTTTCGA AAGCAGATTA TAATTGCTTC TAAGCCATTC AATTGCTTTA	120
	CTTTTCGGTT AATCAATGCT CTATTTTACC ATCATTOGAA GTAAGAGTAT GTCGATATGT	180
10	CTGACCTAAG CTACAGATTA TCTAATCACA TAGTTATGTA CGAACCAATA AGATTATCGA	240
	ATTTGCTTGA AAAACTCAGG CGAACGGCAC AGCGTTGCTT GCGCCTATTA GATGCTTTGG	300
	CCATAGCATA TCACGAAGTG ACCTCACAGT TTTTAAGTAA CCGGAATAGT CTGTAGATAT	360
15	GGTATTGTGA AAAGTTTATT NGCTGGTTTC ACCCCCTGGG AATCTNGGNG CTGNCCTGGG	420
	TTCTTAGGTG GGAATCCGG NCCCCCNNT C	451

(2) INFORMATION FOR SEQ ID NO:197:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1078UP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

	GATCTCCTTC CTTCCTGGTG TCTTGCCAAG CCCTTATTIG TTGACCAAAG TATTCTTCAC	60
35	CGTTGCCCTG TACTCTGTTC TCATAAATTT CCGCGGTAGG ACACTCTCG GCTTTCTCTT	120
	GGGATCTAT GAGGGCTTTG CAATCATCTT CACCGCCGCT AAAGTTTCA CACCATTTTT	180
	GATGAGCAG CTACTTCAGT AAGCCCCGT ATTAGGATTG TTAAAAGAAG TAGGATOGAT	240
40	ACCTTCAAT TCCAGATGAT CGTTGCGGTG GGCTATTAAT TTGTTAGCCA CCTAATACTG	300
	AAATTTACAT ATTATTGCAC TAGTTAATTA ATATTTATGA TGCAATGGGA ATCTATATCG	360
	GTCTCCGTT CCATCTTCTC GTAATTAGAT CACGTCCGAT ATNGTNGCCC CGTACCGAGG	420
45	AGGGACCOGA TTGGNTTAT CTTTATGGTC CCGAGAANTN ATAGAGNGCC NNAANATAGA	480

(2) INFORMATION FOR SEQ ID NO:198:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1079RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GATCGCTCAT TATTTTGGT CGGAGCCTGG GCGCTCTCT GCTTCTTCTC AAATACCTTC	60
AAATTTTGGT CTATATAGGT CTGCAGCTCT TCGTCTCTCG AACATTCCGC CTGTGAAGC	120
TGGTTGAAAT ACTGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT	180
ATCTCTTGCT GGAAGTGTTC TTGTTTCCGA ATGGGTTTTT GCGCAGTTG AGCTTGCAA	240
CTGGTTGTAT CAGACTCGTC CACTTCATCT TCCAGTCCA GTGGATCCAT CCTGCAGCT	300
AGCTTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGGT GTTAGCGCGC TCACCTTCTG	360
CGACTGTTC AAGATGTGCG TTTCAGCAA GAAAAGAGAC AACCGAAGT ATAAGTACAG	420
CACGCGAGCC TAATTTTGTG AGCTTGCGGA TTTAGCTCAG TTGGGAGAGC GCCAGACTGA	480
AGAGAACTT CGGTCAATCG TAATCTGGAA GTCTGTGTT CGATCCACAG AATTCCGATA	540
TTTTTTGCTC ACGTCACCCA CCGGTANGA ACTGGCATTG CCTACCTAAT GGCCAGCAGT	600
GGAAAGCGCT CTTGTGATAT ATATATATCA AGTAACACAT CTATGTAACC TTTTGACACA	660
GTCCCAAGGT GAATCTTGCC TCGGATCTGC CTCATCTGAR TCC	703

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 673 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1079UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GATCAGCGAG CTAGGTACCC GGACGAACAT GCGTTGCGC AGCTTCCCAT ACTTCAGCGA	60
CCGTGTGTGT AGCGCAGAGC TTCGTCTCTG GAATAGCGAC TGCACCTCTG CGTTCAGCAG	120
ATCGCCCTCT TTCAGAAAGC TGCGCATCTG CAGCTCATCG CTCTCAGACT TCCGCCGCAG	180
CACGCCGCCG GGCAGGTTCA CAGAAGCCAG CATGAGCACT GCGTCTGCT TCCGCCAAT	240
ATCCACCTTC CATCGTTTGT TCGCGACCTC CACGATCTG CCGACAATGT GGTGCGCCGT	300
CTCTGGCGTG TACCGCCCGC GCCAAGGAAT CACGACAGG AGTCGGTTCA CCCTGGAAAC	360
GGTGGCCGCC ACGGACGAGT ACGTTTGTGT CTCCAGGAAG TATGTGCGGT GGCTCGCAT	420
CCACACAGGA TCATCTGTAA TCAGCTCTCC TGGCGTCATA ATCAGCGAG AATCCGCTCC	480
TTCCATCTCC ACGTCCAAAT CAAACTCTTC TTCTCATCG TCCAGGTACT GGCTCGGATG	540

GAAGTGAAC CCACGCCGCT TGGGATCGT TATTACCTCG CTCATTACTG CTGAGACGAC 600  
 ACGTTTCARA ACTTCAGAGG CTCGCTAGGC CAGGCGAAAC AGTGTGARG ATACGCTTTG 660  
 5 TTAATTCCTG AAG 673

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1080UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GATCCGGCCA CGCATGTATT CCACTATGTA CGCTATATCG CGGCCTCGCC TCCGTGCGGG 60  
 GCACCGCCTT ACACCTCAAA GCGCAGCCT TTTCATGCAGC CCTTGTACTT TTGCACCACT 120  
 25 TCCTGGCACT TGACCGCATC CAGCGCGTTG AACAGCAGAC AGCTGTCTCT CGCTTCCTTC 180  
 TCGGCTTGC ACACACAGCA TGGCTTTTGC TTGTGGTAC TACTACCTTG TGAAACACCT 240  
 GGCACAGAAG AGGATTCAGG CATGATTAAT GCTACAGTTC TTGGAGATCT TCCAACACCG 300  
 30 CCGCTCCTT GGGGTTTTTC TCACTTTATT TTTGCTTCAA CCGCAGAAAA TTGTGTGCGA 360  
 ATTACAATAT ACAGAGGCGC AGTAACCCCT TTAGTGGCTT TTTGGCTTCT TGGGCTGGAA 420  
 ANTINGACCC CCCAACNVNC C 441

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1081RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GATCTTTGCG AGTGACTAGT GCATGCGGCT ATTTAAAAAG TATCGAGTTA CCCTTGGAAG 60  
 TTTCAGCATT TATAGTACTG ACGGAGCCGC TACAAAGCCA AGGCTTTGAA GGTACTAGGA 120  
 GACATATTCA GCGCATATAA TCACCGCAAG CTGGATTGAG CGATGTTTTG GGTGTGTTTT 180  
 55 ACAGGAGCCA GCGCGGTGGC ATGCGTTTTT GCGTATGGGA TGGTGGACCG ATATCTCTCC 240

TTCAAGCTGC ACAGGCATAC GCACCCGTTT GTGTTGGTAA CACTTTTCGC AAATATGACA 300  
 CTGTTGCTCT CGATCACATA CCTGCTTCCA CTOGATGTGT TTTACTCAA CCAGACAAGC 360  
 5 GGGCGGGAAG ACGAGCGGCC AGAGCTGCCG AACCTCGCGT TGTTCGGGC GGTGATCTAC 420  
 TGGGCGGAGT TTGTGATATG CTGGTTGGTG TTCCCGGTGC TGATTTOGTA CGTGGATCTC 480  
 AAGTACTTGT ATCCGCGCGA GCCACAGGAG CCGGGCGGCC GCAGCGTCT TCGGCGACTG 540  
 10 CGANGCGCCG TTATATGCAA TCTCAAGTTC TATGGTCTTT GTCTACTGGG GGTGATCTGC 600  
 NGGCTGGTAT ATCTCAAGAC GACGACGAT CGCGGGCGTC AGAC 644

## (2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 669 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1081UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GATCCAAGAC GAGCTGCGCC AGGGGAGAAA ACCCCCCAC ATATGTCCAG CGATAOGCTC 60  
 30 AGCATGGAAA ACCCAACCGT GGACTTGCGC TCGTAGTGT GCTTGGGCTG TCGATATAC 120  
 TTCAGCACAG ACATGATGAT TTTTATAAAG TACAGCACAT GGCAGTAGAA CAGTGTGAC 180  
 TGATTGTICA ACCCTGTTTG CGTAATGCTA ACCACATATT GCACTGTGCC AATGCAAAAA 240  
 35 AGCCCGATGA ACAACTGCAT CATCTTCGG TGGCTGTGC TCATCCTATT CGCCGGCTCT 300  
 CCGGTGAAGC CCCATAGTCT GTGCCCCAT AGCACTGGG ACGCCAGCAG TCCGTTAAGA 360  
 AGCCAGCTAT GCATGGCATA CCAGTAGTCC GACCACCTA CCGACGGCT CACCGGCTG 420  
 40 GACGTGTGCG CTTCATTCTG CCAGAGCAG TCTGCACAAC CAGCGAGAGT ACTAGCGCTG 480  
 TATACCGGAT GCAATTAAAC ACCACGTAGC CTTTGGACAA TGCTCTTGG CTCTGCGCT 540  
 TCCAGTTGAT CCATAGTGGC GGATACATCG ACACCGACCA ACATGTGCG TACAAGTATC 600  
 45 CGAGCAACTG TCTCTTCTC ATTCCAGCT CGTTCCAAGT GCTTCTACGC CGGTCTTCTG 660  
 GGTTCAGAT 669

## (2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 654 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1082RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

	GATCCACGAG CAAACTAATTA TTAGGGGCCC CCCACCCAG TCTGCAGCAT TCGAAAGCCT	60
10	TCCTAGCCTT TGTCGATGT CCCAAGGTAC AATTTTCTCG CAGCTGAAAA TACGAAAGAA	120
	GCGCCAAGAA GTGGCCTTCT TTGAATCCAA CGCCGACGCC AATGATGTG AGGCGGGCGA	180
	ACATTTTATA ACAGAGCTCG ATAAGGGCGA TAAGCGGCTC GGCTGTGTTT CTTGATCGG	240
15	CTTGATATGC AATANAATGC TCGGACAGG TATCTTTGTC GTTCCCGCGA ANATCTTCCA	300
	GTTGACTGGC TCAGTATACT TTGCGCTAGG GTTATGGGTA CTAGGAGCTT TAATGTCTCT	360
	AGCAGGTCTT TATGTTTACA TGGAATTTGG AACTGCAATA CCGCGAAG GTGGCGAGAA	420
20	GAACTACCTT GAGTTCATCT TCAAGAAACC GAAATCTTC ATTAAGTCAA TGTACTCAGC	480
	ATATGTCATC TTTTTAGGCT GGGCCGAGG TAACTCTGTG ATGGCAGCTG CAATGTTCCT	540
	TGATGCTGGA AAGTGAAG CAACACGTTG GCGTTGAAG CCGTCTTGA GTTGCGGTCA	600
25	TTTTCTTCTG CTTCCTTGTC AACTCTCTCA GTGTCAAAGC TGGGTGTGTA CTTC	654

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 680 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1082UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

40	GATCCGCAGC TTCCGCAAGC GCGCTTCTC CTCGGTGAC TCCTCGTGGT CGTCGTACTC	60
	CGGCACCATC GACGCTCCG GCTCTCTC ATCCGCGTC GCGTCTTCT CCTCGTCAC	120
	CGTCTCCGC AGCAGCGAGT CGTCTTCCG CCGGCTCTG TCGTCGTGC GCTCCAGCAG	180
45	TGCGCCCGGA AGCGCTGCT CGTCCGGAG CGGCCGAGG TACGGTACT TCACCGGCC	240
	CATCTCCGC TCAATCCGC GGATCACAC CTCCGCAGC TACCGTCCA TGATCTGGC	300
	ATAGTGGTAG ATTTCGACT CCTTCGTGT GTACATCCG GCGTCCAGC TGATCCGCAC	360
50	CAAGTGGTTC ACGAACTCCT GGGCCGCTT GTAGTGGTG AGCTTCTTT TCACCGTGC	420
	GAGGCTGAGC GCGTCTTGA TGATCCGTA GTAGTGGGA TAATCTTCC TCAGCGCAA	480
	AGTGTAGAAA ATCGCAAAA TCTCAATACC ATTTCTCTC TTAAAGTCAA ACACGCATC	540
55	CAACAAACT TTGAGCTGGT CCGTAGCAA CATCGTTAGC CCTCGCCACC TGAAAGCTG	600

AAGACTTTGG TAGTGTACTA TGTGTTCCGA AACAAATCC CACGGTCCGT TTCTGCCCGT 660  
 TCACAGCCTT GCTTCAAGTT 680

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 613 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1083RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GATCATCAAT TTCTTTTGG CTGTTTCTT ATTTACAGCC TCTATTCTG AGCGAACATG 60  
 CGACGCCACA GCAGTCTAA TGAGCTCATC TGTTAGTTGG GTTGCAACCG CGTTACGCAG 120  
 TTCATTCCCT TCTATTGCTT TGGAGCCAGA ATCTCTAGCT TCATCTTGAG CGCTAGCTTC 180  
 AGTTTGGGCT CCCAGTTTAA AAGCTGTTG GTTAAATGA AAAGTATTTT CCTCTTTTAG 240  
 CTGGGAATTG CCAGCAAATG GTTTTCTGTG CGATGACTCA AACGGTACAT CTTTTTTAGT 300  
 TTTTGTTCCT TCTAAAATAT GCGGTGAGGT TGTAGAGCCG AACTAGACA TAAATGGTGC 360  
 CGTAAACTGT TTCGTGGACT GCAGATCAGA CTGTGCTGT GCGTTGAACT GCATGCTAGA 420  
 TTTCACTTCA CTTCACGCG GGGATTGGGT AGTGGGTTGG GTAGTCTTAT AATCTCCACT 480  
 ATCGAAGTTG AAAGTTTLAG ATATATCCTG GTGTCTCCG TGCAAGGAAG ACCCCTGCTC 540  
 AATGATGCTT TCCGAATATG TGGGTAGATT TGAATCATTG CTCCTAGNA GCAGCATCAT 600  
 CCTCCGAAAG AGA 613

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 656 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1083UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GATCCTGAGC GGTGCGGACG AGGAGGAGCG CGAGGAGGAG CCGGAGGCGG TTGTGGGGGA 60  
 AACCGTGAGC CGCAGCGCGA CCGGCGGAC GAAGGGGCGC TTGCGGATG AGGAGGCGGA 120

GAAGGCGGAA GAGGCGGCGA CGGCGCGCTC GGAAGACGAG GAGGCGCCCA AGAAGGCGCG 180  
 GAAGTAGCGT AGATAGAAGG ATATAACTGT AAGTACCAT GCAAGACGAA TCTGAGGCGG 240  
 GGGACGCGC GCTGCGCGG CGCGCGGTA GCTGCGGAGG GCAGAAAAA TCGCGTGA 300  
 CAATCTCTGC GTCATCATCC CGGCCAGAGG ACAAGATGCG TGGCAAGAAG ATTGCGGGTG 360  
 TGCTAGGCGC GACGGGCTCC GTGGGGCAGC GGTATTATCT GCTGTGGCG GACCACCTG 420  
 ACTTTGAGCT GAAGGTGCTT GGGGCATGCG CGCGATCGC TGGCAAGCGG TATGCGGACG 480  
 CGGTGAATTG GAAGCAGACC GAGCTGATGC CGGCGTTTGC CGAAGACATC GTGGTGAGCG 540  
 AGTGCAAGGC TGAAGCATTT TGGGCTGCG ACGTTGTGTT CTCTGGGCTC GATGCGGACT 600  
 ACGCAGGCC CATCCAAGCG GGAATTTGCC GACGCGGAC TGGCTGTGTG CTGAA 656

## (2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 453 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1200RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GATGCTCAT TATTTTGGT CGGAGCTGG GCGCTCTCT GCTTCTCTC AAATACCTTC 60  
 AAATTTTGGT CTATATAGGT CTGCAGCTCT TCCTTCTTC AACATTCCGC CTGTGAAGC 120  
 TGTTGAAAT ACTGCAGGGC CTCTGCACTC ATGCGATTCA CCATTGAATT GCGCTCTTGT 180  
 ATCTCTTGCT GGAAGTGTTC TTGTTTGGG ATGGCGTTT GCGCAGTTG AGCTTGCAA 240  
 CTGGTGTAT CAGACTGGTC CACTTCATCT TCACGTCOA GTGGATOCAT CCTGCAGCT 300  
 AGTCTAGGTG GAGTGGTCTA TGTACAGTGC TGCTGTGGT GTTAGCGCGC TCACCTTCTG 360  
 CGACTGTTCA AAGATGTGCG TTTCAGCAA GAAAGAGAC AACCGAAGT ATAAGTACAG 420  
 CACGCGAGCC TAATTTTGTG AGCTTGCGGA TTT 453

## (2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 590 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1200UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

5 GATCAGCGAG CTAGGTACCC GGACGAACAT GCGTTGSGC AGCTTCCCAT ACTTCAGCGA 60  
 CCGTGTGTGT AGCGCAGAGC TTCGGTCTTG GAATAGCGAC TGCACCTCTG CGTTCAGCAG 120  
 ATCGCCCTCT TTCAGAAAGC TGCGCATCTG CAGCTCATCG CTCTCAGACT TCGCCGCGAG 180  
 CACGCCGCGG GGCAGGTTCA CAGAACCAG CATGAGCACT GYGTGCTGCT TTCGCAAT 240  
 10 ATCCACCTTC CATGCTTGTG TGCGACCTC CAGGATCTG CCGACAATGT GGTGCGCGT 300  
 CTCTGGGCTG TACCGCCCGC GCCAAGGAAT CACCGACAGG AGTCGGTTCA CCTGGAAC 360  
 GGTGYCCGCC ACCCAAGAGT ACGTTTGTG CTCCAGGAAG TATGTGCGT GGCTCGCAT 420  
 15 CCACACAGGA TCATCTGTAA TCAGCTCTCC TGCGTCATA ATCAGCGAG AATCCGCTCC 480  
 TTCCATCTCC ACGTCCAAAT CAACTCTTC TTCTCATCG TCCAGGTAAT GGCTCCGATG 540  
 GAACTGAAAC CCACGCGCT TGGGGATCGT TTTTACCTCG CTCATTACTG 590

## (2) INFORMATION FOR SEQ ID NO:209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1201RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

35 GATCTTGGAG ATGAACCCAA TATGGAACAC GGGCTTGGC AGCTGATGT GCGGAAAGTG 60  
 GCGCGGCGAG TCGTTCTATC CCGGCCACA CGTCTGACAC TTGAAGTTCC GGTGATGGA 120  
 GCGCAGCCGG GGTGCTTCA GCGCTCCAC CTTTGGCGC ATCTGGTCT CTCCATCGT 180  
 40 CTCTGGAAC TCAATCTTGG CCACGAAAT CGCCCGCACC TCGTGGGCG AGAACAGCCC 240  
 AACTGCAAC TCGTTGATGG TCGCAGAGG CGCGCTCGAA TACGAAAGT CCACCATCGC 300  
 TGTGCTGTAC TACCGCTCC GGAGATACAC CGTTTGCAA GTGTGTGTG GCACCTGACG 360  
 45 CCCAGCCGCC ACTCGCAATC CTGTTTACG CCGACCGCTT TGTTTGGCTC CCTTGGCGCA 420  
 ACAACGAAGC TCTGTATAT GTGCGGCTC GAGACCTAA GCTGCTCTT GTGAACACA 480  
 CGCTCAGCC CAGAACTCG TGTCTTTACC TTGAGCTCT GGAATTGGTN CGCGCCAAAC 540  
 50 CNGCTTATTG CTGGGGGAA CNGCTATGCT CCGTGTATC TCAGCTGGAA TNCACANAA 600  
 ACNGACCCC CACCTACCC NCACTCTGG TTATTTGATT TTGCGGGAA TAAACNCANT 660  
 GTTNCATC CTTCACCC CAACTGTGT NTCNCTGTT CNGTNCNTN TTACTIONA 720  
 55 CCTCCNACN CCAATTTT TTNCCGTTG CCT 754

## (2) INFORMATION FOR SEQ ID NO:210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1201UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GATCCTCCGA TTAGCCTCGT CTTAAACTC AACCAAGCTG CTCGTAAACA AACACACGT 60  
 ACCACTTCTG TGTTGTTTCT CTGCGCTTGT TGACCGTCCC GCAACTACTA TGTCGTTACG 120  
 TGTTTTTTTT CCGGAAACTT GCCACCGTCT CAGAATCAGA GGCTGTGAGA TTCTTCTGTC 180  
 GAATATCGCT CTGGACGTTT GCTTACGTGC GCGCCGCCAG TGCTCTTAAC CGGCGCGTA 240  
 GCGCCCGGCC CTGGCCGGTA CCAACAAGCA TGGCAGGAGA CACAGAGTAC TACAAGCAGG 300  
 CGGTGGAGGA GTACGCGCGG CTCAAGCAGG ACACCGACCC GGAGGAGTGG GACAGGCGGA 360  
 TCGGCAGAC GGGCTGCTAA GTGAGAATA TGGCGCTGCA GCTGTGCCAC GCGGAGACCG 420  
 GGGACTGGCG GCGGTGCGCG GCGGACATGG CGCGTTCAA GCGGTGCTGG GCGGCGCAGG 480  
 CAACCGCGAG CGCGTGAAGC ACCGTGGAAG GTGAGCTGGG GCGTGTAAT AGGTGTATCT 540  
 GGAGCGGTGT CAGGTTGACA CTGGACAGT TACGAANCAT TTTTCGGGNN GGCNCGCCA 600  
 ATGGCCANCC CCNATCTNAN NACCCAAACN GGGGTATGAT NTN 643

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1202RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GATCGAAAC GCTGCCACG AAAGCTTGAC ACTGAAGGGA TTTGAGTATT CTCCTGCAIT 60  
 TTCCAAGGCG AATACCAGCT TGTCACAGC TGGCGATCCA ACCTTCCCCT CCTTCAGGCG 120  
 CTGCTTGATC CTGTGCTCTA TCTGCAGCTG AGGTAGCAGC TCTGTGATCA GCATGACGAC 180  
 GGCAGCGCA GAGGTAAAC CTTTCAGAAA GGCCTTTGAG ATTGCATTGT CGATGAAACC 240

EP 0 866 129 A2

GAGCCTGAAG ATGCCCATGG CGAACACCAG GACCCCTGAT ATGCATCOGA TAACCGCAAC 300  
 GGTCAATCAAC GGTTCAGCG ACTTGTCGC CCATGCATCG CAGCTCTGGC CCACCACAAG 360  
 5 GAGCGCAACC GTCTGCGGCC CTACAACCAT CGTCGGGACG CTGCGGAAGA CTGCATATAT 420  
 CAGTGGGGGG ATCAACAGTG CGTACAGCCC TGGCTATGGT GACACATGTG CCATAGTGGT 480  
 CAGCGAAATG GCCAGCGSTA TCTGGAATGA CGTCAGGTC AGCCCGAGAA GCATGTCTTT 540  
 10 CGCATTTTCC CAGAATACTC TGSCAGCCAG CGTATAATGG GCCGTAGTAA GACNCATAAA 600  
 ATTNTTTTCC TNCCTACCGT TGTCNNTTTA TNGNCTGTAC CCNTACGAC TTGTCAAAAG 660  
 CAGTNNCCCC CCGCCCGGAG ACTTCCANCC CTTCCCTACT CCCAATTTGG ACCANGACCC 720  
 15 GGTTCCTGGT GCTTN 735

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1202UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GATGCGCGCC GCGCCCCAGG ACTACGTGGA CTCTCTCTCG CTCACACAG TACTGGACGA 60  
 CCGCGAGCAG CCGGAAGCG ACTGCGTGA GCACAGCTAC ACGCCCGATC CGCTGCAGCT 120  
 CGCCGTCTAC GCGCAGCGCC AATGAGAGCT CATGCTCTCC GCGCAGTGG ATTTTCTTGC 180  
 35 CCGCGCGCCG CAGCGCTCCG CTTGGCGGTC ACCGAAGGCC CAGCGATGAC AGCCAGGTC 240  
 CAGGATATCG TGGTGCCAC CGCCGGGAC AGCGCGGCG GCGCGACGG GCGCCCCAAC 300  
 CAGGCGGTCA CCTTCCCGT CGCGCTGAC AGCGGACCG GCGAGGTGCT CGTGGCAAG 360  
 40 GGCACCGGCA AGACCCCGT GCGCAAGGC CAGACAGAAG AGCAGTACTG CGAGCAGCTG 420  
 CAGCAGTACT TCGAGGTGA CGCGGTGCC GAGTGACGG ACGAGGCTG GCTGACCGC 480  
 GCGCGCGCCG CCGCGCGGC GCGCAACAG CAGGAGGCC AGCGCTGCG CCGCGTCTA 540  
 45 CCAACGCTC TACTTCTCG CGCGCGTGG CGAANCGCC GCNNTGCCC GCGACTGCTG 600  
 TATACGTTCC CNGTTCGGG CNGCTNCNA TNGCGCCG AANNTCTNA NCTNNNNCT 660  
 NNNTCTNNNN GACCCNNNNN CCTTAATTT TTNNTTNNN NNNTTNTCTT TCCCCCTCC 720  
 50 NCTGTACCC TCNCTNCNT CNGGTNNNT CNGTTGGTG NGCTNTCTTC CNVNTC 777

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 756 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1203RP

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GATCAAACAG CTGCAGTTGT TGAAAAGGTT GCTTGAATCC AAACCAAGGA AGGACGTATT	60
TTCTGTTTCTA GGCCTGGATA ACTAATCTCT TCTCCACTCT AGCTGGGGAT AACACCTGCA	120
15 GGACGTGAAC TAACAAGTTG ACTACTATAC AGCAAAATAA CTGGAACAAG TTATACAGAA	180
TTTTGTAAAT ATATTATAGC AGCCCTATTA CTATAATTCC ATCATTGTGT AACGCTTTAG	240
CCTTCGTTCT CAGACTCGTC GTCATTTTCT TCATGATAGT TGATATTTTT GCGTTGCCCT	300
20 GAGCTTTTCC TTAGTGGGCC TGCAATGAGG CTCTACTCTT TTGGCTGTGA GTCACTGCA	360
GAGCTGGTG TATCTTCGTC CTGCTTCCC TCATCGACAA CTTTGCGCTT CTTCTTAGTT	420
TTAGATGAGG CTGATGATGG CCGTTGGGCT TCTTGAATTC TCTTCTCTG CCGTTGGGGA	480
25 TGTTGAATTG GCGGATTAG AGAAGCGGA TACTTTGGCC CTTATATTTA CTGTCAAGTT	540
TTCAACATGC TGGTCTGATA TATAGCTCAT GAACGGGTTT CTTTGCGCTT CTTCCCATAT	600
TGGGGAATGG CTGATAAAGT TCAGAAGGCA GATTAGCTCC CAGGTAGACT GGTAGATTCC	660
30 ACCCCCGTTG GTTTTAGCTC AAANATNATC AATTGGCAAC CNGCTAGANA TAATNINTGA	720
ACATATGCTC CGTGTGGGAT CCGTTGGGAT CTTCCC	756

(2) INFORMATION FOR SEQ ID NO:214:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 781 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1203UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GATCATTTGC TGCTGCTCG GGGAGACCAT CTGGAATGC GACACTGTGT CGATGTCTGT	60
50 GCTCGGGAAG ATCTTCAACA AGTTTCTGAC ACACGATTTT GGGCGCTGC GCTCCCTGCA	120
GGCTCCGCG CGGACCCCG CCTTTGATTT TTCTCTGACG ATCTGCCAGT CGTACAGTAA	180
CCGACTCGGG CGGCAATTCA CGAAGTTCTA CTCGAGATC CTGTACGGGA TTACGAACCC	240
55 TGGCTCGGCC GGCTCAGCG AGACCGGGG CCGTCACTCG AACTTGAAT CCGAGTTCAA	300

GACTCTTCTG AAACTGCATA AACTTACGGC CAACATATGG GAGCATGTGC CGGAAGTGGT 360  
 GGGCTCCGTC GTCCGATTTC TGCATCAGGA GTTATGCTCA GACAATGTGC CGCTCCGAAT 420  
 5 TGGGGCTACG CGACTTGTAG GTGATTGTGT AGCCGCACCC TCCGCTGCCA ACTTCGTAC 480  
 GATGCATACG GACACATATA ATGCTTGGAT GTCGAAGATA GCGGACATAG ACGCCACGGT 540  
 GAGGCGCGAA TGGGTGAAAG CCATACCTAA GATACTGGAT AACAGTCTGA TTGGGCAACA 600  
 10 GATATCTGCA AAGGCTCAAC AAGACACTAA TGGATACCGA CGATGTGGTT AGACTATGCA 660  
 GCTTAGAAGC GCCTGAAAGA ACTACAGTCC CCACGATTCT GGGANATCTC AAAATTCCAC 720  
 TTNTCCNAA TTGTTGGGCC TACCCAAANA AAACNAANCT TAGGAACTTT TCATTTGTAC 780  
 15 C 781

## (2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 765 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1204RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GATCCGCTTG GCTAGGTCCT CAGCCGGCAT GTGTCACGG TATAGGGCCT CGGAGCCAAC 60  
 TAGGAAGCCG CGCACCGTGT CGACTTGAT CCATGGCAAG TAGGTCTTGA GCGATCCTT 120  
 35 CTCCATCGAA AAGTGAGGT CGTCGTCTGG CCAGACACCG ACCCATAGCT TGAAGCCAGC 180  
 ACGGTCCGCA GCAGGACCA AGAACTGCAA CGTGTTCAG TCAGAGGTAG AGTAGACTTT 240  
 GACCGTGTCC GTGTAGGGC GCAAGGCTC GAAGTCGTG AGGTAGTCTT GAGTGTACTT 300  
 40 GCAGGTACCG TGTGCTTCT TCACACCTAG GTTGAAGGCC AAATCGCCA TAGCGTGTAC 360  
 AGACGAGGCA CCAAGCAGAG CTGCGGAAAC AGTGGCAGAG AAACGCATAG CTAACGAATT 420  
 GATGGTGAGT TAGTCTGGCT AAAGTGGCTT GTAGTGGAGA AACGACAGAG AGGACAAAT 480  
 45 ATATGTTAAT ACCAGGTCAG CGCCATCTGC CGGAGGAAA AGAAATGTGC CGCGTGTTC 540  
 CGGCACCTTC CTTAATTTAG AAGCAATTAT TATCACGTGA ATATCACGTG AAACACGTTA 600  
 AGCCTACAGA GAGCTATTGA CGGTGGCTCG GAACACGTTA GCACTGAGTT ATGTACTAAG 660  
 50 GTGGCCACGC ACCATGCAGC TGTCTCGAT GCAATATAAC CCCCAGGCC CCGGCAGTCA 720  
 ACCGCCATCA AAAGTCTGNN CCGGAGNNC CCTCAATGT CCNTG 765

## (2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 776 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1024UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GATCAGGAAG CAATAGGTAC TCAATTGCGG AAGATTCAGA GACAGCAAAG GTCAAGTGCA	60
GTTCAGCAAC ATCGAATCCA CACAAGTTAT GTCGTACAGA GGCCATAACT ACAACGCAAT	120
GGCACCCGGG GGGCAGACGT TCTCCAACAG TOCATATACG AGCAATATGG GGTCCACGGG	180
GGCTCGCGGG CGCAGCTCAG AGCTGTTCOA GAAGTTGAG CGATTTGCGA AGCGCATAGA	240
GGACGTGACG GACCACCGGC TGGTGCAGCG GTTCGTGCGG TACACACCGC TGATTGCGCG	300
GTTTPTTATT GTGGCCAGT TCTACGAAGA CTGATCCCG APTCTGTGCG AATGGCCGGA	360
GCAGGTGTG TTTCTATCCT ACTACCGCG CTACCCCGCA GPTTTCGTAG TGCTGTTTTT	420
GATGGTGGTC GCGGTGCTGA TGATGGTGGG GGCCACGATG ATCCTGCTGC GCAAGCAGCA	480
GCTGTATGCG ACTGCGATCC TATGCGGTG TATCATCTCC CAGGATTGTGT GTACGGGCTG	540
TTCTCCGGCA CTCTTGTGTG TTGCGGAAT TTCAGCGTAA TCGGCGGTG CTGATTACTT	600
CCGTGACTCC ATCCGTGCAG AAGCGCATCA CATTCGGCAT GCTGCCGGAG CTAACAGCAG	660
GAAGGGCAC CAAGGCTACA TCTGCTTGC GCGCGCATAT CATAGTCTTA GTTGTGACT	720
TTACCTCCGC AAAGTGGTGA CGTTCCTCN OCTGGGNAC GGTCTCCCC TCGGIN	776

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1205RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GATCGCACTT CAACCCATTC AAGAAGACGC ACGGCAGTCC GGAGGACGAG AACCGTCACG	60
TGGGCGACAT GGCAACGTG CTGCGGACG CAAACGGCGT GCGGTAGGA TGGCGAAGG	120
ACCTCTAAT CAAGATTTTT GGTCTACGT CGATTCTGGG CCGTACGGTC GTTGTCCACG	180
CCGGCAAGGA CGACTTAGGC CGCGCGGCA ACGAGGAGTC GCTAAAGACG GGCAATGCGG	240

GCCCCAGACC TGCTTGCGGC GTGATTGGCA TTGCCAACTG AGCTGGCTGC TGGCGGTGC 300  
 CGGAAGCTCT GGAAGGTTGC CAACTAGAAG CTCTGATGAC TATGTTAGCA GAATAAACGT 360  
 5 TTTATGGTTC GCTGTGTTGG CGCTGTATGT TACAATTGCA GCAATTAGAA GTCTGCTCTC 420  
 GCGCCCGACG GCACGCTCGG CAGCGAGTAG CTTGGTAGGA TGTTTGCGGC CGCCAGCAAC 480  
 AAGCCGAGGA AGGGCTCGCA AGGGTCTAG CACCTTGGAC ATGTTACTCT GGTGGTACT 540  
 10 GGTGGGAC GTTAGTAGGG TTGGTCAGC AGCTCGAGAA TCTCGCACG GTGCCGTCTC 600  
 GTCTCTGCC CCAATTACG CCAGCNCAG ATTTCTGNC ACTTTGGTTG ATCCCTACN 660  
 ATGAAATNTT CCCCCAAG AGCTGCGGT TATTTCTNAN ATGACATCG TTCCCCGAA 720  
 15 AAGTGTCTAA ACATCCCTGT CCCCCN 747

## (2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1205UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GATCTTCAGG TTCCGCGACA TGATTATCAG CGAGATGGGG TGGCTGGGC GCGCCCCGG 60  
 CTCTGCACA CGCTCGTGA ACTGCTCCG CTCGGCAGG TCTCGGCA GCACCGCAGA 120  
 35 GATCATCTTG TCCAGCAGGA TGTCAATGAA GTGCTCTGC TCTGTACTT GAGACACCGC 180  
 GCGCAACTTG GCGCGGGCT GCTCTCGGT ATCTCTCTG TCCGACATAC CGCGCCATT 240  
 GTGGCTGGTC TCTCTCTGC AGAAGCTGTC CGCGCTGTC TCCAGCTGT GCGCAACGC 300  
 40 GAACTCGTC AAGTGTGTG CGATTGTTT GCGCTGCTG TCTTTGCCC TCCGCGCGG 360  
 CTCCATGTC GGTGCAACA GTGAGCAGC GATGTTGGT ACCAGCTCCC GGTTCGTGAC 420  
 GCAGGCGCG GCTTTTCAT CGTCTGCCAC CTTCTCTCT GCTTCATGA TCGGTTCATA 480  
 45 CTTGCGCGC AGGAATTCCC CCAGCAGGA AGCGCGCTT TTGCTGCCA TTGCAACGCT 540  
 CTCAAGCGC TTGGTCTATC GTCTCTCTC ATCGGTCTC CGCCCCACG TCATATAGAT 600  
 TCGGCTCGC GGTAGCACAC TGGGAAGGC TGCTTTGGT ATATGCGCT AGAAGCAGTC 660  
 50 TCGGCGTCA GTTAGTCTT TGTGATGAT GACGTGTCA CGATGACTG GATATAGAA 720  
 AGTCATCTAT CGATTGAGAA CATAGCTATA TAGAAATGAT TTAGTGAAT ATATCGA 777

## (2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 751 base pairs

# EP 0 866 129 A2

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1206RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GATCGCGTCC	GTCGTCGTGG	GCTCCTCGTC	CTCGTTGAAC	TCCGTCCACA	GCTTGAACGG	60
CCGCGCGGAC	AGGTCCACCT	TCGCCACCGT	CTCCGTCAAC	ACCTCGGFTC	CGAACTTCAC	120
GGACTGCGCC	TTTCATCCGT	CCATGAGGTC	GCTGCCCCGT	AGCCCGTCGG	GGAACCCCGG	180
GAAGTTCTCA	ATCTCCGTGG	TTGTGTCAG	TTGCCCCGCT	GCAGCCACTC	CGTTGCGGAA	240
CATGCCCTCG	TACAGCGTGG	GCTTGATCTC	CGCGCGCGCT	AGGTAAATGG	CCGCAGTGTG	300
TGCGGCAGGG	CCGAGGCCAA	TGATCGTAAC	TTTGTGATGC	ACCATTCGTG	TCTGCAAAGC	360
TTGTCCCAAC	CGTATCTTTG	TTGCTGCTGC	TAGCATCAAC	TGTGCACCGC	TAAGTTTCGC	420
TCGCGCTTGC	TGGTTTATATA	CCTCTGGGCT	TCACCATCGG	TGAACCTTGA	TGCGCGTTAC	480
TATTTCCGAC	GCTPATGTCC	GCACCTGACA	AAATCGGCTT	CGCGGGTGGG	CGACTGCGGT	540
CAGTGGGGGG	TGCAGTACAA	GATACGCACC	GCGGGCCTNT	NGNNNTCNNC	GGCCCTCTCN	600
GNCGCCCGCC	GNCCCTTCNC	AGGATCNTTN	CCTCANCTAN	AACNNGGCC	GGNNGNNTCT	660
TTTTTTTGTN	CNGCNAACGA	AGGCAATNNA	ATNTTTNNTN	GGNCNTNNGT	TNGAANTGTC	720
CNNCNGTGGG	CATCGCNGCT	TATNAACACN	C			751

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 778 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1206UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GATCGCTGC	TGTGCAACCA	CCTGCTGCAG	GTAGGTTGCT	ACTCCACGGG	CGAGATATGG	60
GTCCTGTGTA	ACATCCTACA	GCTGACCTGC	TTTAAAGAGA	CAACCAAGGA	CAAGTACGAC	120
CGCCGCATCA	TCAGTTGGCG	CGGAACGGTT	TGACCGGCC	TGTCTGCAGA	TAAGACCTTC	180
GCTCAGGAGT	TTAACTCCAA	ATGTCTCAAC	TTTACGACCT	GGTGGCACCT	CATGGCCCCG	240
CTAGACCACG	CTGTTTTTCAT	GTGGTGTCTA	GACATTATCG	TGGCCGAGAA	CTCACAACCC	300

TTCAAAAGCA ACCCATCAT CCGGATAAG CTCAACGGCA AGGACTGGGA CTACTACCGT 360  
 GATCTACAG TTGTGTGTCAN CTATAGGATT ATCTGGCCCC TGACTCTTAC AGTGCTTCTC 420  
 5 AGCTATCATT TTGGCTTCAA TAATCTCTAC GACCTCTCTT TTGTGAGCC AGCCTTCCAG 480  
 ATAATAGGGC CCGAACAAGC GACTTGGGGG ACGTGCATGC AACCTTTATC AAGAAATGGC 540  
 ATCACAACTA TAAAAAGTTC TAGTTGCTCG ACTTGTAAATC TCATCTCTAA ACATAATATT 600  
 10 CTTTATATG CTGTATTAC TTANCTCAA CATGATNACN TATGCTGGA AGATTTCNC 660  
 GNTGGCCGIN AGAACNGATT TGGTCAACT TMTATAAAC TGACCGTGC GCGCTCCCG 720  
 TAACCGANA TTCTGTGAIN CMTGATCTA TGANGATGC GGCNCAITNN CANTATTC 778

## (2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 756 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1207RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GATCTGTTC AAAAATTGGA AACGCTTACC ACCTCACCA CACACCAGGA CTMTATTTTG 60  
 TAGAAACAGG CGATCGGCTT GAACAACAGT CACTAGAAAC GGTGCACCA GGCAGCTTGG 120  
 CAACGAGGAG GCACCTAGG GCTCAATGCG TTGATAGTAA AGCATGTACA CGAGCTTTGT 180  
 35 CTCCGAGAGA AGGAACGAGC TCTTGCACTC CGACAGTAC GAGTCTGAGA TACACCACCA 240  
 CCGGTGCGTA GTGGTGGAC GTAAAGCCTT CAGTTTGGCG GACGCGCCT GGGGACGGGG 300  
 GAGTACCTTC GTGGCAGCG AAGATACGCC CGATGAGCTC GCAGAGCTGG CTCCGAGCT 360  
 40 GTCTGCTCG GCTGACGGT CCGGCTTGA GACGGTCTT TCGTTAGTA GTGACTGTG 420  
 ATGGAAGCTC CCCAGTAAG GTCTTGAGCA AGCGGCCATC GCGCCAGGG GAAGGCTTC 480  
 AGCTGGCGTA GGGCACAGG ATTGAGGGG CTGGCTGGG GACGGCTCC GACGAGATCA 540  
 45 CATCTGAGG AATGATATCT CGCCGTCCT TGGTCTTCC TAAGTCAGTT TGTGGCGAA 600  
 CATGCGTTAT GCGCTGAGAA TGGTGGCAT GTGCTTGATT CATGCGCCAA CAGCTTATAG 660  
 CGAATGCCAA ACCCCCACCA TTGTNTTCCC CACACTGCT CMTGAGACAC CCCCCCGGA 720  
 50 AANINAATGC GGTNTTITG TTAACCCN TMAAAA 756

## (2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 771 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1207UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GATCTAATGA GCGATAAGTC ACCGGTTATA GAAAGTTGCG CGAATCCTAC AACTGACTCC	60
AACTCGCCAC AGGAGATATC TCTATTAGAA AAGAATATCA AGGATGTCAT GCGTTCACCTA	120
AAGGGCGTTG ACACGCACTC ATGTGAACAG ATCATTAACG AAATTCTTGT GGTTGATTAC	180
GATGTTGCGAT GGGAGATAT AGCTGGTCTT ACAATAGCAA AGAAGTGTTC GAAGGAAACA	240
GTGTTTACC CATTTTTGCG GCCAGACCTT TTTGCGGGTC TCCGGGAACC TATCTCCGGG	300
ATGTTGTTAT TTGGACCTOC AGGAACAGGT AAAACGATGA TTGCCAGGGC CGTTGCGACT	360
GAATCGAATT CAACTTTCTT TTGCATCAGT GCTTCTCTT TGTATCGAA ATACTTGGGT	420
GAGTCGAAA AACTTGTCAA GGCTTATTT TACCTAGCCA AACGGCTTTC CCGCTCAATT	480
ATATTCAATTG ACGAAATCGA CTCTCTACTA ACTACCGTTC AGATAATGAG AACGAATCAT	540
CCAGAAGATT AGACGAGCTC TTGGTCCAAT GTCCTCCCTA ACGAGCGCCA CGGCTAGGAA	600
CAGAGAGGCG AAGAGGCCAG ACGGTTACTG TCTTGGCGGC AACCCTTAC CGTGGGCAAN	660
AANGANGCTG CNATAAACTT TTTACCGGT CTATNATCCC TTGCCGGAAT ACAACNAAAT	720
GTCTTTGAA AACTTNTGGC CTCCAAAAAG AATTTCGAAC TNATTNNNN T	771

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 740 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1208RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GATCAATTAA TAAATGSTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA	180
TCTTAAATA TTCTTAATT AATAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG	240
GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAA ACTGAATATC TACATATTAT	300

ATCATTAATA TAATAACTCT TTAATTAGAG TTGGTACCAC AAGAATGCTG AAAGCAITTAG 360  
 GGGTGTGTAC CTTAGCTCTC CTAATTAAAG TTTATAAAAT TATCCTTAAC TAATAAAAAT 420  
 5 AATTAATTAA ATAAATAAAT AATTAATTAA ATTTAAAATG TTTTAAAAA AGAATAAAT 480  
 AATATGTTTA TATTTAAATA GATTCAAATT TCCAACAATT CCCATTCAAT TAGTACTACC 540  
 ATCACCATGA ACAATTGTTA CATCATTAGT TTATAGTTTA CTATACTTAG CTACTAACA 600  
 10 TGGTATATGG TATAATANCC CTAATAAACC TTATANANIT TTTACCNAAC TINGATTAAA 660  
 AAAAGGGCGA NCNCTTTTGG NGGACCCCTA CCCNTAAAAG GNGTAATGGT TCCCCAATTG 720  
 GTGGCCGAAA TAANTTGGCC 740

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 782 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1208UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GATCTTAATT TAAATTTTAA ATTAACATTT TATAATTTAG AAATATATAA TCTAGAGATA 60  
 30 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180  
 ATTTTTATTA TTTAATIGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 35 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAGATGTA TTTAATTTAA TTTTAATATT 300  
 AAATATACCA TTTTATTTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
 ATTTAATTTA TATAAATTAT TTAATTTACT TCCCCTGATA TATATAATTA TTAATGTTT 420  
 40 CTTTCATAAT ATTTATTTT ATTAGCTAG TAATATTTCT ATTTAATAGT CTACCCCTTT 480  
 AATTGGATAT TACTACCTAC TAAATATTTA CCTAATAAT ATATTATTAA GAATACTTAA 540  
 TCCTAATAAT TTATTATCT AAGTTATATA AATTAATTAA TCCTTTTTAT TATTATTTAA 600  
 45 ATTATATTA ATTAGTAATT ATATTTATTA TTTTATTAAC ATAATTTTIG ATAATATATA 660  
 TCCATATAAT GGTATTTATT ATATACCNIN ATGAATTAAT GANAACCCCTA TATATGANAT 720  
 TAGTTATAGT GACTTAATCC CNACTCAAT ATATATAATT ATTATAGAN ANTACTTTT 780  
 50 TC 782

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 533 base pairs

# EP 0 866 129 A2

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1209RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GATCAGCCTA TGTAGCAACT GATCGGCGCT GGTCCGTGTC AAACGCCGAA AACACCCAC	60
CAGATTACGC AGACACTCCC ATATTTTGAC CGACTGGAAC TTTGTGTACA CAAAGCTATT	120
CAGCTTGTC A CTGGCCACCG TCAGCGGCAT GTTGTTCAGC CGAGTCGCTA GCGCGCACT	180
GCTGTTGCC TCGCCAGCG ATGGCTCCTT AAGATCCTGC GTTCGCATAT ATTGCGCAA	240
CTTCGATAGG TCTCGACTGA GCGAATTACC GACATGGTCC AGTAATAACA ACACCCAGG	300
GCAGCCCCC CAGCTGTAAT TCACCGTTTT GACCAGCAGA AAGTGCAATT GTAAAAGAT	360
GTACCACTAA TGCCAGTAA ATGTGAAAA GACCTGGTCG TTCTGAAGAT ACGAAATCAT	420
CACTGAAGA TTCCTCAGTC TTCTCGTCC CGAACATCTT GGAAAAATCT GCNGTCGTG	480
GCTTCTCTC CACTGAACC GCAGGGCTTC CAAGGACACT CCTTGCAATT GAA	533

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1209UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGAGGATCGT CGAACTTGAT TATTTCTCTC TGGTACGACG ACAGCTCGTC CGGTTTCGC	60
TTTAACGCCA CCAGCACCAC GTACTGTGTC GACCGCAGCC CGACTGTGTC GCTCCCCGTC	120
TTGATGGCCT CTAGCGGCTA CTCACCTGG AACAGTCTCC CAGTCGGGGA AAAGTCAACA	180
GTATCACCGT CGTAGTTATT TCTGAACATC ACTAACTCAC AGNGCCCCAA TTGNTCTGTC	240
ACACCGCCCT CTTTACTGGT GCTAGTTAAC TGGACAGGAG CTGTGTTTGC CACCCGGGCG	300
CGGGAAGTAG CTCTGGTATT GTCATTTGAT ACGGAGATTT GATATTCTGT GAAAGGTATA	360
TAGATGATTC CGTCTCGCG ATGTGTTGGA GGCTCGGTG CATACTGGAG TCGTCCGAG	420
TGTGNTATCT TCTACATAAC CGTTGNAGGN CAGGGGAGAG GTTTGNNNGC GCAGTTGTG	480
CGAGTACCA TATTAGGCGA TGTGCGGTGA AGAGGTATCT ACTGTGGTG TTAT	534

## (2) INFORMATION FOR SEQ ID NO:227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1210RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GATCTAAATT TATCAGCCCA TGGACGGATG GATTTCAGGC AGCGTGTGCG CGCAGCACGG	60
GGCAGCCAG ACTGCGAGGT GCCAATAAT TCACATAGCA ACGTCATTA TAAACATCCC	120
AAGTCATTAA ACTTACTAAA TATGTGTGCG TAACCAAAAG CACCGTGTAT CATCATCTTC	180
ATAGTCTTAG CTGAACCTAC TGTCGCACCA GCGCTTACT ACGTATTGTA TCTCCCTTIT	240
ACAATGCTTG CCCACTGCCA GTTTTCGCCA CGGCGTTAG CATGAAGTCT TTGCGGCTT	300
TGTACCACGG CTTGACGCT GACTCTAAGC GGACCAACGA GGTAGACGG AGTGCACCCG	360
GGACCGAGTC ATCTCGCTC GCGTGTGCC AGAGACAATT TGAGGTCCA CGGAGCATCC	420
ACGCCATGC AATCTGCCC GTAAAAGTTT GCACANTTCA TCCACACTT GGGGGTTTNT	480
TATCAGNCCA NCGTATCTG GTACGNAAAA NTTTTCCNIN TTTGTGAGG AAATCAGGTT	540
CCCAATA	547

## (2) INFORMATION FOR SEQ ID NO:228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1210UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GATCGAGAAG ATGCGGGGCC GCAACGAGGC CGCCACGCC GAGGCGGGCG GCNACGAGCT	60
CCTGACGGCG GCGGAGCGCT ACGCGCTGGA GCAGGGGCAG GGCTTCCTGG CGCTGTCTGT	120
CCCTGTGCGN GAGCGGGCNC GGCCCTGGC CGTGCCCTGC AACGAGCTTC CGATGAATA	180
CTGCATCACC AAGACTGACT TCGACCGGCT CGCTAGCCAC GGCATCCCGG TCGAGGAGGT	240
CCACGAGGAC AGCAAGGACT GGTACTTCCA GTGCCCTGT GGAGTAGAGG AGGTTAGCCC	300



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GGGCCTAGAG AGCCCCGGGC TGCAGCAGGC OCTGGTCTGC TGGACCAAT GCTCCGGGT 360  
 GGCAGCAGCT GGGACTGCCA GCACCCCGCA GCGATTGAGC TTGCTGGCCN GCGGGCAAGA 420  
 CTCTCACTA TTTTGGCCCTC CNTGCCCCCT TGGCCTGCC CAAGCGCCCG CGCCCTCAG 480  
 GCGGNGNCG GCGCNAAC CCTACCAGA ACCAAANNA CNAAGCCNCC GCGGCCNTC 540  
 GGTGAAGCA ACCCTTTTIN NCTCTGTCT TCCNCCCTG AAAGACCTAN TTCTCTCA 600

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1211RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GATCTCTCC AGTAATGGCG TCAGAGCACA CTGGTAGCG ACCCTGCCA GGTAGCTCAT 60  
 CGGCAAAAG ATAGCAGCG TATGTACCA CCAGCGAGC GGGTGATAAG GAACTGGTA 120  
 CGGCAGCAGC CATAGCTCTG GTGGCGCTGG GTTCAGGCC TCCACTTGT ATAAATTGAG 180  
 CACGAAAGC CACACTTTAC CCCAGTAGG CGAGCCAATA GCACCCCCA TGGCAGCAG 240  
 GGTCTTCGC GCGCGCTGCA TCACGATGTG TTGGCGCTCC ATCCCTAAGA GCGCAGCAG 300  
 AACGTAGTTC AGCGGGTGC CCATCGACAG TCGACTTGT CTCCGAATGC AATCCCAAC 360  
 CGCGTGCAC AGGTGTGCG TGTTACACAC GTTAGCGCAC TAGCTCCGC CGCTGAGGCT 420  
 CAGGAATACC ACCCGGCCA CATGCATGC CACCACATAC CCATATCATN ACATNGGCC 480  
 CCTGTTACA ACAGGAAANT GCCNAACCT CCTCTGCAG ANGGCCAAA CCGCCCCCG 539

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1211UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GATCTACATC ATGGGAGGCT AGGAAGAGCA AGGCACCGC TGCATTTGTA GACTACAGC 60

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TATAATATGC AAATGGCCAA TACCTTTGCC CCGGATCCAA AGAAGGGCAC TGTCAGGCAT 120  
 ATGGTTATCG AGACGAGCTT CAACCACTTG GCTCTAGGCA TGGTCAGCCA GATATTTCCG 180  
 5 CACTAAACAA CGTCTAGAAA ATGACTTGAC CTATGACGTG CCGGGCTTGA CTCATCTTAC 240  
 TATCCTCAGG CCGGGCCCTC TTCTTGCGGA GCATGGCTCT AAACCCGTAA TAAGCCCTAC 300  
 CAACCCGTAT ACAGGAAACA TGCTTACGG CTGTTACACT TATAAGAAGA ATGTTATGCG 360  
 10 CACGCAATTT AATTGGCTTG CGCCAGTTTA AGAAGTTGG CCAACACTAA GTCACCCGAA 420  
 CTATCCGCGA AGGCTACCTA TCATTTACCC TGGAACTGGA TTGTTTGGCT ACTCANTCCC 480  
 CAGCNIGAAA ATTGCCCNNA ATTGCCGCTC CAGAAAGCT ATCCAAAGGA ACTACTCGAC 540  
 15 CAAATCTAAT TTCCCTATA ATGTGAATTA CACTGTNAAT TCAGAANTGA ACN 593

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 536 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1212RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAGATCTGCC AGTACGCTTT CAAGCTGGGC TTGCGGGTC TAGGATAGAG CCGCGCGAAC 60  
 TCAGGACTGG TCGAGACGGG ATGCTGGATC CCGAAGCTCT TCATAAGCAA CAACCCCGGT 120  
 TGCCGCGTGT AGTCATCGAA CGTCCCTCA GCGAATCTG CGAGTCTCCA CTTGACATCA 180  
 35 CCATTGCCCA CGATGCACCG AAGCGTTTCT GGAAGGAACA CGCAAACTAG CAAGAAGCCG 240  
 ATGCCGGCCA TGATGCTAGT GAAACCAAAC AACCATCTCC AACGGTCATT ATCGAATAGG 300  
 ATCAAGCCAG CAATAATGGG CGCCCAAAT CCGGCCACN TTTAGGGCCC CAACATNAAT 360  
 40 TACGCAATG CTTGCCGGG GTTTTTCGGN GGTGTGATT TCNCTTACCG TACGGGCCCC 420  
 TGAGAAAACG AGAACTCGA GGAAATGCTG CCCCCCTNTT AAAAAAATAC NCCCATCGNG 480  
 45 CAGGNIGAAA GCANITACNC TTGACTATAA ATCANCCCC GANAANNTTA NACTCG 536

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 586 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1212UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

5 GATCAGCAGT GTCTTCGGG ACGTCAACGG CTTGACGGTC TTGCGTACCG TGGCCAGCGT 60  
 CCGCACGCCA TGAAATGCCT GCACTGCCTG CCGCAGTCCA CAGTTGCGCA GCGATGCCAG 120  
 ACACGAAAAC ATCCTCGTTA ATGCAGCTTG GGTCTTCCG TCGTCACTGT GCGTCTCGAT 180  
 10 TAAGCCCAGG TTATCAGTAA CATCAAATT TTACATAACT GCCACGTGAT ATACACGTGA 240  
 TAAAGATCTA CACCCATGCC CCTTGATTGT GTAAAAAGC AACTTTTGAA AAATTTTCTA 300  
 CGTTTCCATC CGATGAGATG AGCTTAGCCT AGTGGAGTC CAATATCAGT GCACTAAGTT 360  
 15 TATCCAGTGA TACTTGTTCT CGAGCTTTCA GCAACAGCAT CAGTTTACAA ATGCGACCAG 420  
 CAGTTATCCC TGGAAAGAAA TCCTACGGTC CGAACTCCCA TGATAGTTTG ATACGGCCCT 480  
 TACAGACGCC AGCGAAAATC CCACATCTCC NGGNGGCTTC AAATNNNCTT CCGNGGTTCT 540  
 20 AAAGCTTAGG GGNATTCOCA TGCANGGGTT TATNAAATTT GANAAT 586

## (2) INFORMATION FOR SEQ ID NO:233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1213RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

35 GATCTTTTTT AGAGAGTTCA GTGTGCGGAC CAACACGGTC GGAGGCCCTT CAGCTACTTC 60  
 CAGAAGGTCG TAAAGAGTCT CCAGTAGCCC CAGGGTGGC TCGTGGTCAT AACAGTCCAT 120  
 40 CTGAGGTAGC GTGTTAATAA CCGCTTTCAG CATGCTCGTA GAGGACTTCT TTAGTAGGGC 180  
 AGAACTTATA AACTTAAATG TCTGCTCTAT GCATTCAGGG GTACGAAGAG CTGCCAGTGT 240  
 CCGAATGTCA TCAGCCGATC TGCTCGTTTT ACTTTGCTCA GAATGCGGCC ATAGTTTAAC 300  
 45 TNCNGTCCC AAATTAACCC GGTTTCCCGG GACCTTTTIN AACAAAAAGG AAAAAAATT 360  
 CCGTTTCCCC CCNCTNCCC NNNNTGGGCG AAAAAATTTT TNCNCGGCG AAAAAATTAC 420  
 CCCCCNCTT AAGNCCCATT AAAAAAAN NNNNNNTTTT TTTTTTTTNT NGGNGCCCN 480  
 50 NAAAAANNIN CCCNNTTTN NAAAAANGG NGGNTTNNNG NNNNANANN NANNN 535

## (2) INFORMATION FOR SEQ ID NO:234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1213UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GATCGCCAC	TTCACGA	ACT	CCAGCTCCG	AGGCCGAA	AC	GTGTCGCA	GTC	CCGCTC	60
GCGGAGCGC	CCCACGTC	A	CATACACGT	A	GAAGCGCCG	CCCTCCGCG	CTGCCTGCTC	120	
CCCCGGTAC	CGCCGCCCA	GCGCGTGAGT	CACCCGCTT	ACCTGGTA	CC	AGCCCCCG	180		
CAACCGCAG	TTCATCTCG	TTACGTATGT	CCCCAGCTCT	CCCCCGTGC	CGCC	CAGCGC	240		
GCCCCAGC	AC	TGTGCCAGCA	CTTGCTCGTG	CACCGCCCC	CGCGCCGCA	GGATGCACTG	300		
CAGCAGCAG	CGCCGCTAT	CGTCGGGGT	CGTCTCCGTC	ATTGCTCTCC	TGCGCCCCCG	360			
ATGCACGCA	ATCCGCTCT	GAATGCCCTT	GGCTGCCCC	GGCTTGCGGT	GTCTGGGGTT	420			
GATTGCCAG	AATGCTGAA	C	AACTGACA	CATTTTGCCA	AAAGAAACG	CAATGTCTCT	480		
CGAACGAAT	T	CGNCTCT	GTTGAACTAA	CCGCGCGCC	CAGTTGGGTG	AAGCCGCTGC	540		
TGTTCCACC	TATCCGGTAG	GGTTCAGCT	TCCTGTGNTT	CCACTANTGG	NAAACNCTG	600			
CTT						603			

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 527 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1214RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GATCGTTCAC	GTCAGCCA	AT	TCTGTGTG	GT	AGCCACTAC	ATTGTAGAG	TTATAGATTA	60
AACCTCGAAT	GCAATCAT	TG	GGTAAGCA	CAGCTTCTGT	AGTCTGCCTA	TAGCAGAACT	120	
TTTCATCTTC	AAGGGTAT	GT	CTTGAAGCG	GCTTTAAGGA	ACCCCTTCATC	GAAGTACTGG	180	
GTCTTTCTAC	CCCTCCGGG	GAGCAGGATG	TTAGCCGGAG	CTTCTGAATC	AAACTCTTGC	240		
ACTTCAAACT	CTTGTCGTG	G	ACCGAACGCA	ACTTTAGCTG	CGCCTTCAGG	TTTGTTTTCT	300	
TTACTGCCAG	AACTTGTTGG	CGTGATGGT	AGGAATTTTC	TCCCATCTGG	GTTAAGTTCC	360		
TTCCATATCN	ATTGACACTG	CACGCCCCAA	CATTCAATTT	TCCANANCCC	CTACCCCCCC	420		

NANATGTTAA TTTTTCNGGT TTAAAGGACT TATCNCCT NTCAATTTT CTNAATNAA 480  
CTOCATTTGT CCNNAACNAA CAATTNAATT CCCCCTGTCC TTCCCNAA 527

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 597 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1214UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GATCAAGACC TGACGGCTTC CTAAAATCGC TAAGTTTAGT ACATAAATTG CGGCAAGAAT 60  
TACCCAAATC ACCTGCTGTG GAGATACGAG GCAAGCTGAG OGGGTGGATG TGCCCATTC 120  
ACACCACTAA CTCCTTGGTG TGTGGCTGTC ATGGTACTGC TCGCTACCGC CGTGTTCACG 180  
GCCCTGTCTA ACGGGAAGCG ATGCCCGTAA AGCCAAATCA TGTAACACCC AGCGATAAGT 240  
CCACGAGCAG ATGCTGAGAG GCTCGACCAG AAGCAAGTCG CATGGGTGAT GCTACAGATG 300  
CCTATGCGTG TGACAGGTG AAGCAACTGT GTTCTGCTTC AAGTAATAGC CAAACTTGGC 360  
CGGTAGAGA ATGACACTGC GGTGCTGTG CATATGTTGG CACTATGCAA GGTACAGAT 420  
TGCAAGCTG CCCGAATGTT GGCCTAAATT CGAACAACCA GCCAGCTATT GGTATGGAAT 480  
TATATACAAC TTGGTGGGG AGGAATTCG GTGAAAACG GCGCACCAGG NAACTTTACT 540  
GGAACGGGAA NOGGGNAATT TCCCCCNC CCGGGTTT TGGAACCGC CCNTTG 597

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 754 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1215RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GATCAGAGCA AAGTGATTCA AAGCGATTTT GGACGACCG TAAGCTGCCA GCGCAGGATG 60  
GCCATCTGA CTGAGCCCCG AGGTTACGCG AATGAAAGCG CCTGCGACT TACGTAGCAG 120  
TGGAAGCGCC TTGCTGGCCA GATTACGAC GCTAAACAGA TTAATCTCGA ATAGGOGTCT 180  
CCATTCTTG ATGTCCGCT CCGGATGCG TTGTTGGTAC GAGACACCG CGTTCGCTAC 240

GACAGCGTCT AGCCGCCCAT ACTCCGAGGA CACCTTATCG ATCACGGCTT GCACCACACG 300  
 CTGTCAGTG ACGTCTCGA CAACATAGTC GAAATTTCTTG CCATGTCTCG CCTTCAGCTC 360  
 5 CTGCAATTTG GTTTCGCCCC GTGCAACCCC TACTACAACC ACGTCGGGGG TTGAGCACAA 420  
 TCTGTCAACG GTTGCCGGCG CAATGCCACG CGATGCACCT GTCACAATTA TAACCTTCAT 480  
 TCTTGCTTGG TACTTTTATCT TCAATGGGCC ACGAACGCTC CCGCTGTAG TTTATATATG 540  
 10 ACTTCAGGGG CTGTTGGCAC AGCTCACTAG CACACTACCC TTCACATGTC ACACCAGTTC 600  
 GAGAATGAAT GGCACAGTTC CATTGTGAAT CATGATTATC AATACAATAT GTGTGTGAAT 660  
 TATTGATTTG TAATATGCAT AATATAGATG GTTATGATTT GTAATACAGT AAATATACGG 720  
 15 TAAATATAAA GTATTTTAAG GAATATTTAT AATT 754

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1215UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GATGCCCCGG GGCTACGTC ACTGCAGATT GGCGCAAGCC AGGAACAAGA CGGACACTAA 60  
 GTCAATCTGT TTATGTAGAT TGGGTGGCGA GCAGCGCAG CGGCGCGCT GATCTAGCG 120  
 35 TACCGCACCA ACGGCGGGAC GCATGCGGGC CCGGCGGCT AAACCAAGAC CGTGTGCCCC 180  
 GGTGCCAATG GACCGCGGGT TCATCCACCC CGCTCAGCCG GAATGTAGAC CAAAAAAGA 240  
 GTGTGGTTCC AGCTCTCAA TTGGGCTGGT CTCAAGGGGT CGCGGCCCCG CAATGGCCTA 300  
 40 TATAAACGGA CAGCGGAGAC AGTCGTGCA CTGTGAGGA CAGGCACACC GATGGTGAGG 360  
 GTTATCATTG TGACAGGCGC GTGCGCGGC ATCGGTGAGG CAACCGTTGA AAAGTTGTGC 420  
 ACAGCCCCCG ACGTTGTGGT GGTGGGAGTT GCGCGGCGG AAAAGACTTG AAGGTGCTGA 480  
 45 AAGAGAGATA TGCCAGTAAA TTCGACTACG TTGCTGGAGA CGTCACCGAT GAAAGCGTGG 540  
 TGCAGGCGGT GCTCGACAAG GTGTCTCGG ATTATGGCG GCTAGACGCC ATCATAGCGA 600  
 ACGCAGGCGT CTCGCGCTTC GAACGCATCG CCGAGGCAGA CATCCAGCAG TGGGAAGCGA 660  
 50 CGTTTGAGAT CAATTGTTTA GCGGGTAAG CCTGGTGAGC AAGGCGCTCC GATGCTAANG 720  
 AATCCCAGGG TTACGGTGAN TGTGGTTACC TCNNGANTCA ACNAGGTAGN TANCCG 776

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

# EP 0 866 129 A2

(A) LENGTH: 546 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1216RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GATCAAGTCT TTTATCACTA CAAATGAGCA GCGCTTAAAT TTCCAGAATC GTTTACAGCT	60
GGGTACGCTT GCAAGCAAAT TTGGCCTTTT TGAGCTAGCG GAGGAACAGT TCGCTCAGCG	120
CAAGCGCCTC ATGCGGCTTA CAGAGCGCGG CGAGCTTTAC ATGTATTACA AATCTCTCAG	180
CGCGTTCTAT TCCTTAGOCA AAATGCCGAC CTGCTTAATA GATACTCTGC GTGCGTTTAA	240
TAACGAGCCG CACTCGTCCC TCCGTAACAC ACTACTGGCT GCGCTCTATC CGAACACATA	300
TCCACTGGCT CCGCCGCAAT AATGCAGAAG AAGAGGTCCA TAGATGAGCT GAACCCAGCCA	360
GCGCCANCAG AATGTACTCC CACTTATGCG AACTCCNANA NTGGAAGGCC CTGCATACAT	420
TTCCGGTCCC ACCNACTTCT GCGTTCCTTG GCTTACCACT CTTGTGAACC GAATNGTGCG	480
GCATGCCTTG CCCAAAAACC CCTGGAAATC CATAAATACC TCNCGGGGGT TANTGTGCGT	540
CCCCCG	546

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 593 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1216UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GATCTGTGAA TATATGCTTG GGTGCGATTG GTTTGCCAGT GCTATAGAGA GCGGTCAACG	60
GCGTACGCAC GGCAACTCTT CGAGTGTGCA GCGCAAGTAG CCGATCATA TACAGGTGAT	120
GGATGGCTCC TGTATACCTT CCCCACTGC AAGCCCCGTA GTTGCTCAGG TGTACTGCG	180
GCAGATGGTC ACATCGCTTC GGAGTATATA GTCTGCGCTT TGAGCCACTT AAAAGGGGCT	240
CGCCGGCTAG CCGCGCCGCG TGGTCAAGTG AATTGCCATCT GCGCCGAACG GAAACGTAAC	300
AGGCCGTGTG AACGTGGTGC TCATCCGTCA GCAGGCCGGT CTCCCAATGT ACTTCGCATA	360
TGTTATTTTA CGTTTATGTT ACCTATCGAG GGTGCTCAG GGTATATGCC GCGGTGCTGC	420

CCTGCCACGG AACCCGCAGC CTGCAANCT CCCTAATTGC CCATGGTGAA TTGAACTCNC 480  
 AAGCTTATAT CTCCTTGCCCT GATCCCCCAT NATGCATTG AAGTTCNCCA NAGGACAAGA 540  
 5 AACANACNCA AAAAACNAAA TGGTTAAGTA AAATIGATTT GGTGTTCOCN CCT 593

## (2) INFORMATION FOR SEQ ID NO:241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1217UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GATCTCGTTT CTGGGGATT TTTATTGGGTT GGAAGAGGAC CTGGGGCTA CACCACTGAA 60  
 GGTGTGCGAG TTCTCCAGTT GAGGCTATT GAAGTGATA TCTGATGATA GAGCGCTCAA 120  
 ATGTTCTGAT CCTGACATCG AATAGAGCGC ATTTTCTGT ATGTAGCGG CTGGGTCTCTC 180  
 25 GCGTGGGATA TCTTTGATGT TTGGAGTGGT GTTGTGCATC ATGTACACCA TATTTGATGT 240  
 AATCGGTTGA ATACCATGAG GAAGTGGACT CATTGATTG GCTGGTGGCT GCGGATGTGT 300  
 TACCATTGGC GTAGAGGTTA GAAATTTGGT GAGTTTGCCA AAGGAAGAGC TGGCTGGCTA 360  
 30 GCAGAATGAT GGACTGGCGT TCAAGCGCCA TGTTCNTCC TTTGAGGTT AAAAATTAGG 420  
 AAGGGGACAA GGACTCCCTT GAATCCTACT ANCCCTTCT AAAACTTGGC AATATTGGTC 480  
 CCTGAACAG ATGNCNCCNC CACATCCCC TATTAAATTT TTTAACAACC ATATTGTGG 540  
 35 ANACCTNGAA NTTGAACTTG CCNGCNAANN GATTCCCTIN CCTCCCCAGA TN 592

## (2) INFORMATION FOR SEQ ID NO:242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1218RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GATCTTTGTG GGCACGAG ACCACCGAG TACCGCCGT GCTTGGAGC TACCACTGAA 60  
 AAATGTTCTG CATGAATCCC ACCTTGATAA TACCATGGA CCACTGGAAG TTCTGGGACC 120  
 55 ACCGAGCAGC GATGGGTGGC ACACGAGCCA CTCCATCAT AGAGTGATC GCCAAATTTT 180



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GGAAGTACGA GAAAAGAGAG ATCGAGTTGG AAGCGATGTG CGCGGCAGTG GTTGAGTGGC 240  
 5 CGATCACAGA CACAAACCCG GAAGTCCAGG ACACCCACAC CAGCTATCGC GCGGAATCGG 300  
 CCACGAATGC ATACTTCGTC TGCACCGTCT TCGCGTGCCG ACAGCACCCG CCTGCAACA 360  
 CAGGCCCAAT GGATGCTCCG TACTGGTGTG TCAGCTTTCC GCNAAGGCGT TTACACCATC 420  
 10 CGTGCTTCCC AGTTCCCNCG AAAATATACC CCGCTTGGT ATCTTCCNT GAAAAATCAC 480  
 CGCCGAAAT TCCAGTTGA ANCTCTTTG ATTCCCCCCC CMTGCCCTCC CCAGNINCGG 540  
 GANATTCACA ACNAATNC 558

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 604 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1218UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GATCCACAGT TTCCGCACTG AACTTACTAT CCTCAGCAA CCGCAGGTCA TGTCAAGCG 60  
 30 TTGTGACATC AGGCTTCACC CCGTAGCTCA TAATGCCTGG GACGGATGCC TTGGTAGAGT 120  
 AACAACCAAA AAGGCATGTT GGATCAGCTG CATAAGCTAG TAAAAAGAG CAGACGCGCG  
 CTGAGCCACT AAAGGCAACG ACCCGCCAAT ATATGATAAA TAGAGAATAT AGAATGTTGC 240  
 35 CACTAGGCCA AGATGACCTG CATTGAGATC CAGCGACAAA GTGCCAGGAA TTAAGGGATC 300  
 TTCAACATTC CTGATCATAT GAGAAGAGCA ATACAGGGTT AAAACGGCGG CGTTTAAAT 360  
 TTACAGACT CAATCAAATG TTTCACAATA CCTGGTTTGG ACAAGTCCGA GACATCCCCC 420  
 40 TAACTGATCT GCTTCCCCCA GCCAAGGATT TTGGCCATA TACGGGCCAT ATTTTGCTTG 480  
 ACGATTCTTT TGCAATCCTC CCCGAACCAC AAANACCTTA GGGGCACNAA CGGCCCAATT 540  
 CCCNANNGAA AAAAAAATA GGTGCTTTGN ATNNCCGNA CCCCCCCCCC CCTTNTTTC 600  
 45 CCNG 604

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 550 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1219RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

5 GATCCTGATA TTGTACCGGC TCATAAATAC TTTGGATATC TTOGGACAAT GTATCGTACC 60  
 CGATACTTT CAGCACATGG ATCAGTATAT CATGCTTCTT CCTAAATGCA GCAACAGTAT 120  
 10 TGAGGACTTC CTTCAGACTG TCCGTCTGAG TATCTATCTT CATAAAGATG AACTTTTCGG 180  
 ACCTCTTCTT CATCAGCTCT CTGATGAGTG ACGTTGAATT CTTTAAATAG CGCTTCCAC 240  
 TGGTTTGATA ATCTTGATAC AGTGGTCCAT AGTCTCCCT GGAAAGAAAT GAAGTCGGAA 300  
 15 GAAATCAGTT TTGGCAGCAC TCTCTCAGTT TCTGATTCAA CTCCGTTAG ATATTTCTTC 360  
 CCACAAATGT TTACGGCCCT ACAGTTGGTT TCTTTTGANA CCTTCACTTC CNTCCNAAGC 420  
 CATGAAAATG ANTCATCNC CCCCCCCCCA CTTTGTNAAA NTTCOCATTC GCAAATTNQN 480  
 20 CAGTTGAATT CCCCCANCCG GGTGTTCCOC GCGTCCCCC NAAAAANAC NGAGGGGGGT 540  
 TTTAAAAAAN 550

(2) INFORMATION FOR SEQ ID NO:245:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 598 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1219UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GATCGGGGCG CTGCGGCGCG CGTCGGAGTG GCGCCACGTG GCGCGGCCCT TTTGGCCAAA 60  
 40 TCCAGGGGT GGGCGGGTTT CGAGCTGCTT GACCTTCCGC GGCATGTCAA AGTGCGGGT 120  
 TAGTTTGGTC CTGTAGGCGA ACTGTAGCGG CGATGCGACC GTCTGCGCA CGGTGGGGAG 180  
 CAGGCCCTCG GCCAGCAGCT GGGGAGCAAA GAACTTGAAC GCATTTGACA CGGTTCGCTG 240  
 45 TTTGAGCTGC AGCTGCTGGT CATACTCAG GAACTGATAC TGGCAACCGG AGCACTTCCC 300  
 GAAGTACTTG CAGTTGATGA GGTGCTCGTG GCGCATTTCA GCAGAGGTCT GCACTCCAG 360  
 CAGAGACGCT TGGCGTAGT GCGGTGTGTC TTGTGCACTT GGATGGTGAC CAGTGGGCC 420  
 50 TGGCCAGCCC AAATTGGCAC CCAGCACTAC TGTTTCTCTG TTGCTATCC TCCGGGGCTG 480  
 TCCAACAANA CCCATCCCTC CCCATCCACT TTACNTCCAC ACATCACTTT CATCAGCNCC 540  
 GGTGTGTTCT CTGCTGCATC GCCCCCGAA TTINTCAGA ATGATTACTC CTCNCNG 598

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 747 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1220RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GATOGGCGAG TTGTGGCCCT CAGOCAGCCG CTTTITGGGC ACGOGGGGA GGTGTCCAT	60
GTACCCGTCG GGCACGCCCC CGTCGCCCTC GCGATCAGC TGCAAGTGCT GCTGTAGCTC	120
CTCGGCATC AGTCTCAGCA TCACATTAG TAGCGGGTG CTGTGGCAT CTGCCTCTG	180
GAACATGTCA GCCAGCTGCC TGCGAAGTTC GGACCGTGT CCGTGGTGT CTGTGAGAGT	240
TAGTATTCTT GGCCGAGTC GGTGCACAT TGGCATCACT TACTATTGTC GCTGGGCATT	300
CACCTCCCTG GATCACTGGT GCTCCCGTG GCGTAAGGG GCAACAGACA GGCTTTTTTT	360
ATTTTCCTCT ATAATACGCT GCTCTATGTA GCGTATACTA TACAAGTCTT AACTAAGGTG	420
AAGTGAGAAG TCATTATTTA GCTGCGTTTC GGCCGGTCAT GCAGCCGGCT ACCATATTAG	480
CATGCCGCTG GCTTGACCG CTTTGGAGGT GGGGAATTG TTGATGCCCC AGGACCTTAT	540
GGAGTTCAC CTCACGGAGA GGTTCGGAG ATCGAAAATG TCACTTTCCG CAAATTGCGA	600
CACACGTAA TACTCGCAA ACGAGTTCTC GACACCGCTG AGCTGTGCT CGACGTGCTC	660
GACATAGGAC AGAAGAGGCT TCGTTGGGC TGGGGGGCG GCGGCGCAA CCGGAAGNGC	720
CCCCCANAG CTGGCGCCNG GCGGCC	747

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1220UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GATCCAGAAT ACTGTGCA CCACTTCTTG AACCGGGT ACAGCGGG GTCCGTGCG	60
TCCAGCGGG CCTGTGCG CGGTGAAC AGCGCGGT CCTCTGTA CAGGTAGCTT	120
GGGTGAGT CCGAGCGCC GCGAACCAC CAGTCTGG GCTTGCCCG CGGTCCAC	180
GTCTCAAAT AGCGTAGTT GAGGTGACG GTCGCGGT GGGGTTCAC GGGGTGATC	240

ACCAGAGAAA TGCCGCAGGC GAAGAAGGCG ACGCCGGCCG CCGGCTGCCC GGTCACGGGG 300  
 TCCGTGGGGA GGTGCAGGTT TTTGTGCTCG GCCCGCATGG CACTGACGGC TGCCGGGCGAC 360  
 5 AGCTCGCCGT GGA CTACCGA GAGGTAAAG CCGGCTTTT CGAACGTGGT GCCGTGCTGC 420  
 AGCAGCGACG ACGTGCCGCG GCCACCTCC TTGGCTCCC AGGAGTGGC CTTGAACTTG 480  
 ACCGTGTGCA TCGCTCGAA CCGGGCTGTA ATCTCGGCT GCTTGCGCG CACGAGCTCT 540  
 10 TCCATGGCT CGCGCATGTG GGGGGTGTGG GGGGATGCCA TTGCTGGGGC GCCGCAAGAG 600  
 GCGAAATNAN CNGTGCGCCC GCGGGCTTAT ATAAAAGCGT GGCACGGGTG TTTTGCCAC 660  
 GNCACCANGG GCTGCNAAAG TCCGCGCCAA NANANCCAGG GTCCCGGCCA NAACACNTCG 720  
 15 GCGGGCGGCC NAACGCCGCG NCNCACAATC ACNCCGACAA TCGCGCNCNG GGATTCC 777

## (2) INFORMATION FOR SEQ ID NO:248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1221RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GATCTCTGCT GTTGGGCTT GCAAGCATCT TCCTCGCTAA CTCGTTGGC GTTTACGTTT 60  
 GAGGTTCGGG GGACGTATGC TANACGAGG GCATTGCGGG GTTGAGGGGA AGAGGTTGAG 120  
 35 ATTATGAATG ATATATACTG TTATACCGGC TCGGGTGGC TGTGCGGTC ATCAGAGGG 180  
 ACTTACAAGT TCAAAGGTC TTCATGATA TTTACCAACT TGTAATAACG CTCTGTGAG 240  
 TCTGAGTTGG AGGAGCGGG CTGGTGGCCA TACTCCATCA ACGTGTTTAC CATTGCGGT 300  
 40 GTATAGCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCT OCTTTAGGAA CATCAAAATG 360  
 GTGGTGTTC ACAANCNGGA AAACCTATCC TGTTAGTNNNA GAAGGGTTGA GAACACCGCT 420  
 AATCCCTTAG GCACTCCACC ATGGTTTAT CCGTACCCA TTACCCAAAT TTCCCCAAG 480  
 45 TGCCTTNA A CTGTGNCGAA CCCCCGNA A TNCCCGTTT TTAACCCN AAAAANG 537

## (2) INFORMATION FOR SEQ ID NO:249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1221UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

5 GATGACCOCT ATCAACGCOCT TGCAGGCTGC TATGGAGGGC TATCAGGTCA CCACTATGGA 60  
 CCACTGCGCC AGCTACGGOC AGGTITTTTGT CACCACCACC GGCTGCAGAN ACATCATCAA 120  
 10 GAAGGAGCAC TTCTTGGCCA TGCTGAGGA CGCATTGTG TGCAACATCG GCCACTTCGA 180  
 CATCGAGATC GAAGTGGCOCT GGCTAAAGGC CAACGGCGTC GAGCGGTCA ACATTAGGC 240  
 ACAAGTCGAC CGCTACTTGC TTCTCTCCG CAGACAGTC ATCTGCTTG CCGATGGTTA 300  
 15 GACTAGTCAA CCTAAGCTGT GCCACTGGCC ACTCTCGGT TTGTCATGTC TTGCTCTTC 360  
 TCCAACCACT CTTTGGCACA GATGCTCTCN TTCAAGGGCA ATNAAAAGGC CTTCAAANAA 420  
 ATTNNTTNTT TTCCCAAAAA ACGGCNTCA AANCGGNTT CATTTCTTNC CNAAAATTGN 480  
 20 AAAGGGGNC CCATTTCCCC CTAAATTTGG GTTTTNTTTT AAAACATTCC CCCCCCCCCA 540  
 TTTCGGGTT CCCAAAAGGG TTTTNGGGG NOCCTTAAAT NITA 584

(2) INFORMATION FOR SEQ ID NO:250:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 535 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1222RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GATCGAATAA TAAAAGTGGC TAATACTTGG TAATAATATA ATAGAAAGGG AAATAGAAGA 60  
 GAAGTCAAAT GGGAAATAGT CAACGGGTA CTAGGTGAGT GTTCAGTGC ATGGAATGTT 120  
 40 AGTCAGAGAG GTTTATCAA AAGGCGATC GTCTGATGAT AGCAGTATCA CGAAGTGCTC 180  
 ATGCGCCCTG CATACAATGG CAGGCTCAGC GCAGGATCAA ATGGATAGCA GCGGGGTAC 240  
 CCGGAACGG ACTCAGTGGG TGGAGTGGCC CCGGTGGTAC TTGAGGCGGT TGAGGTCTTT 300  
 45 GTAAAGTTTG CCACAGACCT CGACCGGTA AGGCTTGTCC TTCTGAAAC CATGCGCGTC 360  
 TGGATAGGGC TGGTTGGACT CCGGTCCAT GATGCTAAAA GTGCGGTCTT GGGTTTTCAT 420  
 GAAGCTTTTG ATTCTGGTGG CCGTGGTTT ATGGTACTTG AGTCCCGTTT GATCCTGGTT 480  
 50 AGTCTTATCG CAGCCCATGA GGGACNNTG AAGGCTTNTC CCNCCTTGT CCNEN 535

(2) INFORMATION FOR SEQ ID NO:251:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 581 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1222UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GATCTGCTC AGACCGTCAC CCACGTTGTC TGCAAGGGCC TCCGCGCTT TANCTGCTG	60
CCACGGCTTG GAGCAGCTA GCTGCAAGCC AAACCGGGC AGCTCGAGC AGTGGGCTT	120
GGCAGCGCC CACTCGAGT TGGTGCCCTG GATCAGGGC ACAGCGAGG CCATCTCACT	180
GTACGTCAG TCGGGGCCA ATTGGGCGAT CAGGCGCGG AACGGCAGT TCCGACGGT	240
GGTCAGCGA GAAACGATCT TCTGTGATG CAGGTCCAGC GGCTTCTTCT CCTGTGCAA	300
GTAGGGTGT TGTGATACT GGGGTACAG CTGGGCTGC CGGGCGGCT TGTGTCTCA	360
TTGCTCCTC CGCTGCTGA CCTGGGCAC CTCTGGACC GGGCTCCG GCGCGCGCG	420
GCCCCGTGA TCTGTGCG GGAATCTCT CTGGATGGG TCAAAATTCC ACNATTTCTC	480
CCTGCNCGG AAGGGCCCAA NTTTTCCCA ATNANCCCA ATGAACCAIT GVINCCCCN	540
TGGTTNCAA ACNAAATTTG CCCCCCGG AGATTNCCC A	581

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 544 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1223RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GATCGGTTTT CACCTCAATT CGTTTCTGGT CGGCAGTTG GTGATGCTGC TGATGCTGAA	60
GCTGTAAATG CTGTTTCTGC TGAGCAAACT GCTGCTGCTG TTTCATCCAG GGATTCTCCG	120
GAGGAGCTGA GTCCGGTTTG CGCCGTCTCT GCTTGTGGTT CAACAAGTTG TTATATAGCT	180
GGTTCATACC TTGGGAGGTC AGGAATGAC TGACATTGCG GTCGCCCTGC GGGTGGTCTA	240
GCAACCGAG CATGGCTCT CTCTCCTGTA GAGTTTCTTT TGCCGCCATC TCAAACTTCC	300
TAGATTCCAT TATCAGCGCT TCTTCTCAG CAATCTCAGC CGCCGACCTC GAAAGCAGCC	360
TCCGTCAAAT ACTTCTTCCG CTGTATTCC CTGGTCTTG GAATAGCTA GGATGGTAGT	420
AGCGGTTTCC CCGGTCTTT CGCCGTGAAA TTATTTTGG CATACNGGT TAAAAATCTC	480

CCCGTANTTC CTCCAACGGT CCTNNANNCG NCNTAAANAN ACNGGTCNGT AAATNATAGC 540  
 NNCC 544

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1223UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GATCGCGCGC TTGAACATGG ACGTGGACAC GGCGAAGTGG CGCTGGAGCG CGCGCACCGC 60  
 TGCGTCTCTGG AGCTCTGTGT GTGCCATGGT GCGCTCTGTC TTGAGCTGGC GCACAACCGC 120  
 GGCGGATATG GCGTGGACCC TACTGGCGGC GAGGACATCT GGTAGCGCGG CCGCCTGCTC 180  
 GGACTTGACC ACGACAGTGG CGACGCGGAC CTGCGTGGTC GGCGCCGTGA ACGCCGTGTT 240  
 GACTGCAAAG TGGTCCGAGG GCGCGATGGT GCGGGGAGGG AGGGGTTTTG GTGAGGATGC 300  
 GTGTGCGCGG CCGGACGGCG AGCGAGATGA GCTGGCGCTG CAGCTCGGCA TCTGGATTGC 360  
 GGTCAAGTCC TGAATCTGCT CCGTGGTCAG TTCTGCGTAG TCTCCGAAA AACAGGAAAA 420  
 ATGGTGGCG GCATNGTICA ACATCCTTGG CCCCCGCGT TAAAAATGGC CGAACTGGNN 480  
 GCGATTTC CCGAGAACCC ATTTTGTAT CCCCCCTCT TCTGNNCC GATTTTTTTG 540  
 CAAAANINAA AACCCCCCT AAGAAGANN CGGGGNGCC CCNCGCGGN TTTTTTTTC 600  
 CNCCCCCA 608

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1224RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GATCAGTAAC AACCATAGCA GCGCACCTA CGAAAGCATT CGATACATT TTAATAAATT 60  
 CGACAGCAGG TAGTAGTCTT CTCCGGATT GCTTTACAGG CTCGCTAAAG ATGTGTTCGT 120

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AGCTCTTCCA AAGAGAAATT TGTGTAACCT CAGAGTCAGC AGCGGACTCA AAACAGCAACC 180  
 TCAACCAAGC GGTGACCGC ATAGGTTTCAT TCAAGCCCAA TAGTTTTTGG AATAGATCAG 240  
 5 GGGGAAGAGT TGAACATGC GTAGGGGGTC TCGTTTTTAC TCGOCTAACT AGTTTTATCT 300  
 CTACTTTTGA AAGATAGTGC TAGTCGGGAA GCTCAACATT GTAAGTCAAC AAGCTAGGCA 360  
 AAACTGTAGT CAAGATTGAG TTCGGCTCAG GGTMTTGACA ACAGAGTAGT TATTCTCTCA 420  
 10 CTCCCCAGGC AAGATGTAAT GGTATAGAAA ATCCAGTTGA AGCCATAAOC AGCTCGTGTG 480  
 CACAGTCCAC CAGAAGATAG GANACATCAG GTTGAAGAAT TCCTCATCTA GGTATCTGC 540  
 TGCTTTTCCT GTTCTGCTTT GGACCAACCC ACAACCCNAA AACCAACGCN AAATCAAANA 600  
 15 CCNGGTTTCT TCCTTGNTCC CCCCNATGA AANAGGTTTT GAAANGGTIN TCCTCTTGC 660  
 CGGGCCAANT AAAAAAAGG CCCNCAGGT CNACNATATT ANCANCCCC NAAAAAGGCC 720  
 TTCTGNTCTA A 731  
 20 (2) INFORMATION FOR SEQ ID NO:255:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 762 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (vi) ORIGINAL SOURCE:  
 30 (A) ORGANISM: PAG1224UP  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:  
 35 GATCGGGTGC GGCACATGCC TCATCGGGCA GGTGGGGTGG CGGAGGCATA AACCCACCCC 60  
 TGGTGTGTGC AGTGAATAGG TATGGGTACA GCCTTGGGCG CCACGAATGT GCGGAGACGT 120  
 TTCAGCTGCC AGAGGGACCC GACCGCACCG GTGGACTGTT GGCTTGGTTG GACGCTCCAG 180  
 40 GGTTACGAGC CGGCGCCCTG CGGAGCACAT GATGTCGAGC TGTGCATTGG TCCAGGTGG 240  
 CACTAACCAT GCCAAGGGCA TCCGGCCAAG GCGGATGGG CTGGACGGCG CCAGGGCGGG 300  
 ACGACTATCA CTAAGAAATC ATCGATTAAA ATATAAACTA CATAAAGTAA AGGGCGGACT 360  
 45 GAGTGCACCTC TCAGCGCACT AGCAGCGAGT AGCGGTAGTT GAACCACTTG CNTGGATCC 420  
 GTGGCACGAA GCGGAAGTAA CCGGAATCC GATAGTTTCA AACGAAGAAC CGAAAAAGCC 480  
 TTAAATGGC TTCACNCTA GTTCCCCCAA CNGGTCTCC TGTTTGGAAT TAGGGTGGGC 540  
 50 GGAAACCCAA ACTGCCCAAT TGTINTCCAA TTCCCCGGNG GCCCCAATTT NAATTTCCAA 600  
 ACCNATCNEN ATCTCGGCTG NATCCCCCCC NTGCCCCCCC TCAATGGCCC CGAACCTTTT 660  
 NTGCCCCCCC CCAAGGGCC CTGNGNATT TTTTCCCCNG CCCNCCGNT TNCCTTAAAA 720  
 55 NAAAGCNGCA TTTTTCATTT CCCNGGAAC NCTTTTGTGT TT 762



## (2) INFORMATION FOR SEQ ID NO:256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1225RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

GATCCTTTTC TTCTCTCTTC CCTCCTCCGA GGATTCOCTT TTTGAGCTTG CCCACTGCGC      60
CCAACCCACC GCCTATGACA CTAGTACCGG CGGACAGACC AGCGGATAAG CCTTTATTGG      120
CAAAATCGCC AACCTTTGTC TOCACCTTGG TAACAGAGAC AGTGTACCTA GGAGAAAATT      180
TGAAGITCAA GTAAAGAATA CCACCGTCTC CGCCGTTAGG ACCAGTTAGC TGGACTTCCA      240
TTGGGGTTTC ACTGTCTGGG TOCACCTCAG CTAGAGCGAT GGTTCGGGTG CCAATGAGAT      300
CGTCACTGTT TCCGGCATCC CAGTCCATGA CCTTGATGCG CAGGTAGTTG TTAATCCGGT      360
TATTCAACTG CAGGGATGTG TTCTCGTTCC AAACAGGTTT AAGCGTCTTC TTCTGGGTTC      420
TTGGTCTTGT ATATTACCTC ATCTGAATTG TCGAGGTTAG AATTTGACAT AAGGTCCGAC      480
TTGCCGTTCC GGTCCAGCAGG TAGAGCCTGA CTGCATTTAG AACCTCCAGT GTTAGGTCCG      540
AGTGTGTGTA TCAGTTTGCT TGTCGCATCT CNAACCCAAA AAGGAACCAC AACCGTTANN      600
TCCTTTTGNG ACCCAACCTT NNTTACAANN AGGTTTAAAT TACANTTTCN ATTNTTTTGN      660
TGGAANGAAC CCCNAAGNGT CCNCTGTITT TACTGANCNT NNTCCCNAAAT      710

```

## (2) INFORMATION FOR SEQ ID NO:257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1225UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```

GATCCTACTG GAACCACCCA CTCAGGAGCA GGTTAAAAAA CCAGCCAAAG TAAAGACAGA      60
GACAAACGTA AGCATCCCAA AGCAGACCCC TACTCCAAAG TCTAAGTGGG CTTCAGCTTC      120
GTCTTCTAAA GTGCTACAC CCCTGTCAAA GCAGGAGCCC GAAGGCGCGT CTACCATTTT      180
TGACGCTCCT TCTTCTTCTT CCTCCACTCC GGTGCTGGG CACTTGGATA TCTTTAGCAA      240

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ATTTAGGAAA GCATCCAGTG ACTTTGACAA GCOCTTTGTG GCOGAGTCGA ATGAAGTTGC 300  
 CGAGAAGCCG TCOGGAAGG CCAAACGGCA AACTACTCCC GCTGCCAGCA AATTAAAGCC 360  
 5 CGCTGCAAAG AAAATAAAGA CGCCCGCGCT CGATGAAAGC GAATCTGATT TTGACCTTGA 420  
 CCTCAGCGAC TCCAGCCCG CCATCGCCCC TAGAAGTAGA GCCTOGGAG CTGTCCCAA 480  
 AAAGCCAACC TACGTAGTTG ACCTTTCCGA TGACAGTTTT GTTGATGGAG ACGCCAGAG 540  
 10 ATGTTGAGGA ACCGATACTG ACGAATCCTT CCAGCTCTGA CTAGCACTCT AGCTCGGCA 600  
 TTGACAGTNC NCTACCTTAT GGAGGNTTCC GAAATCCNTT GAATACCCCC CGTTTTTTTAC 660  
 TAAAACCCCC NCTTTCTTTT TCACCCCCA ACCCCAGGG GACGAATACT TTTTCTTTA 720  
 15 CTTTCTATCA NGGGGTGTGT CINCNCOCNT 750

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1226RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GATGCTCTC GCATGGGAGC ATCAGATGTC ATATGGGCGA AGCCTTTCCA TATGGGGCT 60  
 ACGAACGATA CGAGTTCCGC TCCTGCTTGC GCTGTTGGG TCTGTGAGCG TGCTGCTATT 120  
 35 GCTGTGCTG ACGCCACACA TGTGGCTTGG ATGGCATCT CCGGCAGCAC GGGAGGTCCC 180  
 GGCTTCACCA GAGTCACAGG CCGCGCTTC ACCAGAGTTA CAGGCCCCGG CTTCACACA 240  
 GCCACAGTCC CCAGCAGGT CTAAGACGCT ACTGCAAGAC TTAGTCTAG ATAGCAAAAA 300  
 40 ACCGGAGGGG GCCTCTAGC CACAGATGCA GTGCAAGGC TACTTTGAGG GCACATATCT 360  
 CCGGAGCCT TCCTGGGCAA ATAGGTGTT GGCATGGCA GAGACTTTC TTACGGCTAC 420  
 GCAATACACA GCGAGGCTGT TGGAGCGGTG GGCATATTT GCTGATTGTT TCGTTATTCA 480  
 45 GATTTCGGAT TTTCAAATAC NCTATCCAAA CAAAAAATC TGOCCAANT CCATCAGCGA 540  
 ANTTCCCTT TCNNGGCAA AAAAAAAN NGAGGANATT TTGCTNTCC CCNGAATTT 600  
 NCCCGGAAA ATTTTAAAG NGGNTTTTT GNAAANGGC CCCACAAA NANAAAGG 660  
 50 GCCTTTTTTG GAAACGGC CTTTTCCC GGNGAACA AATTNNNNN GGGGACGCC 720  
 NGAATTTTC 729

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1226UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GATGCTTCA AATTTCAGC CGTTGATATT CAAAGAGTGG TCAAGTTCCG AAAGATGGTC	60
CTTCTGTTCC TCTGTACGTT TGGAGGCCCC GCGTACCGGG GCGTTGGGCG TTGTCCTCAC	120
GGTGGCGTGC TGTCCTATGG GGACATCCTG GATGTTGTTT TGCAACGCAT TAGCAAATGA	180
GTTTTTGTAG TGGTACTTAG GAAGTTTATA ATTAGGCTC AGTTCCTATAC TGCCGCTAAT	240
ACTTTGACCT GGAACAATCA TCGTTATGTG CTCACCTCTG GCGTGTCTC TAGCGTATTC	300
CCGCCGTGCT TCAGCATTTG GTTGTTCCTG GATCGTTGGG TATGGATCCT CCCACTTCTG	360
TAGCCAGTTG GTATCCAGCT TCTCACCTG CTGATGCGAT TCTGGACGCG GGGGTTTCAG	420
CAGGCGTTAG CAATGAAGTT GCGTTGCGG GTTCAAAAAA AAANACCGGN GGGGCGNTGG	480
TAANCCCGNC CCTTTAAGGG CGCCCCATA TTCNCAATNA CCNNNACCGC NCCCCCATN	540
ACGCCCCCAA AANATNTTIG AAAAAATTGC CNTACCTTTT TGNGGGAGCC CACNCNCTTA	600
NATAACCCAT TTTTGAAGAN AGCCNNTCT TTTNTTAAAC NCCNCGGTTT NONANTATGC	660
NGGGGCAAAA TTAAACCNCC CCCCCNAAAT GNAATCNMTT TCCCCCNAA NACAAAAAAT	720
ATTTTNNTTT NGGGCNGGGA AT	742

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1227RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GATGATGAA CAGACTGGAG AACAGAGAAA GGTGGTGCCC CTCGAAGTCG AACGGTTTTT	60
CCGCTCGAT TTTGATGAGA TATTACTCCG GGATACGATG CAGAGGAACG CAGCTATGGA	120
AGAGGAGGAC TACAGGGAGC TGGGAAAAG AGATATTGAG GTGGCGTTCC AGAACACCGG	180
CGTGACGCTG GATGACAGGC TCCAGTGTGT GCGGGCCATA TCGCTCTTCG GGAGGTATGT	240

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	ACGGGATATC GACGGGATGT CGGAAGCGCT TCGGACGGG GACAGGCACA TCATGGTGT	300
	TGCGCGGACA AATGACGCCA TTACGGGAT GCCAAGAAG CCGTGGGAGT ATCCACGGAA	360
5	CATCGACAAG TTGGAGCAGG CAGGCGGCTC TCGAGCGAA ATCCAGACG CCATCCAGGC	420
	GAATGTGAGA CGCTTTGTGC TAACCCACGT GGTTCGGAC ATCGAECTCT CTAAGGTGGT	480
	TGGGAAGAT TGCTCCAGCC GTGTTTGACA AGCGACTTCA TCCCAAGAGC ATGCAGGGGA	540
10	TATTCTTTTG CGCCAGGAT GGCAANGGT TTACAGTTC NIOCAANANN GGGCGGACCT	600
	TGCGTTNAG ANGTTACCC CCGCTCTAAC GGTTTATTTT GGTTCACN CCCCCTTGGN	660
	TCCGAATTNG AAAACCTCC NOCTGNCCN NOCCAATNAN TCNCTTGAAT CCCCNTTNG	720
15	GAACNNNNN TTNCCCCAN CNCC	744

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 768 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1227UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

30	GATCATTTGC CGGACCAAGA AATATTTTCA CTCTCGAAG AGCTGGCCAC TAAACTTCGT	60
	GTCTGGTTAG GTTCGGCTCC AGCTGATGTG CTAGATATCG AGGTGAGAGG TAAGCTTATT	120
	GAATACTGCA TGAATACTGC ACTTTATTGC GGTGGGAAAA TAGAACATCC TACATCGACG	180
35	ACTTTGATGA CTGACCATGA TGAAGACGAA TCTGAAAGCT CTGATTGGGA ATAGTCCAGG	240
	CAAGTTAATA CCCAATGCTC GGTCTTAGCC TCAAGGGAGA TATCGGTAAC AGCTCTATCT	300
	ATGCTGCCAG CACGTACGAG TTTTACTTAA ATTGCGCATA CAGTTCATGG TATTTGACAT	360
40	AAGCTTAATG TTTCATTGCG AACACAAGGC TTGCGGATGT GTAAAGTGCG CCGGCTCTCT	420
	GCATTCAAGA CAGCATACAT GAACCTTCAG TTTTATACGC CGATCATGTT GATTTCTAAT	480
	AGGGCTAGTC CATGGCCCTT ACCTATAATA TACTACCATC CAGCCCNCG AACCGNAACN	540
45	NNATTTTMTA TTTTAATNAA ATTTTGGGG NATNCCACAC NNNCCCTANC NNGGANTTCC	600
	AATGTTTATT TAANTNAAAA ANCAGTTTGA AGGGTATTCC NNNCCCCNC CCCACNGNT	660
	TCAAAACCAA ACNANACCGT GAAGCNGIN NTCCCCNCA AGGAGNGCC CCCCCTTCN	720
50	AAAAACGGIN NOCTTTNOCN CCTTGNCNA ANATTCCCCC CGCTGCCC	768

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 738 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1228RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GATCCATTGG	CCCCAACGAT	GCTAATGAAG	TTCTTGCCCTC	CAAAACCCAC	ATTGTGCACA	60
CCCTTGTAAG	ACTTGAAGTT	CTTCACTCT	AAGCCAATCA	GCCTCCCCAT	CTTTTGTAGA	120
CACTGAAGCT	CAGTCTAACT	GCTCTCGATG	TTGTTAGTGC	GCTGTTAATA	TGTCCAAACA	180
AACGGCATCA	TGGTTGTGAA	GAACGCGCG	TTCCCATACA	GGTCAGCAC	GTAGCCAGC	240
GGCCCCGCGG	GGCCGAAGAT	CACTGAGATC	GGCAGGAACA	GGGGGTCCA	CAACAGCACC	300
AGAAATACCA	AAATCGCCCG	AAACGTTATG	ATGTACAGGA	TCACCAGAGT	CACCGCCTGA	360
ACCCAGATCT	GGCCGTGGCC	CATCCCGACC	ACCATCGACT	GCCTGAATTA	GTATATTCCG	420
TCCCACTGCG	TGTTTCATAC	ATACCACCCC	AGGGCACACC	AGGGGGTAAC	AACCCCAAAG	480
CNGTCCCTAG	GGAGCGCATG	CAAAATATCC	ACNCTCCGCA	TGGCATCTCC	CNNTTGGAAA	540
GGGNCNCCCC	NAAATTTGGG	CCNAAANCCC	TTAAAAGGNC	CCTGTGNCN	CAANNACTTC	600
NAATTTCCCG	NTTNGGCCCC	CCCCCCCCTC	CAACGGGATT	TAAAACAGGN	GGGNGNGGGA	660
AAAACCNCG	AGGGGNTTTT	TTTNGCCCT	TTCCGAAANA	ANCCNCCCC	CCNCGGAAAA	720
AAATATTTTT	TTTTNGGG					738

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 748 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1228UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GATCATGCCA	TTCTTACGCT	TTGCCACAT	GGACGCCCAA	ATGAATTTCT	GTGTATGCCA	60
GGATGCTGAC	GATGCAGCTG	AAGCAGGAGA	CGACAGCGAT	GTGACGCTG	GTGTATGAC	120
GCCTACTATT	TCACCTGTGA	ATACTTGTTT	TTGGCCCTCT	GTAGACATAA	TCTTGTTAAG	180
GACAAAGCTC	CTGCTGTCCG	TGTGTATCAG	GTCAAGTAAA	GTAAGCGCCT	TAAATGCCAA	240
TTTGGAGATA	CCGAAGATTA	AGCATGCCAA	ATCGTTAGCC	GOCCTAACCT	GCCATGGGTG	300

# EP 0 866 129 A2

ATGCTGGGAA CAGGTAAATA TGGCCTGAGG TGCTGTGTAC TTACCTGATA TAAAAGTATG 360  
 CAGTATGCGG GGGCCTTCGT ACGTCTGCT GTAGTCTATC GGATCCTGGA TAGATGTTAG 420  
 5 TTCATCGGTA AATGGTTGGA GATAATTTTC GTCTCGGAG GCTGTATAG TAGTTTCTTG 480  
 TGTTTGAATA TTCATGAAAT GGTGGGCTA GCTTTCAGCA GCTGCTTCTT TAGTCTTTC 540  
 TCATACTGAC TTCTTCGCAG ATCTACNCCA CCGCCTTGGG GCTGACCCCA GCACACTTAT 600  
 10 GATTTTANA AGGAATCCCC GTAATCCAAN GCGCTTNCNT ACCCTGTCOC AATNGTTNCA 660  
 TCAAAANGTC ANNCCCTCNA TTTCCTCTTT TCTCNCCAAA ACNCCACNT TAATTGAANA 720  
 NGNCCCTTTC ACCCGGAGAG GTGGCGNC 748

## (2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 653 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PAG1229RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GATCGTAACA ACAAGGCTAC TCTACTGCTT ACAATACCT GTGTACATC TAAGTCGTGT 60  
 ACAAATGATT TACTCTCGG CAGTATGACA TTGCAATCCG CCGGCAAGCG CCCAGACCTT 120  
 TCGTCTGAA CACCAGTTGC CGGCTGCTA TGGTTCAGCG ATGCTAAAAG CACCTTATTC 180  
 35 GTATCCATCT ATAATGTGCG AGAAAAAGAA TCATCGGTT CTAGCATGGA TTCTGACTTA 240  
 GAGGCGTICA GCCATAATCC AGCGGATGGT AGCTTCGGG CAATGCCCGG TCGGACAGCC 300  
 GCAAAAACCA ATTATCCGAA TGAACGTTC CTCTGCTACT AAGTTCATT ACTATTGCGA 360  
 40 TAACATTCAT CAGTAGGTA AACTAACCT GTCTACGAC GGCTTAAAC CAGCTCAOCT 420  
 TCCCTATTAG TGGGTGAACA ATCCAAGCT TACCGAATTC TGCTTCGGTA TGATAGAAGA 480  
 GCGACATCG AAGAATCAAA AAGCAATGTT CGCTATGAAC GCTTGAAGTC CACAAGCCAG 540  
 45 TTATCCCTGT GGTACTTTCT GCACCTCTAG CCTCCACTCC CGAGAACTAA GATTGATAG 600  
 CACACTTTCA TGTTGTATC AACTGAATC AATCAGGACT TTACCTTGTC TAC 653

## (2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 528 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1229UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

	GATCAGATAC CGTCGTAGTC TTGGCCATAA ACTATGCCGA CTAGGGATCG GGTGGTGT	60
10	TCTTATGACC CACTCGGCAC CTTACGAGAA ATCAAAGTCT TTGGGTTC	120
	GGTCGCAAGG CTGAAACTTA AAGGAATTGA CGGAAGGCCA CCACCAGGAG TGGAGCCTGC	180
	GGCTTAATTT GACTCAACAC GGGGAAACT CACCAGGTCC AGACACAATA AGGATTGACA	240
15	GATTGAGAGC TCTTTCTTGA TTTTGTGGGT GGTGGTGCAT GGCCGTTC	300
	GTGATTGTGC TGCTTAATTG CGATAACGAA CGAGACCTTA ACCTACTAAA TAGTGCTGCT	360
	AGCATTTCCT GGTTCGGCAC TTCTTAGAGG GACTATCGGT TTCAAGCCGA TGGAAGTTTG	420
20	AGGCAATAAC AGGTCTGTGA TGCCCTTAGA CGTTCCTGGC CGCAGCGCG CTACACTGAC	480
	GGAGCCAGCG AGTTATACCT TGGCCGAGAG TCTGGTATCT GTGAAC	528

(2) INFORMATION FOR SEQ ID NO:266:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 756 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1230RP

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

	GATCCCGGTA GCGCTCTGGC GGCATAATGT CTGCCGTATA GGTGGACTCT GGCTGTATTG	60
40	TCCGAGGGG AATGGCATGC TTCTTGTAAGA AATACAACCG ATCATAGGGC GAGCTCATAT	120
	CCACCGTAAG TCGCTGGGAC ACGTACTTTT TGA CTGAGCC ATCATTCGG CTGTTCAATTG	180
	CGACTCTAAT CTGATTGAGA ACCCTGACCT CTAGTGCTAT AGCGCAGGGC GTACCTGTCT	240
45	GATGATGGC TTTTCAATGC TCGAGCGTGC GCAGTGTTAC ATCGATCGTC GCGGACGATG	300
	TTTAAGCAGG ATGCTGAGCT AATATGTATC GGTATAGGCT ATTGGCAGTA GACCTGGGTA	360
	TATACGCTA GATATGGACA AGATGCTGGC CCTAGACATC CAGAACTTAA CCAGGCTCGG	420
50	GTAAAGCCA CCCAGATAAC ATTGGAACAT TAGAACAATT ACCACCGCA ATGGAGGGGA	480
	ACCCAGTCGA AACCCACGG CATCCAATAG TTTCCCCCAA CNGCGAAANG GCAGAATGCA	540
	CCGCCCAATG CTGCCCAAC GCCCAGGCG ACCCTGACCC CATTGACCTN GAAGCCCTGG	600
55	GGCNAACTG CATTTTACCC CCCCCCATTN GGAAAAANTG ACCGAATAAA ANNCCCCCN	660

AAAAANAAAN GGCCNCCCCC AATTACTTTT TNNCCNNGG CCCCNAACCC CNGGGCINNAA 720  
 AAAANNANIG GGGGGGGGTT TCCGNNMTT AAAAGG 756

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1220UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GATCTTCCGC TCCACTTGGT TGGGCTGGCG CATGTCAAAG GTTAGTAAAA GCCCCGAATC 60  
 GTGTACTGAC GCGAACTTGT TGGATCTTCC GGAAGAACAC AAGGACGTAT CCGCGCCCAA 120  
 GGACGGGAAA TCATAGGTGG GCATCCACTT TACATCAOAG ACGGAATCTG AGCCTGAATT 180  
 GAAATTCAGG TCGCTGCGGT TCACCTTGTA AGAGTGGGAC CGCAAGTCCC ACACCTTGAT 240  
 GCAGCCGTCC TGGCCACCGC TGATAAGGAG ATGCGTCTGG CCCATGTTGA AGTCCACGCT 300  
 GTTGATGGAA CCGAGTGTCT CCGACAGGCT CCGTGAATCAG CCGGGAATCC TTGCGCGAGC 360  
 CCGGGTTGAT ATCGTAGATG GAAACCGAGG TCGACGTCCC GCATATGGCG ATGTAATTCT 420  
 TGTGGTGGTG GAACCCCGCC CTGTGAGTCC CGAAATCCGT GCTAATCTTG CGCATGTTT 480  
 CCGGGCCCAT GCTGCTCGAA GAACTTCGTC CCGGCCCGCC AAGGNTCCCC NGTTGTTTNT 540  
 GTTATTCCGT GCACCCCTGCT GCTCCCTGTA CCTCCGTCN AACTTGTTCA GCGCAAATGG 600  
 TCTTCCCCCN CCCCNC AAC CATGCCCTT ANCTTCTTTG ATTTTCTTCC AACCTTGCCA 660  
 CCCCCGGTGG CTTGGAGGGG GGGTACCCCC CCGAAACCC CNGCCCCCC CAATTNTCCC 720  
 ACGCCCNCCC GAATTGGTT TNCCTNNGG NCCCCNNGG GNCNNAAAA CCTCCCTAA 780  
 AGNA 784

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1231RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:



EP 0 866 129 A2

GATCATCTGC GTGAAGGGCG ACAGAAGCCT GGGATGGAA ACATTGGAAT TGATGCATTA 60  
 ACGCAAACAC ATGGGTCATT TCCTCAAACCT CAACAGAAAG GGGACGAAGC TGCGCACACA 120  
 5 GTGCTGCAA ATCTTTAGOC GAGTCTGAA AATTCAAAGT CCGTAGTTCT CGTATGTTGA 180  
 AGCCAGATCC ATAAACTATC TTCTCACTCG CCGATGCAA AGTATCAAGG AATAGGCGAC 240  
 AATCGGTAAT GATTGGCTCG AGCTACGCA GATATTGGCG CACTTCTGAT ATCCGTGGGT 300  
 10 TGTTGATOC ATGATGCACA TGAATAAAG GAAGAAGCTT CGAAAGAGGT ACACGGCCCG 360  
 GGTAGCCGTG TGATGAGAGC TGTTAGTTG GCTTCAACAT CAGCAAGTTT CTCTATAGGG 420  
 GACGAGGGT CGTCAACATC ATTTATTAGA CACTCCAGC ATTTGTTCTT GAAAAAAGT 480  
 15 NGTGCATGNA CAATNGCNC CCCCCCTTTT GAAANGCGG AGAAAATTTT CCTNNAANAC 540  
 NAATNCTING GTNNAANTGC TTNNAAANCC CCTTNAATTA AACCCCTNNN GGCNCAAAAA 600  
 AATTNTTTAA ANCTTTTINA ACNCCCCGGG AAACANAAAC CCCCCCCCCA AAAAAAACA 660  
 20 NGTTTNTCC NCCCCCCCCC CCCCCGANNT TTNNAAAACC TTNNAAAAT CCCCCCCCCC 720  
 CNAAAAANCC CNCNAATTTT TTTTTPAANC C 751

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 762 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1231UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GATGTCAGC GTGCATGAC TTGGCATTC AAAGGGATGT GATCCCTGAG GGGAGGCTTG 60  
 CAGCAGGCG GCTCCTTGT TCACATCATA GCTGTGAG GCGGACTGA TTCAGCTCTC 120  
 40 AAGGCGAGCA CCTTCCAAC GCGCAATAGG GCGCCCTCC TGGGCTGTG ACGGAATAC 180  
 CTCAGACACT GCGTTAAGAT ATATGTATTT AAGAGGGCAC CAGCTGGCTA TCAATTGCC 240  
 TCTCTGCTCT TGTTCCAACA CCAGGCAAGT ATCATGATGT CTGCTGAGG AAAAATGTT 300  
 45 AAGAACAACG GCCAGAAGGA TGAGGGGAAG AATGCGGGC AGAGAGAGGA GCGCCAGTAC 360  
 AGGGTCGGG ATGAGCAGG CTGCGGCGC CAACAGCAG CTGACTTGG GCGCCAGTA 420  
 CCAGCAGGCG CCAAGCTCG AGCAGTTGA CAGACTTGG NGCTTCCNA CATTTGGGCC 480  
 50 CCCCACCAAT TGGGNCCTCA GCAAAATNGG CCGCNCNCT TTATTTTNG GGGCGAATGG 540  
 GGCNAACT ATCCCCAANT TGGGGNAAC TCCCCCCCCA GNAGAGAAC NCATTTTTC 600  
 55 ATTGAAAAC NCACCTTNNN TTGNNAAAG CCCCCCCNA AAAGCCANG GACTGTNTT 660

TTTNGAAAAC GNCCCCCTTT NIGTCNCNNN ANAAATTTT CTANAATTG CGNGGATTCC 720  
 TCCTTGGGG CCATTCCNTT TTTACCTTT TAACCCCCC CC 762

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 746 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1232RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GATCTTATTA ATGAATTTT CCCCACGAAG CTTGTGGAAT TTGATTCTA TGCTTTGCAA 60  
 GCATCAACT TGGGCTGTG TCATGCGAAA CTAACACGCC GCGAAACAGA TACTGCCCAA 120  
 GCGTTAGCAC TCGCTCTTTG CCGTGCTACA AACAGTGTC GAGCATTAGC GTGTGACTTA 180  
 TTTAGGGTIG GAATATACAA AAGTAAGGCG TACATGCGA TATCTCTCTT GTGTGCTCT 240  
 CTCTTACCTA CATCTAGATG TATTGAGGGA ACTTCCCCGC GAGATTACG GCCAAGGCCG 300  
 TOCAGCCCGT AAAGTGCTGC ACCCGTTCAC CTTCACATCG TTCTGGTTGT ATTGTTCGGT 360  
 AACAAAAACC ACCTTTCCCC AAANTCNAAT AATGTNTTCA ACAGGTTGTT CCCCCATTG 420  
 AAAGGGATAN NGTTTAAAC CCGGNCNAAA CAANNAANGG GNNGVTTTTT TTGGGCANAA 480  
 ACCCCCCCCC NAATTNAACC GCGTGGGGCC CTNCNCAAAA TTNTTTTTTT CCCCCNVGG 540  
 GGNCCCCNCC NAANAACCCC CGNGTINNA ATATATCCCN CTTTINOCAG AAGNGANTCC 600  
 CCNNNAACCC GNGGATNT TTTGTGNTT TAAAAANNCC CCCCCCCCCC CCNGGGAGGG 660  
 NNTTCNCNC CCCANCAATTT NNACCNAGN GAGTTTTTTT TCCCTCCCGG GGGAAAAAAC 720  
 ANTGTINNTT TINNNCCNA AAAAAA 746

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1232UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

EP 0 866 129 A2

GATCAGTTTG CCGTAATTGA TACAAAAGGC AACTGGTCCG TGGGCGACGT TCGAGGAGT 60  
 AAAAAGAAGT CCCGGCGACT GCGCTTGTTA AGGAAGTTTA GCGGGACTAT TTTTGACCCA 120  
 5 GAGGAGTACT CCAATTGGAA TATGATAGAA TGGTCACATA TTCACACAAG ATTGCTTTGTG 180  
 ATGAATAGGT CAACTTTTCAT GGAAATTGAC TTTGTAGACG GATGGCAGCA GGAAATTGTC 240  
 CAAGCAAAGA CGTGGTCTAA CTTGCGGAT TTTAAACGCC TTTCOGATGA GAGCAGTGT 300  
 10 CTACTIONCT GCAAAGAGAT TATATTCTTA GACCACAAGC AGCAGGGAAC AAGAGGGGCG 360  
 CTATCTGGA AACACAATTG GGATAGCAA GATTCATCTC TAAAGCTTGC TATACACATT 420  
 TCTGGCAGCC ATATGAAACA ATATTTACAT GCATTCCTAT TTCCACCATG ACTOCCCTGCA 480  
 15 GTGCTTATGT GTCTTCTTC CCGGTCCGAA AACACTTTCC ATTTTTCAG CCATCCCCC 540  
 GCTGNTGTGT TTTTNCATT TACACNCCNG NTTTTACCGA AATTACCTCC CCGTGTGTC 600  
 NAGAAACCGA GTTINANAGA ACCACACCCC CTTTCATTTT CCTANNVTG CCGCCCCC 660  
 20 CCAGGGCGAG AGTTTGGGN CCCCCNTTTT NTGNACCATN TTNCCCCNCC CCGNAGGGT 720  
 TCCCCACNT AAAANCCCTG AAACCCCTTT TCCCCCACC ATTTTNGGTN GGGGATN 777

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 734 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1233RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GATCAGATG CTGTGGCAT TGCTGCTGT GGTGCTCTG TCCCCCTCAA GCGCCGAAGT 60  
 40 AGACAAGCTG CCAGCAAGCA CTGATGGTA CAGGAGCTTT TTGTTACAGT TCTTAAGCAG 120  
 GTTCGCGGTC GAGTCGCGT TGTTCAAAAC AGCGCCCGGC TGCACGCTCG AGCTCGACTC 180  
 CCCCCCGGC GACGACGCG TGGAATACAC CTCTGATCCC GGGTCGGCAT CCTCGCTCT 240  
 45 CGCAGTCCCC CCGGAAGCAA AAAATTCTTC CACGGATGTA TTCCCGTGGT TGCCAGCTG 300  
 CGCACCGGC GTACCGCAG CGCTGTGAC ATTGGACGTG ATATTCTCCA TCAGCAGCTG 360  
 CGAGCTGATG CCCCCCGG CGCTGTCTT GCTCGCATCT GTAACTGCT CAGACCCGA 420  
 50 GTTTGTGTTT GTGTCACG AACGAGAGT TCAACCATGT GACGACGAG GCGGTTTTG 480  
 CCTTCAACC CNAATTGGG CCTTCTGCT GGAACNCAA CCGGGGAAT TTCCCAACT 540  
 NIGATTCCN AANTGCGCG CCGCTTCC AAATTANAAT CCGCAATTG GNTTGAAATN 600  
 55 GNCNAAATNA AACCCTTT TCCCCNNN CCCCCCNG GCGCAANGA GCGGTGGG 660

GNTTAAANNC CCCNACCCCC AAANTTATAC CCTTTTTTTTG NNCCCNCCCC CCNNCCCTNT 720  
 TTTTTTNCCC NTCN 734

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1233UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GATCCAGCTT CCATATAAGC TGTGTGTTGC GGTGCGGACC TCTACAGAAG TGGTGATATA 60  
 TGATACTGTT ACCACGAAAC CCATTGCAGT GGTGGGAAAT TTGCATTACA CCCCCTAAC 120  
 GGACCTCAGC TGGTCTGACA GGGGCCACT ACTCGTCGTG TCATCAACAG ACGGTTCTG 180  
 CTCTATATC TCAATGGAGG ACAGCTATT TGGCGAGCCA TACAGTTCG AGGCACAGCG 240  
 GACGGATTCT CTCATACTT CCACTCCAAA AAGCAACATC TTCAGGAACA CCCTGCGGTC 300  
 CAACCCGGTC AACGTAAAGC GGAAGCACTC TGTAGGCGGC CACAACGACT CACCCATAAA 360  
 GCGCGCTGCC AAAAAATGTC GCGCTTTCC CCGTGGTGG TCGATGAGGG ATCTGCGCGG 420  
 GCACACAACC GCTACTCTCT AGCAAAGATC TCAAGCTCC GAAGGCGCAT CCAACCGTC 480  
 CTGTGTTAAT GACAACAACG GGGCACCTA GTATCCCCNC ACGCATCTCT ANAAGTTNG 540  
 ATTCCNNTAT ACTNAAATAC AAACCCGANA ANCNNTTTTC TTGTINACAA ACTTTTTTTT 600  
 GACCTGCATC AACTATATCC GNGNGGTCA TTCTTGCGA ATGCCCCCTC CCCTTANAA 660  
 CNCCCNACN TAAACCTTCC CNCTCCATA TTTACTCATG AATCNCNGCG AANTCNCTGC 720  
 GGATCNCCA NCTTTTGGT AGINTTCCCC TTTTGTTC C 761

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 728 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1234RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GATCACAGTG CTGTGGGCAT TGCTGCTGCT CGTGCTCTTG TGCCCCCAA GCGCGAAGT 60

EP 0 866 129 A2

AGACAAGCTG CCAGCAAGCA CTGATTGGTA CAGGAGCTTT TTGTTACGT TCTTAAGCAG 120  
 GTTCGGGTC GAGTCGGGT TGTCAAAC AGCGCCGGC TGCAAGCTCG AGCTCGACTC 180  
 5 CCCC GCCGC GACGACGCG TGAATACAC CTCTGATCCC GGGTCGGCAT CCTCGCTCT 240  
 CGCAGTCCCC CCGGAAGCAA AAAATTCTC CACGGATGTA TTCCCGTGGT TGCCAGCTG 300  
 CGCACCGGGC GTACCCGAG CGCTGTGAC ATTGGACGTG ATATTCTCCA TCAGCAGCTG 360  
 10 CGAGCTGATG CCCCCGCGG CGCTGTCTT GCTCGCATCC TGTAACGTG TCAGACCGA 420  
 GTTTTGTTC TGTGGTCCC ACGAAGGAG ACGTCCAACC ATGTGTACAA CAAGNCGTTT 480  
 TTGCCCCA CACCCATTG CACTTTCTG GINGAACGCC AACCCCGAT TTCNCAACG 540  
 15 GNATTTCNT ATNGCCCGC CCCCNCNNA AATANAACC CAATGTNGNN TGAAANGGNA 600  
 NAAAANAACC CCTTTTCCC CTTTTTCAA CCCCCCCCN AAAGGCCNNT GNGTGNNTAA 660  
 ANCCCCCCC CCAATTTAA TCCTTTTAA TTGCCCCACC CCCCACCTT TTTTNNNC 720  
 20 CCTNNNCN 728

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 782 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1234UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GATCCAGCTT CCATATAAGC TGTGTTTGC GGTCCGACC TCTACAGAAG TGGTGATATA 60  
 TGATACTGTT ACCACGAAAC CCATTGCACT GGTGGGAAAT TTGCATTACA CCCCCTAAC 120  
 40 GGACCTCAGC TGGTCTGACA GCGGCACCT ACTCGTCGTG TCATCAACAG ACGGTTCTG 180  
 CTCCTATATC TCAATGGAGG ACAGCTATT TGGCGAGCCA TACAGTCCG AGGCACAGCG 240  
 GACCGATTCT CTCATACCTT CGACTCCAA AAGCAACATC TTCAGGAACA CCTGCGGTC 300  
 45 CAACCCGGTC AACGTAAAGC GGAAGCACTC TGTAGCGGC CACAACGACT CACCCATAAA 360  
 GCGCGCTGCC AAAAAGTGTG GCGCTTTCC OCTGTGGTCG TCAANAAGN ATTTGGGCCC 420  
 GGACCACNAA CGCCTACTCC TTANCAAAA ATTTTTCAAA NCCCCAAAG GGGGTCCCAA 480  
 50 CCGNCCCTT GTTTTTTTGA AAAAAAANG GGGNCCTCA TTTTINCCC CCCCCCNC 540  
 CCAAAATTTT GGGGATCCCN NNNCCNAAA AACAAACCCC AAAANCTTT TTCCGGTTAN 600  
 NAAANNITNN CNNTGACCC CCNCCCCC TTCCGGGNGG TCATTIVINC NAATNGCTCC 660  
 55 NCCCCCTNA AAGNCCCN CNAAAAANC CCCCCCCC NTTTTCCC NNNAACCCC 720

GGGAAAATTC CCNCGGGAN NNNCNANITTT TTCTTGGTCT CCCCCNTITTT NTTCOCTINA 780  
GG 782

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1235RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

20	GATCCTTGAG AAGCCAGATA ACGACGAGGA CGAGGAGCCC AGTGACGATG AGGATGCCGA	60
	CGACTACGAC TCGGATTCTC CCCGGCCCCG CGACAGCGC AGCGAACTCA GAGACCTCC	120
	TGCGCCGGCG ACATTGCTA CGGAAGTCA CGATCCAGC GTCTGGCCT CCCCCTTGAC	180
25	CTATTCTTTC CGCTCCGTCA TGTCCACTA TGGCACAC AACTACGGAC ACTACATTGC	240
	CTTCGCAAG TTCCGTGGTG TGTGGTGGG CATCAGGAC GAAACAGCGT ACATCGTGA	300
	TGAAGCTGAG GTCTTGTTCA CACCGGGGT TTTTCATGTTG TTCTACGATA TGAATATGAC	360
30	GAGGCGACCG GGCAGTTGCG TGACGACTTG GCGTGCTAC AGGAGCCCAG TCCGTGCTGT	420
	CAGATGGGGA CGGAAGAATA CGACTCATTG ACCGGGTCA CCAAGACCTC GATTCAACGA	480
	NCCAGCTGTT GCTCCCGCA ATAACTTTG TTTGGGGCTG GCGGGCATA TTNCTCCAT	540
35	GCATGTTTCAT GCCCCACCG GACATGTTTG ATCCANATAC TTTTGTGTTN GTTNCCTCC	600
	TTCAGNGVIT CCCCCNAAGC AAGATTCCTA NNCTACTTGC CTNGTGTGTC CNOCTGGTT	660
	TGGNACCCCA AATTCCTINT NNCCVITINT GGGCCANCCC NNGGNAACC CNOCTTTTT	720
40	TTTCAAACCA GGVTTNCCCT TTINGCN	747

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1235UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

EP 0 866 129 A2

GATCACACC GTGTCTTTT CAAAGGTGAC CTGCAACTTC TTGTTATTCA AGATGATAGT 60  
 CTCACGTGTC TTTGACACGC TAGCAGGGTA AAATACCGAC TCCTGGCGGT CAGOGTTTTT 120  
 5 TGCAGCCATG TTATCCCAAT GCAAGGTGCC TATTGGGACC AAATTTTCCC CTCTGTGTGT 180  
 CAAGGCTCC AAAGCTCTCT CTATGAACCG ATCTGCTAGC TGCAAGACCT TGTTAAGCAT 240  
 TGGTATTGCT TCATATTTGT ATACCATTTT TATACATGTC CCGGAAGGA CATCGTGGAA 300  
 10 CTGCATAAC AAGATATCTT CCCATAGAGC GTTAATATCA TTAACAGGGT ACGTGTACTT 360  
 GTTAGCGCT AGTAGOGAAA CCTTTGTGGC AATCCACTCC AAATCATGGA TCTTAACCTC 420  
 AGATAGTCTC ATCAACCGTT TAACGCTGTC CTGTGTGTA TACGTGCTC CTATGGAAAT 480  
 15 CAAAGTTACA ATCCGCCCAT CCAAGTTGGC CAATGNGTTC CCANTGCTG NCTTCNGCAT 540  
 AATATCACCG TAAAAACCGT TTANGGAATC CCNACCCCC NACCTINGGG AANAACATTG 600  
 CATTCOOGGT TAAAAATTGAA CGANACCCC CCATTTGTTC CACNCCCC TGTTTGAACC 660  
 20 CCNCCCCGN CNCCGNACCC NNAAAAANAA CGTTGCNA ANGTTCATIN AAAGTTTGT 720  
 TCCCCCGGG TTAAANCC NAATTTINAN AAGCTTCTT TTCCCCGGG GGGTTG 776

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1236RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GATCTCCCTC CGTGAAGT ACGTGAAGT TTTGAGACTC TGCAAGTGT CTTTTGATAG 60  
 CTTCGATGCC TTAGCTCCCA TGCTACTAT AACGTGTCC CGGCTCAG CTAATGTGGG 120  
 40 GCTGCTATC TTAGTCCCTA ACTCTTGGAA GGTGAGAGG CCATAAGCA CGATCGGGA 180  
 GCTGCTCAA TTAATGCTC TGAAAGCGGT GTGTGGTCC ACTTTCCAG ACCCAAGGT 240  
 ATGCCGGTGA CTTGACCTCC GGTCCGATG TGACCTGGG AGGCGGTGG ATGCCGCC 300  
 45 TCATGGCTGT CGGTGCGAA GGACTATCTA CCAGGACTT GGCTGCTGC GCAATTTGCA 360  
 CTGCAGCTTG CAGTGAGGT CTTGCGAAG CTCACGGCA GGGCAGGCA GTTACAGCA 420  
 TGGCACAGG CAAGCCCCG GAGTTGACG GAGTTGGTTG CCAGATATTG GCGGTCCAA 480  
 50 ATTCTGANTA GCGCTTTATA TNAGANCCCC NCGTTGAAC CCAAGNTTT TTTATGGGA 540  
 TGGTTGAAT TCGCCCCCT GCGTTAACC CCCCCAACC CTTNCCCCG GCAAAANCA 600  
 55 ATCTNCCCC NGTTNAAAA ANCCGAACN NNAAAAATTT AAAAGAGACA AATCANNNCA 660

CCCGNGAAAA AGAGCCCTNT CTTTGTAGAA TTCCCGGGGG GGGNGTAAA TTNAACCTTT 720  
GA 722

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1236UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GATCTTCGTC CGCTTGGGT CAGGAAATC AAGCGGGATG AGCTCTGTG TCAGTTTACC 60  
ATAAAAGAGC TGTTTACAA GGTGAAITG CTGCGCTCT TCATCCAAGC TGAGCGGGAC 120  
GGAGCGACTC TCAATTTGGT AGAGGACGTT CCAATGCAT TCGTCACAT CTGCTGTCT 180  
GCCAATCTCC AATGTGTTT CTAGCTGGTC GGAATAATT TTGCAACAT AGGTGGAAGT 240  
TTCAGGGGCT TCGGCTCTG GACTCCCGAC CATGGTGATA TCTTTACCTG AGTCATCAIT 300  
CTCAACAGCC TGCTATCTT CAAGCGGACC TGGCTGGTG TTTTCAACCN TTGGGNGGNN 360  
GAANTCCAAT ANNCCCCCTT TCTGGGGTTC TTGAAAGNA TINGGANAAT TNNITGGGCC 420  
GGTINTTACC NTTTTINGANA GAGACCCCTG GNNITNCAN ACCNAAATNN TCCNNGGGG 480  
CNCOCGNCG AATNTTTTIN TITCCAAANT TTCCNAAANN CCNCTTTTNT GCTTTTCCCC 540  
NTTINGNGG NAGCGCCCCA GGGGNCOCG CGAANTATC NGGGGNTGG AAAAAAATAA 600  
NAATTTCCCA NAGGGGINTT TTTTTTCCN TNGAGAAGG GNGGTANAA AAACCCATTT 660  
TTTCCCCCN NTAGANAACC CCTTTTNCNC CGGGGNTCC NGCCGGGGG ATINTTNGG 720  
GNGCNTGN NACCTCCCTT CCCNCTATA NAAATNCCCC CGGGGGGGG TTNNVTTTC 780  
CCCNAAAN 789

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1237RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:



EP 0 866 129 A2

5 GATCCGGT GAAGACATTG TCAGGTGGG AGTTTGCTG GGGGGCACA TCTGTTAAAC 60  
 GATAACGCAG ATGTCTAAG GGGACTCAT GGAGAACAGA AATCTCCAGT AGAACAAAAG 120  
 10 GGTAAAAGTC CCCTTGATTT TGATTTTCAG TGGAATACA AACCATGAAA GTGTGGCCTA 180  
 TCGATCCTTT AGTTCCTGG AGTTTGAGGC TAGAGGTGCC AGAAAAGTTA CCACAGGGAT 240  
 AACTGGCTTG TGGCAGTCAA GGGTTCATAG CGACATTGCT TTTTGATTCT TCGATGTGG 300  
 15 CTCTTCCTAT CATACCGAAG CAGAATTGG TAAGCGTTGG ATTGTTTACC CACTAATAGG 360  
 GAACTGTGAG CTGGGTTTAG ACCGTCCGTG AGACAGGTTA GTTTTACCCT ACTGATGAAT 420  
 GTTATCGCAA TAGTAATTGA ACTTAGTACG AGAGGAACAG TTCAATCGGA TAATTGGTTT 480  
 20 TTGGGCTGT CCGACCGGC ATGTCCCGCA ACTACCATCC GCTGGATTAT GGCTGAACGC 540  
 CTCTAAGTCA GAATCCATGC TAGAACCGCA TGATCTTTT CTGCACATT ATAGATGATA 600  
 CGAATAGTTG CTTTTANCAT CGCTGAACCA TACAGCCGCA CTGTGTTCAA CGAAGTCTGG 660  
 25 CCCTTCGCG ATTGCA 676

(2) INFORMATION FOR SEQ ID NO:281:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 709 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1237UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GATCCCGTAC ACGAAGAAAA TCGGACGGGC CAACCAAAACC CAAAGTTCAA CTACGAGCTT 60  
 TTAACTGCA ACAACTTTAA TATACGCTAT TGGAGCTGGA ATTACCGCG CTGCTGGCAC 120  
 40 CAGACTTGCC CTCCAATTGT TCCTCGTTAA GGTATTTACA TTGTAATCAT TCCAATTACA 180  
 AGACCCGTAT GGGCCCTGTA TCGTTATTTA TTGTCACTAC CTCCCTGAAT TAGGATTGGG 240  
 TAATTTGCGC GCGTCTGCG TTCTTGAT GTGGTAGCG TTCTCAGGC TCCTCTCCG 300  
 45 GAATCGAACC CTTATTCCCC GTTACCGTT GAAACCATGG TAGGCCACTA TCCTACCATC 360  
 GAAAGTTGAT AGGCAGAAA TTTGAATGAA CCATCGCCAG CACAAGGCA TGCGATTCCG 420  
 AAAAGTTATT ATGAATCATC AAAGAGTCCG AAGACATTGA TTTTATCT AATAAATACA 480  
 50 TCTCTTCAA AAGTCGAGAT TTTAAGCATG TATTAGCTCT AGAATTACCA CAGATATCCA 540  
 TGTTAGTTAA AGAATATCA AATAAAGAT AACTGATTA TGAGCCATTC CGCAGTTTCA 600  
 CTGTATAAAT TGCTTATACT TAGACATGCA TGCTTATCTT TGAGACCAGC ATATGACTAC 660  
 55 TGGCAGATT C AACCAGATAC TATCTTTAAG ACACCGAAA TGCGCAACA 709

# EP 0 866 129 A2

## (2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 820 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1238RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GATCACGGCA	ATGAAAACT	AAGCAAACGT	TACAGACTTT	GAGTGGTACA	TCGCCCTGCT	60
TTGGGATCTC	TGCATAGTCT	CCCAGGACCT	GCAAGACAAG	ACCTCGCGC	AGAAACTGGG	120
TGAGCAAATT	AGAAACATCA	TGGTGAAGGT	TCCTGACCTG	CGGGATCGCA	CTTTGGGGCA	180
GATTGTGCAG	CTGGTGAAGA	GCGAGGACAT	CACGGCCCCG	CTGCCCGGTG	TTCTGAAGGA	240
GTGCATCTGG	TGCGTGGGCG	AGTATTGCTC	GTTCCTCGAC	AATAAGGATG	AGTATATTCT	300
GCTATTGGCA	GAAAATTTCG	AATTATATGA	GCTTGAACCT	CAGCAAACCT	TGATCCCTGC	360
CATTTTGAAG	ATTTATAGCA	ATTGGTGTAA	CGAGTCGGTG	GTGCACACGG	GTCCGTATTA	420
AATGGGTAC	CGAGCGGATA	ATCACCCAC	TAGAAGATCT	AATAATCTCG	AAGAACTTCG	480
AAGTCAGGA	GCGGTCTTCC	GAGGCTCTCG	AATCTTACCC	TTTCTCTGG	ACNCCCCCTC	540
CNAAATNNTC	TGNATCCCTA	NCNGCTGGCA	NCTTACNAAT	TCCTINGCCCA	NTTCINCAAC	600
CCTTTGAATT	NACCNCNNIN	CNCTGGGGCC	CCCAAAAANC	TCNNNNNAAA	CTNTTNTTCN	660
ATGGGAACCC	CCTTTNCCCN	AAANGAAGCC	ANANNNNACC	GNAAAACNEN	CTTGAAGNGA	720
TTTCCCGAG	TTTTGANAAC	ATTTCNNCCN	AATTTTCCGG	GACGGCCAAA	AAGGGTTTIN	780
CAAATTANIT	CGGGGGGGGA	AGGGGAANGG	GGGGGNGNNA			820

## (2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 875 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1238UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GATCAGAAAC	GGCCGGCTGC	AAGAATGGAT	GGCGATGAGC	TTGAGCAGT	TGAGGCATCG	60
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EP 0 866 129 A2

CTTATGCAAA AAAAGAAATT CCTCAGATCA CGTGACAAAG TTTCGTGATC TCTAAATGTC 120  
 GACGGTTGGG CGAAATGTGC CGTCTCTGTC TATAAAATAT AACTAGTIT CTCTACCACT 180  
 5 AGACTGATTG GGAATATCTA AGCTTTCAC TGTATGACGC AGGAGCACTT CATAATCCAG 240  
 TACCTTCTTT GGCTTATCCA CACTAGTCAT CTCATOGAAA ATGTCACAGC CAGTGCAGAG 300  
 AGCCGCGGCT CAATCCTTGA TATCCAAATA TGTCATAAG GAAAGCTAA AATACATGCT 360  
 10 TACAACGCAC TTCTGGGGCC CGTATCGAA CTTTGGTATT CCGATTGCTG CGATTATGA 420  
 CTTGAAGAAG GACCTGAGT TGATTTCGG CCCATGACG TTGGGGCTCG TGGTATACTC 480  
 AGGTATTTTC ATGCGTTACT CGATGGCCGT CACTCCCAAG AACTACCTCT TGTMTGGGTG 540  
 15 CCCACTTTAT AAACGAGTCC CGGCAACTC GGACAGCGTT CCGCTGGCT CAAGTTTCAA 600  
 TTACTTCGGC GAGAGCCCTG CTGTCAAGC ACCGAGAGA CCGCATAGG TCGTTTTCGG 660  
 TCGCACAGC TTGCATTACA GCGTGACCA CTACATAGAA TATTATTAG CCGACTATCC 720  
 20 TACAGTTTC TAGAGCTAGT CGAGATGCTT TTGGCTGATA CTGCTGGGT GGGCCAGGCC 780  
 GTATCTTGCT CCTCTGGCT TTGCTGGGT GCGCAGCTCC CANTTGNCC TTCNCGATNN 840  
 TCTGTGTCC CGTATCCATT GNTAAATGT CTCCC 875  
 25

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1239RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GATCAACTTA GAACTGGTAC GGACAAGGG AATCTGACTG TCTAATTAAA ACATAGCATT 60  
 GCGATGGTCA GAAAGTGATG TTGACGCAAT GTGATTTCIG CCCAGTGCTC TGAATGTCAA 120  
 AGTGAAGAAA TTCAACCAAG CGCGGGTAAA CGCGGGGAGT AACTATGACT CTCTTAAGGT 180  
 45 AGCCAAATGC CTGTCATCTT AATTAGTGAC GCGCATGAAT GGATTAAOGA GATTCCCACT 240  
 GTCCCTATCT ACTATCTAGC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGCGG 300  
 GGAAAGAAGA CCTGTGTGAG CTTGACTCTA GTTTGACATT GTGAAGAGAC ATAGAGGGTG 360  
 50 TAGAATAAGT GGGAGCTTCG GCGCCAGTGA AATACCACTA CCTTTATAGT TTCTTTACTT 420  
 ATTCAATTAA GCGGAGCTGG AATTCAATTT CCACCTTCTA GCATTAAAG TCCTATACGG 480  
 GCTGATCCGG GTTGAAGACA TTGTCAGGTG GGGAGTTTGG CTGGGGGGC ACATCTGTTA 540  
 55 AACGATAACG CAGATGTCTT AAGGGGGACT CCATGGAGAA CAGAATCTCC CAGTAGAACA 600

AAGGGTAAAG TCCCCTTGAT TTGATTTTCAG TGTGAATACA ACCATGAAGT GTGGCCTATC 660  
 GATCCTTAGT TCTCGAGTT TGAGCTAGAG TGCCAGAAAT TACACAGGAT ACTGCT 716

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 793 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1239UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GATCATCTTC GATCCCCIAA CTTTCGTCTC TGATTAATGA AAACGTCCTT GGCAAATGCT 60  
 TTCGCAGTAG TTAGTCTTCA ATAAATCCAA GAATTTCCACC TCTGACAATT GAATACTGAT 120  
 GCCCCCGACC GTCCCTATTA ATCATTACGA TGGTCTAGA AACCAACAAA ATAGAACCAA 180  
 ACGTCTATT CCATTATTC ATGCTAATAT ATTGAGCTT GCGCTGCTT TGAACACTCT 240  
 AATTTTTC AAGTAAAGT CCGGTTGCG CTAGAGTACA AGTACCTAG GTTAGCCAGA 300  
 AGGAAAGGIT CGGTTGGATC CGGTACGA AGAAATGG ACGGGCCAAC CAAACCCAAA 360  
 GTCAACTAC GAGCTTTTTA ACTGCAACAA CTTAATATA CGCTATTGGA GCTGGAATTA 420  
 CCGCGGCTGC TGGCACCAGA CTGCGCTCC AATTGTTCT CGTTAAGGTA TTTACATTGT 480  
 ACTCATTOCA ATTACAAGAC CGGTATGGC CCGTATCGT TATTTATGT CACTACCTCC 540  
 CTGAATTAGG ATTGGGTAAT TTGGCGGCT GCTGCTTCC TTGGATGTGG TAGCGTTTC 600  
 TCAGGCTCCC TCTCGGAAT CGAACCTTA TCCCGTTAC CGTTGAACC ATGGTAGCCA 660  
 CTATCTACC ATCGAAAGT GATAGGCAG AAATTTGAAT GAACCATGC CAGCACAAGG 720  
 CCATGCGATC CGAAAGTTA TATGAATCAT CAGAGTCCGA GAACTTGATT TTTATCNATA 780  
 ATNCNCTCTC CAA 793

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 836 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1240RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

EP 0 866 129 A2

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GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT 60  
ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT 120  
ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA 180  
TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240  
TGTACATGTA ATACCATTA AATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA 300  
TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT 360  
CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420  
GCACCTCAAT GTGACATTTG TCATATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480  
GTTAAAATAA AGATAATAAC ACCAACTGTT CCATACAATA ACTCTAGGTG ATTTATAAGA 540  
ACCATAATAT AAACCTTTAC CAATATGAAT ATACATACAA ATAAAGAAGA ATGAAGCACC 600  
ATTAGAATG CATATATCTA ATTATCCACC TATTGTACTC TCTCANAATA GTTCCTACCT 660  
GATGANAAGC TATCCATATT ANAAGAATAT GCATACCTTA AAAATAOOGT TANAATTGAA 720  
TACTAACATA ACCTATAANA CCNAATTCAC CATAATAATG AGAGGGTGAG GNGAACCATA 780  
CMTACNATAC TAATTTAATT ATTGATTICT TCCCNMTT ATTATTAAAT TTTAAT 836

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 860 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1240UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

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GATCTAGAAT TATTAAAGTCA ACTATTAACT AATATCTATA ATAATAATGG TTTATCATTA 60  
AAATCATTAAGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA 120  
AATTATGTGA ATAAAATAAA TAAATATAAT TTTACTAATTA ATAATAATTT AAATAATAAT 180  
AAAAAAGATT TAATTAAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATTCTT 240  
AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTAAA GGGTAGACTA 300  
TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT 360  
TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT 420  
ATTAAATAAC TTAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAATTAAA 480  
TTAAATACTA TTAATAAAT ATCTATAAGT AATTTCCTAT TTATTTTATA ACATTTTAAA 540  
ATGTTTTATG TTTAAATAGA TAATAACAAT TAAATAATAA AAATTAAGAT GCCACAAATA 600

TTUCCATTIT CCITTTATGAA TCAATTACTT ATGGTTTCCT ATTTATTTTA CTATTTTATC 660  
 CTTCATCTT ATGINITTTA CCTAAGAATT TAANAATATA TACTCCTAAA TATATATTCC 720  
 NAAATTATAA TAGTTATTAA ATTITAATTA ATCCANTATG ATCCNTATTT ATAAATATAT 780  
 AAGAANATTT TAATATATAT ATATGAATNT TATATONCN TGAACCATTG NAATNNATTA 840  
 TAGTTTACAC CCOCTANATC 860

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1241RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GATCTAAATA TATATAATTT AATTATATAA GATTAAATATA AACTTTTTTA TTATAATATT 60  
 TAAGTATTAA ATTATTTTAA CTATTATTAT CATTTATTTAA TAAATTAATT ATTTGATTAT 120  
 TAATACTTAT TATATAATTA TTATATAATT TACTTAAATC ATCATTATTA ATATTTTATAT 180  
 AATTATAAAA ATAATATTTA ATATGAATAC TATTTAGTCT ATGTTCAAAT TTAAATTTAG 240  
 TTATTTAAAT ATTATTAGAT ATTATTATTT TCCTTAATAA ATTATTAAAT AGATTATCAA 300  
 TAATTAATAT ATTATTTATT AATTGTTTAT TAAAATAATA TATTTTATTA TTATAAGAT 360  
 TTAATTTATT TAAATATGT AAATTATTAT TTTTATATA ATATCTATTT TTATAAATAT 420  
 TAGTTTGATT TATATTATTT AACTTTTTTA TAAGAATTAT TATTAAATTT AATTTTAACT 480  
 TTAATTTCTT ATTAATTAAT TTATATTTAT TTAATAAATT ATATTTCAAT TTATTTATTT 540  
 ATTTATTTAA TTAAATTAAT TATTTAATTA ATATTTTATC ATTATTTAAT TAATTAATAA 600  
 AATATTATTA AGAATGTAGT TAAAATACT TATAAAAGGA TCCGAACCTA TATTATTGTT 660  
 TATGAGACAA ATCCTTTTAC CCATAAGCTA TATAGTTTGA CTATCATTTG AGANTTGGGT 720  
 NNNCCCCCTA TGCTNNCATC CTGVTGTCOC CNCTAAANGA ATTINTTTINT TNANANATGA 780  
 AAAANITATT TATCAAAGAA TTATAATTTT TTAANAAGGG GNANAAGGAA AGACCCG 837

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1241UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

	GATCTGTATA CTAGAGCTTA TTTTACTTCA GCTACTATAA TTATCTTAT TCCTACTAGT	60
10	ATTAAAGTAT TTAGTTGATT ACTAACTATT TATGGTGGTT CATTAAAGATT ACTAACACCA	120
	ATATTATATC TATTATCATT TTTATTTTTA TTACTGTAG GTGGTTTAACT TGGGTAGTA	180
	TTAGCTAATC TATCATTAGA TGTAGCATTG CATGATACTT ATTATGTAGT ACTACATTTG	240
15	CATTATGTAT TAAGTTTAGG TGCTGTATTC TCTATGTTTG CTGGTTATTA TTATTGAAGT	300
	CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATTCATT CTGATTAAAT	360
	TTCTTAGGTC TTAATATTAT TTTCTTCCCT ATGCATTTCT TAGGTATTAA TGGTATACCA	420
20	AGAAGAATTC CTGATTATCC TGATCTATTC CTAGGTGAA ATTTAGTATC TTCATTTGGT	480
	TCTATAATAA CTATTATATC ATTAATGTTA TTCTTTTATA TTATTTATGA TCAATTAAATA	540
	AATGGTTTAA CTAATAAAGT TAATAATAAA TCTATTAATT ATATAAACT ACCCTGATTT	600
25	TATTGAATCA AATAATATTT TCTTAATGAA TACTACTAAA TCACATCTAT GATTTATATG	660
	AATCACCCT CTTAATCNAT CAATTAAACC CTCTAATCCA ACTTTAAATA NNCITTAATTA	720
	TAAATTANNA ATAAATTTAG TGAANAATT AATNGTAANC AATNTTTTNA NGGANTTTAT	780
30	CTCNNTCCAA CCGAACTAC TTTTATCCTT AANNAAAACC TTAAATNAAT GGACCNCANA	840
	NTCNNAACNN GTTTTC	856

(2) INFORMATION FOR SEQ ID NO:290:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 831 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1242RP

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

	GATCAGTGC TAAATGTCG GGTACATTAG TGCACCCGTA CACCGCATTG CGACATTACG	60
50	ACGCTTCTTG ACTAACCAGG TTATCAGTGT TATATAGTTA CATACGAAGC TCTGGTACAA	120
	GGAAGAGCCG GCGGAAGTC CACTTCACCC TTAAATTGOC ACATTTTCATG AGCATTTACA	180
	ACAGAAGCAC AGCTGTAAAC GTTCTCGAA CTGCTGAAGT TTCATATTGT TCCTTAAGGG	240
55	CCCTTGATGT TGCAGTTCAA GCTAGTTCTG TTGGGAGACT CGTCGGTGG TAAGTCGTCA	300

ATTGTTTCATC GCTTCGTGAA GGATTCGTTT GATGAGTTCC GGGAAAGCAC AATCGGCGCC 360  
 GCATTTCTGT CCGGTACCAT CAAGCTGGCG GACCAAGAG ACGCAATGAT CAATTGAGA 420  
 5 TCTGGGACAC CGCGGGACAG GAGCGGTACA AATCGCTGGC TCGATGTAT TACAGGAATG 480  
 CGAACGCCCC GTTGGTGGTG TTATGACGTT GACACAGGAG GATTCTCTAG CAAAGGCACA 540  
 GAGCTGGGTT GAACGAATTA AGAGCAGGTT GGTAAGAGA ATTCTGGTAT CTTCCTGT 600  
 10 GGGCATAATT GATTNGGGGA NGAGGANOGG AACNAGGTG ATTGAACOGA GAACNCAGGC 660  
 TCCCCAAACC CNGGGTGANT TCCCNAGGT TTNNCCAAA CCGGCGGTT NOCGGATTIN 720  
 TTCNNGGAT TGGGGGAANN CTAAACNGG GCNATTCNT NCGGCCCCC CGCNTCCCC 780  
 15 ANITTCNTT CAAGNCCCC CAAAGAACAC CCTGGGGNTT ACCCCCTCC N 831

## (2) INFORMATION FOR SEQ ID NO:291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 878 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1242UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

30 GATCTGTGTC ATTGTGAAGG AGGAGACGAA AAACGCTACC ATCAGTGTG CCGTCGAGAA 60  
 CAAGCAGCTC ATCCCATTC A TTTCGCTGGC GGAAGTGGAG ATTTCGAGG ACGTACTGT 120  
 GAAGGCTTC CCTAACGGCT CTGAGAAGAT CGTCTTATG GGGCCACGG ATGAAGCGAA 180  
 35 GGAAGCAAAG GTGAATGTT AGAATTACTT GAACACTTTA GCAAGCAAG TATCTGAGAA 240  
 AAAGATTTTC ATTCTCGCA AGTTCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGAA 300  
 ATACAAGGTC TCGTTATCT TCCCAACGGC CCTTGGTGAT GATACTGTGT CGTCTACGG 360  
 40 ACTGTCCGCT AATCTTGATG ACGGATGCG ATATGCTCGC CAGTCGTCTA AGCAGTACAT 420  
 GGTAGAATCT TTGGAGGTAT CCAAGGCTCA CGAAAGAAT GTCGCTCATG CAAAGAATTT 480  
 AATGTTCTAC TTCGCCAGTT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG 540  
 45 ANITGAANTT TTGINCTACC CACTCCCGGA GGGATTTCG CCGTTTAAAN AAGNTTTTNA 600  
 ATNCACANTT TTCCAAAGG GNGAATTTTG GGNACAAAA AAAANTGINT TCCCCGNCNA 660  
 TNCCTTATTT NTTAACNACC CCCCCTCCCC NGPTTCNCC GNTGAANACC NAANTATNAC 720  
 50 CCTTCCCCC AGNGATTTAC CNGGGCCNIN CAGGGGANTC CACTTTTTIN CTCCGGANTC 780  
 AANAAAGGGA AANACCNGN GCTTTTGCCA GNTGANAAA AAATCCNCC CCCCAGAGG 840  
 TAAGANCCN GNAAGGNGG CCNTTTTGA GAATNCCC 878



## (2) INFORMATION FOR SEQ ID NO:292:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1243RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GATCGCTAAT CCCGAGGTTT GTTTTGAAGT CTGTGATCAG TTGGTCTCC ACATCTTTGA 60  
 GAATTTCTAAT AGCCTCCGAT GGCAGTTCCT CCAATTCCAT TCGCACTGG GCAGACTGTA 120  
 TCTTTAGAGA GTAAATTTTC ACACACAAAG AGTCAATCTT GTCTTGAACA TCGTCAATCA 180  
 TATACTTCAG TACATCGTTC ATGTTTGGTA GATTCAGTGA GCTTTTGAGT GCGCCTTTTC 240  
 CTAGCGCCGA AAGGTTCCCC GCTTCATTGG ATGAGAAGCC TAGAACTGAC ATCATGGCGT 300  
 GGCAGCATGT CTTCGCAAC TGTGACAACC AATAATTCAA GACTGCGGGG CCTAGATAAC 360  
 AGGGCCCTTG CCCGTCGAG TCATAGCCTG AAGCCTCCAA GAAGGATTTT CATAGGTTAA 420  
 CATAATTATC ACGCTCTATC GGTGAGAATT GAAGTTGGAT TAAGTAATGA TGCTGCTTTG 480  
 GGATTTTAAT CTGATATTGG ACATCATTCT TTGTATGACG GATACAAAGG TTGAAACGTG 540  
 GGATGATATC AAGAAGTTCT CTTCGGTGA AAGTCACACC GTTGACACGT TGGAGCTTTG 600  
 CGAATTGTGT GCGGGATCTA GATGCATCG ATTTGTTGCC AGTTCCTCG TATTCTGGCA 660  
 GACTGTGTTT GATATACTTT GGAGATCCCT TGAAGGGATG CACTGCCATT AGAAATACAC 720  
 CTTGAATCCN CTAGTGAATG ATAGGNTTAC CCGAACCCCC ANTTTGTATA CCGNCAGAG 780  
 TTTGTCATC GGGCCCTTCN NCTTCTGCC CACATTGCTT CCNATTTTA TCCTGAAATG 840  
 CTTA 844

## (2) INFORMATION FOR SEQ ID NO:293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1243UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GATCTGTCC CACCACGGGC GCAGGAAGT GTACTGGCTT TTGAGATCA ACTCTGTCAG 60

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GACGTGATC TTTCGTGCT AAAAAGGCGG GAAGCCGCAC AACACGGTGT ATAGGAAGCA 120  
 GCGGATCCCC CACATGTGCA CCTTCATGGA GTAGCGTTGG TCCTTCACCA CCTCGGGGCG 180  
 5 GGTGTACCCG ACAGTCCCCG ACGGCGTCTG GTGTGTGTA GCATAAATTT GCTTCGAGAG 240  
 TCGAAGTCT GCAGCTTTA TCACACGAT CCGCGCGCC CCGATGCCAG GTCGGAACAG 300  
 GCGCTGCTCT TGTTTTGTCT TTGGTCTGTC CGACTGTCTC AGCTGCTGGC GCTTGCTGGG 360  
 10 TATAAATCA ATTGGGGAGA ACAGCAAGTT TTCTGGCTTG ATATCCCGGT GGACAAATGCC 420  
 AAGCGAGTGC ATGTGTTTTA CCGCGAGTGC CAGCTGCCTG ATTACATGTC TAGAAAGTTC 480  
 CTCGAAAAA TAAGTGAGTC GCACGATTTT TCCAAAAATC TCCCCCGCG GCAAGCAGCT 540  
 15 CCTGGACTAT GAAGTAGTAT GACTCGGTCT CCTCGAAGT CGATAAACGT CACAATGTTT 600  
 TCGCCCGAGG ACACCGCCTT GTGGATGGTG ATCTCCTTCA GAACTGCTCT CGCGATGTGG 660  
 CCTGTTCGCG CGGCTCNCNC CACTTNNNNC GGGCCCCCCC NCGTGCCCCC ATCGTTAANA 720  
 20 GGNCCCTTTT GCTGATCNC TTGACGGCNC CGTTTNNNTAC NGNCNAAGTN CCTTTTCGGN 780  
 CGNCCCTCAG CGNCCNNNG ANNCCNCGN AAACCCCNCC CNATTTNCCC NAACTTNTCC 840  
 CNCAANCCAA GNNCCGAANC CCCCC 865

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAGL244RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GATCCTGCCT TATCAAGAGC GCCATCGAA CTCCCCCGG GATGTGTTG AGAGGTAGCG 60  
 AGCTCACTC CACAACCTC TCATCTGAAT CGTCTTCTA TGTACTATCT AGCTCTTCAG 120  
 CGTCGCGCGA TGCAGATTCC GCGCTGTCTT TCACCTGTTT CAGCACCGCC TGTCGGTTAA 180  
 45 GCTCAGAGAG GCAGGCATGT GTGCGACCCC CGTATATCTG GCCCAGGTAA TACCCGTTGG 240  
 CCAGCGAAGC CATCGTAACG CTCAGTATGA ACGTAAAGTT GATACCTGCC ATCCTAGTTT 300  
 CTGTTTGGTA TTCTGCATGC TGAGTGCGCA AGCCAAGTTG GTTGAAAATT CCTTCAAGCT 360  
 50 GACAATCGCT GGTCTGCGC GCAGTTCAAC ACAGCAAAC TCAGAGAGAG GTATAAACGC 420  
 CATATATAGG AGGAGACTAC TCTATTCATC GCTATCTTT TCAGCCACA GTTCTCTGCG 480  
 CTGCAGAAIT GTGTGTGAT TCGCCAGCA TTTTGTTCAT CGTCTGACA TATTCGTCCG 540  
 55 TTATGATTGG GAATCCGTGG AACATTCCG CGCCAGCCTG TTAGATTAGG CCACACCGCC 600

CTTGTTAGAC CATAGTGGGC GAGTGGGATT ACAGGTTATC CNTCGAACAC CATCCGTAGA 660  
 ACCAGTGGCT ACNCTCCGGN GTTAAACCCC TACGCTNCCC TTCCACTTNC CGATAGTCCA 720  
 TACGCGGAAT TTGGGGGGCC AAAAAAGTGC CCNGCAGGAA CNCAAACGAA GNNTCAAAGC 780  
 CNTGINTTGG GCNGGTGCCN TTTCNCNAAA NCAGTGGGTA NTINTAANCC NGCCNCTTAT 840  
 TTTCCCAT T 851

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1244UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GATCAATCTG ACAGTTGGAT TGATACCAGG TGCTATCTCC TTATCAGCCT TTACAGTGAC 60  
 GAAGGAGGGA TTGGATTGGG GAATGGAGAA TAAAGATATT TTTGATCCAT CACCAGAAGG 120  
 ATTTGATCCC TCTTTCAGTG AGCATGCCCA ACTTTTACTC TCGGAACGTA TAATGGGAAA 180  
 CTTTCTCGTT CCAAAGTCTG GCATCTGGAA TTATGCATTT ATGGGTGCTG GATTTAACAG 240  
 AGAGCTACGT TACGAGCTAT CTCCTGCATC ACCACTOGGA TTTTATGATG AACAGCACCG 300  
 TGCAACGCAT TTTCTACAAT TCAACGAAGT GGCAGCTGAC GATACTTTGG AAGCAGAACA 360  
 GGAAGATTTA TTCTCCTAAG TACATATTAA GGATAGAGCC AACTTGCAA CTAGCTTCAG 420  
 TTGGGTATGA ATCCCATATA TGTATATATC AATACACGGG CCACTCATGG CTGGTGACCC 480  
 ATTTAAGCAA ATACCATATT TTTTAATGTT GCGGTGATTT TATAATCTCG ATATCATGAT 540  
 TTTATTTATA GGAGATGACT TTTCCCTCTA CAACGCCACA TTATAGAAGA CGTCAATGC 600  
 AGCACCCAGG CTGAAGCCAG AACGGAAATG TTGGAACCAG AACAGGCAGG TTTGAATAGC 660  
 TCGACATATG AACCTCCCCA GAACATGTTT TTTTGAACA TCNAATGANT TTCTGCCAAA 720  
 AACANGAAAA TGGACNCCNN GCATCATTC AAAAAACCN TCCTTGAACC TGACAAAAAA 780  
 TATGCACCCN GATTTTTTGA TCACGGANNG TTTTCTTTAC NCCAATTAAA TAGGNCOCOC 840  
 NGAGATTTTT ACACCCNCC 859

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1245RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

10	GATCAAAAAC AGAGTACCCCT COGCAOGAAC TTCCCATATG AGGCCCAGAG AGAACAACAT	60
	CGCCGATCAC CTATATCAAC AACGGAGACC TTGGTCTGCC GAGAAGTCA CAGCTTATCT	120
	TATTATCGAT CGAATGGATG TTGGAAAGAA GATACAAAAT AACGCATAAT TGCTGAATAT	180
15	ATTGCACGCT TCTAACGCAA ACGACGAGCC TCAOGCTCAG ATTCCATCAA GACCAAGATG	240
	TCGTCTCTCT TAACTGGGCC CTTGACGTTT CTGACAATGG TTCTGGAAGT GTCTGCAAG	300
	AACTCAACGC GGACCTGGGT GACACCACCA CGAGAACCGG TTCTACCTAG AACCTTGATA	360
20	ACCTTAGCTA GAGTGACTGG GGTCTTGGAG TCCATTTTGA TCTATTGCTT CTGGATATA	420
	AAATATCTAG TAAAAAGTGC TGAATAGGTG AGAGGAAGAT ATCATGAACA GGCGGTTTTT	480
	TTTGATGCCC CGAAAAATTT TTCAGGTCTG CGATGCCCAT CGCAGGTGAA ATGTGCTTGG	540
25	GTTCTTGAAA AATCACATCA TACGATAACT ATGCGTGAC CCAAAGGCTT TGGCAGCAGC	600
	GAAGTGCGCG AAGGTTAGCC AGCCGAGAAC GAAACCTGAG AACAGGTTAA GCTCAGGTGA	660
	ATTGTTTGCT TCTATTGCTT TACAGTTCAT CTTCCGGTAA TTGCAGTATC CGTTGATTCC	720
30	CCNCAGCTGA CCAGCGGTIN ATTCCCGTTT GAACCTTCAG AGNTCNVIGAA ACCCTNGTNT	780
	TTTCAACCCN TGACACNTAT ATNCCCCCT TATATGACTT CCGTGNATNC CCG	833

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1245UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

50	GATCCGGGTA ATACAACGCC TCGGACCCCT CGGCGGCTAA CGAGAAAATC GCGCTAAGCT	60
	TCCAGCCTAA TCATAATAAA AGGGGCATTG GTGGAAGCTT TCTGGTACTT ACGCGAGTAA	120
	ACAAAAGGCG CAAGGACGTT TCAGAAGAAG CCAGAAGCAG CAATGAGOGA GATCAACTCG	180
	ATCATTCACA GAGTGAATGT ACTGGTCTCA AAACTGCCCA AAGAGAAGGA TGCAGGCTCG	240
55	GAGAAAGAGT GCGCGCTGAT CAAGTTGGGC GGCATGGTAT CTAACCGCGA ATCGGGCCTG	300

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TTGTTTGGAG AACTGGGCGA GCAGATGGAT CGCAGAGGG TGCTACGGCA GCCATGGATT 360  
 GTGAGTPTTG TTGTGCGCTT GGGCAACGAG CTATGCGGGC GTGGGAGGTT GGGCGAGAGC 420  
 5 TTCTGGGGCA AGATATTGGT TCCGTGGAT GGACAGACCC CGTTATTGAC AGTTACTAAC 480  
 AAGAATCCAG GGTGCGAAGT TTTCGGGTAA TGTTGGGGTC CATGGCGGGT TGGTGGAGGC 540  
 GCTGCTGGAC GGGGCGCTGT CGGTACGGC TCCCTGTGG TGGCAGAATA TGGCGTGTGT 600  
 10 GCTCAGCTG TCCTATNNAC CNCCGGATT NTCCGGAAGT TGNIGNCCCC CCTTTACCCC 660  
 CCCCCTNNCN AGNATGGTTG GNGACCNITT GNNCGNITNC CAACTTCCTT NNNCCCNCT 720  
 TTTTITGNAC NTTGAANCNA TTTTCCCCC TINAANICAA CCNACNGTT NNNCAACCC 780  
 15 CCCCCCCTT TGGGAAAANN AGNAAAAAN ACCTTTTCCA CCNCGATNC CCTTTGNCA 840  
 NCTGGAACNG NNNNITCNC CCTC 864

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 830 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1246RP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GATCAACAAT GATTGTGGCG ACGGGGGGGG GGGCGTTCAA ATTCTACGAC GTGCTGCTGT 60  
 CGGAATTTC GGGCGTGTC GATATCTCC GGCTGGACGA GATGGACTGC CTGACGAAGG 120  
 35 GGTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGAGC 180  
 GCGAAGGCAC GGTGGATGCG GTGGCGGATG ATGAGATGTA CCGTACATG CTAGTGAACA 240  
 TAGGATCCGG GTCTCGATT CTGAAGGTGG AGTCGCCCAA CGAGTGCAATG CGTGTGGGCG 300  
 40 GCTCGTCATT GGGGCGGGC ACGTTGTGG GACTACTGTC GCTAATTACT GGGCGAAGA 360  
 CGTACGACGA GATGCTGGCC TGGGCAAACC AGGGCAATAA CGGGAACGTG GACATGTTGG 420  
 TAGGCGACAT ATACGGCACC GACTATGCCA AGATCGGCCT GAAATCCAGT AATATGTCAT 480  
 45 CGTGTTCGG GAAGGTCTTC CAACGGGAGA GCGTACCGC GCCCCTCGGC GGGCCTGACT 540  
 TGGCGTCTG CGACCTGAC GTGTGAGATC CGAGATTGGA AATGAGAAAT CCNCAAGCC 600  
 GAATNTTCC ATCCTCTGTG TACCATCTC CAACAAATCG GCCAAATGCT TNCTGCAGCC 660  
 50 AAATCCCCAA CTCGAAAAA NNTCTTTGG GTCNITATNT CCCCCTTTT TACCCCTGA 720  
 CCTTTACCC CCCCCTAAT CNGGTCAAN GNTTTTACA NCCNCCCC TNAGGNTTAA 780  
 55 GGTNTTGGCC CCNNGCCCT TMTGCCCCA AAAATTTCCT NNCNNTCTN 830

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(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1246UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

GATCGTAGAG CGTGAGACGG CACCGGCGGA GCGGCCAGCG CCGGACGGTG TGCAGCCAGG      60
GGGGTTTCTT GAGCTGTACC GCGCGGCAGC GATATCTAGC TGCGGCCAAC GCTTCAGAGG      120
GAAGAATGGG CAGCGCAGGC CGCGCGCGGC GCGCGTCGCG GCAAGCGAGG CCGAGAAGAT      180
CCACAAGGAA AACATGGCGT ACATCGAGGG GCTGTGGGAG GAGCAGCGGA CCGCAGAGCG      240
CCGCGAGCTG TTAGAGAGCC TGGACCCCAA GGTGCTGCAG GCGTTGTACC GTCGGTTGGA      300
TGCACTGCA GCAGCGGACG GAACGGCGGC CTTAGTGGCG GAAGTCGAGG GAGCGGCAGG      360
CAGCTGGGTG GCGCGCACCC GCGAGGAGCC GATGATGCGG CGCTGGATG ACGCGACCGT      420
CGACGCGCGG CTAGCGCGGC CACAGGCTTC GATGCCAGAG GCGCGGCCCA CGTACGACCT      480
GCCAGCGCGG CTGGAGGATG CCGACGACAT CGCGCCCCAG GAATACCACT TCATCAGCAG      540
ATGGACCATA TGAAGGACAG GACTTGCTAC GAGATATCCA CTTCCTCGCG AATGAGACTG      600
TGGCGCCCCG ACTGGACATC AACGACCCCA ACTTTATGAG CAGCTGCAAG AGAATACTTC      660
CGGATNTTCC GAAAGAAANA AATAACTINGA ATGGATGAAG GCCACTGAAC CCTGACACTC      720
TTCTNCTAAC TCNCGATTTT TGCGGAATGC CCTCCAACTT AGGGCCCATG TCCCCCCCCC      780
CCGGAATTIN NCCCCNNAA CNGCCTCNC CCTTCGAAAA CCCCCCTTIN CCGGCTNTCC      840
TCCCATTTGC ACNTCCCCA C                                     861

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1247RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

GATCTGGCGG CCGAGCTGGG GCGCTGTAAT GCTCCCTGCG GTTACTGTGG CCGCGCGCGC      60

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```

GTGTCTTATT CGGCATCGCG TAGGGTTCAC TAAGCCCCCTC CAGGACGGGC AAAAAAGCG      120
CAGGGGCGTC ATAGAGCACC ACAGGGTCTG GGTGGGAAG CACGTGCATC CGCGGGTGT      180
5  GCTTGCTCAC CGCCTCGTGC GCCTTGCCCC GCTCTGCCAC CGGCGCAGGC GTTCAGAGCC      240
CGGGGGCGCG GGGGGGCGTG TGCACGTGTAG CGGCACGGGC GGGGGGAGG CTCGGCTTGC      300
GGACCGCCTT GATGACCGGC TTTCGGCCCC GCGCGGGGCG GCTGGCCCGA GCGAGGGCCA      360
10 GCGCGGCGTG CACACGCATC AGCATCCCAT CCACCGCTTT CCTGTGTCTT TCCACCAAGC      420
TGTCGCCGTA AGCAGACTCT GGGCTATCTC CTCGGCTCG GACGAAAGGC CTCGTGCTG      480
CTCGACTGCG TCTGCCCGTA CTTCCGTCGA AGTACGGCGC CAGTGGCGGC GCGCGCTTCG      540
15 CCTCGCGGCG CGCGGGGCGC GCGAAGGGCA CGTTAGGGCG CCGAGCGCGC GTCAGACCGT      600
CCTCATCGAA TCGGAACGCG TCGCGCGGTC GCGCCAATCG CCCACGGAAC CAGCCCCCGG      660
GGGGGTTCNG NGGCGCGGCG GCGCCCCCTC TTTTNAAAAC GACNACCNCT TGNAANCCG      720
20 TTACCCCNEN CNNTCAAAC NCCNGGAAA ATTTTCGNEN ANNNNNNNNN CCCCCCCCC      780
NTNCINNGAA ANAANGNCCN GGCCCTNNGG      810

```

## (2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 630 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PAG1248RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

GATCAGATAC CGTCGTAGTC TTAACCATAA ACTATGCGA CTAGGGATCG GGTGGTGT      60
TCTTATGACC CACTCGGCAC CTTACGAGAA ATCAAAGTCT TTGGGTCTG GGGGGAGTAT      120
40 GGTGCAAGG CTGAACTTA AAGGAATGA CGGAAGGGCA CCACAGGAG TGGAGCTGC      180
GGCTTAATTT GACTCAACAC GGGGAACTC ACCAGGTCCA GACACAATAA GGATTGACAG      240
45 ATGAGAGCT CTTTCTTGAT TTGTGGGTG GTGGTGCATG GCGTCTCTA GTTGGTGGAG      300
TGATTTGTCT GCTTAATGCG GATAACGAAC GAGACCTTAA CCTACTAAAT AGTCTGCTA      360
GCATTTGCTG GTTGGGCACT TCTTAGAGG ACTATCGGTT TCAAGCGAT GGAAGTTGA      420
50 GGCAATAACA GTCTGTGAT GCGCTTAGAC GTTCTGGGCG GCAAGCGGCG TACACTGAG      480
GAGCCAGCGA GTATAACCTT GCGCGAGAGT CTGGGTAATC TTGTGAACTC GTCCCGTCT      540
GGGATAGAG CATTGCAATT ATGCTCTTC CAGGAAGAAT CCTAATAGC GCAGTCATCA      600
55 CTTGGGTGA TACTTCCCTT GCGCTGTAC      630

```

## (2) INFORMATION FOR SEQ ID NO:302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1248UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GATCGCTAGA TGCCCAGGAT GAGACTGTC AGGTTAGGCA GGTTGTGTAT GCGCCGCCAG 60  
 AGGGAAACCC AATGACTTTG CATAGAACAA ACCCGCCATC ACCCATGTCT TCGCTGTAT 120  
 AGAGACTAAG GTATCTGACG ATCCCTTAGC GACTCTCTCC ACCGCTCGAC GAGGCCATTG 180  
 AGCTCTTAGC AACTGCACAA ACCTACTCGA ACTCTGTTTC CAGACTTCTT TCTGTTTGTG 240  
 TTCAACTGCT TTGCGATGAA GTACCCCCCA GGCTATTTT CTTACCCGCC TGGTGTGTGT 300  
 CTATATACCC GGTGTATTT TTGATAAAAA ACTCAGCTCT TCCTCTACGG CAGAAATATA 360  
 TATCCAGTCC TTAGCGCCAT GCGAAAATCT GCCTTTTAC CGCTGTTTCT CCCAGTCTTA 420  
 GCACTGGCAG AAAAAAGATG TATGGGTAT AGGCGCTGGC CCGCGGAAA AAAAAAAAAA 480  
 ATAGAAAAAT AGAAAAATAA AAAGACGTGG GCGGCCCCGC GGGCAGACGA AGAAAAATA 540  
 GCGGCCACC CCTCCCAAGC AGACGAACAG GCGAGACATA ATAAATCCCA CACCAGGGAA 600  
 GAAAGTCTTG TGCAAGCTCC CGGCTCATAC GCTGCCATCT GTTCATCCG GNTTGCAACC 660  
 AGTATGGATG TTCAAGCATG TCCGANGCTC CGCTGCCCTG 700

## (2) INFORMATION FOR SEQ ID NO:303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1249RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GATCATGCAA CATTCTTCT TTTCCCGCTT TCTGCCTGTG CCGGACGGTG TGTCCCGCC 60  
 CCGCACCTCT GAGGAAGAGC TTGCGGACTG CAGCGAGCAT GCGACAGTA CCTGGGGCGA 120  
 CTGCTGGGC ATTCCGATAC CCAGCGGGT GGCGGCTCC GAGGCCACTC GCAAGCATTC 180



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TAAACCACTT CCATTGATT GAATCAAATT ATATATACCA TTAAGTAGAG CTACCATGCG 240  
AACCTTAGCT GGGACGCAGT AAAGATTGGC GGTTCOCAGA TCAGCTTCTC GGGGTGATC 300  
5 GATGGCCTTT TCTTCGCTAT CAGCTTCTCG TACCTTAGCA GCACGTCTC GTTCAGGTAC 360  
AAGATGTGCT GGCCCTTGTA ATATCGCAGT ATGTTAAGAG CCTTGGCTGT GTGCAGTATG 420  
TCTGTAGTCG TGAGCGATGT CATGCTACTG ATTTTCATCGA TGTGATCTC GGTGCGGTTT 480  
10 TCGACTAGCA GCTTGATCAG GGTATCGGAC CAATAGGCTC TGTAGAGAGC AGCCCAAGAT 540  
CAGAGAGCGG CTCTCCGGC ACCCAACTTG TTCTCCTTCT TAGAGAGCTC CATACGAAAC 600  
TCAATCAGCA GCGTGCCGTA CCCCATCCGC TGGTACTGAG GGAGCGTCCA GAATACACGC 660  
15 CACATTGTAC CGTCCGCCA NTCCTTTCCN TTGGANAATN CCCACCAAGT NGGTGCCCCA 720  
CTCACTCCCC TGTGTTCTTG CANTAAAAA AAGGTCAANT TCCTATNACT CNTGTGNTCC 780  
AAAAAACTTT GANAAAGNIN GTTGGNACC ACTTCCTNNT NCCCCGTCAA TTCAAAT 837

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1249UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAOCTGCCGA TGGACNGCOG TTGGCAGGTG ACTGCCCTAC GGTCTTTAGT CCGCGCAAAG 60  
CGGATGGCOCT TTGTGGGCAC ACGCAAGAAC TTGGCAATGA TGTTGACCAC GTCCATGGTG 120  
TOCTTATCTT CCTTGATCAT TGTGAAGTGC ACGCAGTTCT TGGAGGGGCC GTACCCCCAG 180  
40 TTAATGACAC CGTCTCTGTC TCTGTCTGTC TCACATAGT CCTCTTTGCT GACTCTGGTT 240  
TTACGGTGTG CCAGGGCAAT CTGGAATGTG TTGGACGCGG AAGTGACCGA TTCAAGCTCA 300  
TTGTTGAACG CCTTTCGTAG CAGCTGGTGG ATCTTCGTCC GTGCAGCTTT GTCGTCAAAG 360  
45 CTCTGGTGG TTTCATTTT CGTGACGTTT CTGTACACGG CCTCAATCTG CTGCATGTCC 420  
TOCTGCCCCA GTAGCTCTAC CAGCTGGTTC CGCAGCTCTG CCTCCACCGC GTGGTTGTGG 480  
CGCGGTTGCG GCTCTTCAGC CTGCTGTGCC TTCACTGGT CGGCAGAGGT TTGGGTTTAG 540  
50 CAGGCATTTT GAACCCATTG TCCCGCAAGT ACACCACTGT TCATCTCTTC TGGATCTCAT 600  
TGACCATGAA GTCCGAATAG CGCTGCTTGA TCTGCCCGCT AAACCCCTGT ACTCTGCTGA 660  
GAGGTACTCT GTGATCCAAC GTGATTCTT TGAGTCCATC GGTCTCCGNT TTGGCCCCCT 720  
55 NCCNCAAAG TTCTGGCTG CTCNNANCC GCTCTNTAAT CCCCCGAAAN TCTGTACNNT 780

TCNCNATTTTC CNNNINNNCC TACCTNAACC CTTGTINAAC CTTCCACCCN ANAANTCATA 840  
AATATTCCCC NOC 853

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1250RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

ATCTTAATTT AAAATTTTAA TTAATTTT ATAATTTAGA AATATATAAT CTAGAGATAT 60  
ATAATCTTAA AATCATAGGT AAAAATACAT AAGATAGTAA GAATAAAATT AGTAAAATAA 120  
ATAGAAAACC ATAAGTTAAT TGATTCATAA AGAAAAATGG AATTATTTGT GGCATCTTAA 180  
TTTTTATTAT TTAATTGATT ATTATCTATT TAACATAAAA CATTTTAAAA TGTATATAAA 240  
TAAATAAGAA ATTACTTATA GAATATTTAT TAAATAGTAT TTAATTTAAT TTTAATATTA 300  
AATATACCAT TTTTATTAAT AAATAGATTA TTAAGTTTAT TAATATTAAG TGATATATAA 360  
TTTAATTTAT ATAAATTATT TAATTTACTT CATTCATATA TATAATTATT AAATGTACCT 420  
TTCATAATAT TTATTTTTAT TAGTCTAGTA ATATTTCTAT TTAATAGTCT ACCCTTTAAT 480  
TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT 540  
AATAATTTAT TATCTAAAGT ATATAAATTA ATTAAATCCT TTTTATTAT TATTAAATTA 600  
TTATTAAATTA GTAAATTATA TTTATTATTT TATTAAATA ATTTTTTGAT AATAATATAT 660  
CCATATTAAA TGGTAATTTA TTAATAATAT CCTTTAATGA TTINATGATA ACCNATTTAT 720  
TATGANATTA GTTAATAGTG ACCTTAATAT CCNATCCNA ATATATNTAT TTATTNTAA 780  
NAACANANAA CTTCTTATNN CATATTTANT TINANTATTN ACCNNTCCN NNNT 834

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1250UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

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	GATCAAAATT TCAACAATTT CCATTTTCATT TAGTACTACC ATCAACATGA CCAATTGTTA	60
	CATCATTTAG TTTATTAGGT TTAATAATTAA CTTTAGCTTT TACTATACAT GGTATTATTG	120
5	GTAATATTTA TCCTTTATTA TTATCTTTAT TAGTAGTTTT ATTACTAATA ACTTTATGAT	180
	TTAGAGATAT TGTAGCTGAA CTACTTTATT TAGGTGATCA TACTTTAGCT GTAAGAAAAG	240
	GTATTAACTT AGGTTTCTTA TTATTTGTTG TATCTGAAGT ATTAATTTTT GCTTCTTTAT	300
10	TTTGAGCTTA CTTCCATTC A GCTATAAGTC CTGATATTCT ATTAGGTAAT GTTTGACCAC	360
	CAGTAGGTAT TGAAGCAGTT CAACCAACAG AATTACCATT ATTAAATACT ATTATTTTAT	420
	TAGCATCAGG TCTAACTATT ACATATAGTC ATCATGGTTT AATTGAAGGT AATAGAAAAC	480
15	ATGCTTTATC AGGTTTACTT ATTACTTTCT GATTAATTGT TACATTTGTA TTATGTCAAT	540
	ATATTGAATA TAGTAATACA TCATTTACAA TTACAGATGG TATTTATGGG TCCAGTATTT	600
	TTGCTGGTAC TGGTTACATT CTTACNTATG GTTAGTTTAC TAATTAGGTA GGINCTATTA	660
20	NGAANAACAA GAAATTNCT TTAACNCCN CCCCCTCGTT NGANATNNAA CCNCACCTAT	720
	TATTACNNT TTINAAAATA NTGAANACCC CANNATGTT NTAANGAAAG GNNTAACGTN	780
	NACNCACCN TAGNNTTNG GTCCCCCCCC NTGCTACCC ATTTTGNCCC CCCCCACAN	840
25	AACCCCC	847

(2) INFORMATION FOR SEQ ID NO:307:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 825 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

35	(ii) MOLECULE TYPE: DNA (genomic)
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	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1251RP

40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:
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	GATCAGGAGG GTTTTGCGGT GCTGCGGAC GGCGGGTTAG AGGTAATGCT CCTGCGAGAG	60
	GATGACAAGA CTGTCGCTGT GTACCGGGAA GTGCAGAAAT AGTGTATACT ACATAGTCAT	120
45	AGTTATAATA AACAAAGCCG GCGGGCTCT AACGAAATGG GGAGTTGCCC ATGCCACCGG	180
	GGCCGCCGGG GCGCGCGGG CCGCCAAAGG GCGGTTTCCA GCGCGCACCG GGGAGGAAAC	240
	CGGCGGGCT GCGCGGTTC GCGGGTCCG CCGGGTCGAA CTGGCCGCGG TAGGGCAGCG	300
50	GGCGCGTGG CCGTTGTAGC CCGGATCGA ATATCATGCC GCCCTGCGGG TTGGGCGCGG	360
	GAAAGGGGTC AAACGGGTTT GCGCGCTCT GCGCGCTGG ATACAGGTGG CTGTGCGCGT	420
	AGCCTGCAGG GCTGCCAGG AGCGGCTGG CCGCGCCGGC CCGGGGGAG AGAACCTCGT	480
55	ACTCGTCCTC GAAGCCAGG ATGTCTGCTG GCAGCTGGG TGCAGGAACC TGCGCGCGGA	540

TTGGCGGAGG CGCGCCTCCG CTGAGGGCGT CMTAATCACC GGGCTGTGCT TTTGCGCNGG 600  
 GCTTCTCMTG CGCCACCAG GGAATTTC CTGNAAACT TNCOGAATC CNCCCCCTTA 660  
 5 AACTGGCCN CNCCCTTTIN CCTNNNGCT NTCTCTCTGC NNCCCNMTT CCCCCCAAN 720  
 ACCCNOCTAC CCNNTCTINT NGNTTCNNC OCTACANCT TTCNNCTNC TCCCCCNCC 780  
 ATNTCTCTNT TMTATCNAA AATTTCTIN CTTTTTACCC CCCCC 825

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 856 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1251UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

25 GACTGTTCG TGTGAGGAA GATAATCAAT ACCGGAATCC TCTGAGCTTT GCTTCGGCCT 60  
 CCATTGCGCT ATTACGAAAT TCGGTGCTG CTCTAACGA TGTGTACCG TTTATACAAC 120  
 CGCTGTGTGA TCGCTTTTGA GCAGAAGCCG GTTTTGCAC CGACAGAGAT GACAACCTTT 180  
 30 GCTACTCTC CGATCCAGTA TTGTTCAGTG CTGTAGTCAT CTTGCGATCG TTGGTAAACA 240  
 CATATACCCC ATGCGAGTTC GAGAAGATCG ATACCAAGTT GCTTTCGCTC TCATTTCAAC 300  
 CATTAATTTC GCGCTTTTGA TTGTAAAGGT GCAGCACCAC AGAAATACTT GATAAAATCT 360  
 35 TAGGCAATGG CCATATTGGG AAGTTTATAT TACTAGCAGC ATGGTTGCTC ATCCCGGCGT 420  
 TGTGCTGTTC GTTCAGGGG GCGCTGTAC TACCTTTAGT CCGTGTGTAC TCACAGCTTG 480  
 TTACCGGGCC GGGCTTCTAT GCAACTATTA TATTTGCTTC TAATATATAA GTACTGACAT 540  
 40 TTTCATACGC GCCTAGCTAC CGCTGCTTTC TCTTGGTGA CTCTCTCAG AACAGCTTCT 600  
 TGGAATTATC TTGTACTATC AACCATGGAG AACTGTTCAC GCCACACCC GACCAAAGG 660  
 AGAACOGAAG GACAATTTTG ANCTCCCTT TCCCCGAAT TANGENTINT GAANATATNA 720  
 45 ACCGGGACCG GGTTCCTTNN TCCCCGGGT ANTTNCCNT TAAATTCGTN TAAANTTANN 780  
 AANGGTINTAT GGGNGAANG AACCCANCT GACCCNAAAN GTINGNIGGG GTTTAACCTN 840  
 CTNNVINGCC GTNCCG 856

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 834 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 55 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1252RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

10  GATCTOCTAT TAGTGGGTAG CTAGCTAGTC GGCCCGGCTG GCGGGGCGCG AACTGGTACC      60
    GGGTGGGAGG CCGAGTGACT AACACTCCGG GTTCTTCTGT CTCCTGCCAT GCGAACATA      120
    ACCATGGCGA CTTATATAAG TTCCGGCGGC GTGCAGTCGT ATGAGCCCGT ACGAGCAAGA      180
15  CGTCCAGCAG TTTCAGCGC GGTAGTCGGG GCGTGCAGT TGTGTATATA TTGCCACCOCT      240
    TCGGAAGTTG GACAGCCGTA TGCTGGAGGC GGTCACTAGT AAGCAGGAGC CCGTGACTCA      300
    AAGTAGAAGT CGGATTGTAA AGGACAACAG ACCAGTGGCG GTACGGACAG CAGCGGGCCA      360
20  ACGTAGTAAT AAAATATGAC GAGAGATATA CAGAACCACC TACTCTTGA GACGGCCACG      420
    GAGGTAGCGA ACAAGGTCCG GGCATCTAC TGGTGCTGA AGTCGAAGGC ACCGGTGACC      480
    TGGCTCAGT ACAAGGACCA CTACCACTGT ATTGGGCCCC TGAATCCAGA CTCGGTGACG      540
25  ATAGAAGTGG AGGCGCTGGA CTGGGAGGAT GACAGCGTGT TGGACCCGGG AGATTGCTGC      600
    CCGGTAAAC GTCCCTGCA GCACATGCGG AACCCCGCGT TGAATCCGT ATATGCCGGT      660
    GGTGTGTGAA GGTNCCCCCG GTTATCTTGT TCAACCTGTT CCGGTACCC CTTCTCCAC      720
30  AATTGAAGCC ACCTGTTGAA CACTGCGGAT CCCCCCCCC CAAANAACCA NAAACAAAC      780
    CCATCGTGA GGTNCCCCNG NCTGTCCCG AAATTAANGC CGANCCNCC TCAN      834

```

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1252UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

    GATCTTTATC GCAACNTTTT GGTCTGTITT CGAGTTACGG GCGTGGGGA CCACACCGAA      60
50  AGCGCCAGCT CCGAGTGTTT TGCCGAATAT GTAGTCGGCT TTGTTACAT ACGAGGCTGG      120
    TTGACCTGTC ACCTTGTTGA AGAACTTCGT CAACATGTTG GCGTGAGACG GAGGACGATC      180
    CTGGGCGTTC GATGCGTCTT CGTCGTGCTC CCCTACACCC TTACCGAGTT TTCGGTGGG      240
55  ACTAGTGAAC ACTGCCATAG CCTCGCAGTT AAAGTGATGT GGCAATATTA TATTGTAGTT      300

```

EP 0 866 129 A2

TTGTCTTTT CTGATTGTT TTAGGCTGCC GATAGCCAC GAGGTGAAGT TTTGTACACT 360  
 TCACACATCC CAGCACTGCC ATCAGACAG ATGTTGAAGA TCAAATTTG CAGCTACATG 420  
 5 CTGCATTGTG GTGCTTGGGT TAGCAGTAGC GGCTAAGTTG CAACTACATT GTCCCCATTC 480  
 ACTCAGAAGT ACCTCGGTTA AGCTCACTAT GCGCTTATTG CCGAGCGAAG CCGAGCATTG 540  
 TTACAGCAAT GATGAGAAGA GGCTATTGGT ATGTTAACAT AACGCCAGTA GTGTTATATT 600  
 10 TACCACTAAC CATAGAAAAA GTACAGAATA TCGTAGOCT ACGAACTGAA TGAATATNTT 660  
 GCTTCCCCNC CCCGNCNTA TACCAATGAA TAATAAATTG GATTGTCTAA TATCTNCCCC 720  
 ATATCCNGCC GGGCCCCGA NNCCCTNCAA CTATTGGTN CACNCCCN TGCCNCCN 780  
 15 TTTTNTTTIN TCNNGGAACC CCCCCCGT CATCTCGNN TGNVINAANA TGANTACCT 840  
 CCTTGNTCC CCNCCCT 858

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 841 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1253UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

GATCCTAACC AAGCTGATTG ACTCCAACIT TOCACTTGGC ACATTGACA AGCTGTTGCA 60  
 35 GAGCTGACG GCGTGGGG GTGGTGGCTC CATATTGGGA TCAGATGGTG GGTGTACAGA 120  
 CACGGAGGCA TTGGGACATG ACCGAAAAG CAAGAAGTTG GAGCCCCGCT TCCCGGGGCC 180  
 TCCCGGAGC GTGGCACTG GCGCGGCCA TCGCGATAT AATCTGAAT TGGGCTCAA 240  
 40 CTAATTGGC GAGAGCAAC GCGAGCCAG CGTGATGCTC CCGAGGTGC AGCAGCGCTG 300  
 GAACACAGCT CCTGACAAAC AACCCAGACA ACAGCATAGA CAACATGGGC AGGCCGAGGA 360  
 AACGGGTCA CCACCAATGG CTCTTGGTA TCCCTCTCA ATGTTAATGA ACAGCAATTA 420  
 45 TACATTCCCT GCGGCCCCC AGCAGCGCT CCGCCGCAT CCACAATGC GTGCTCGAC 480  
 GCAGCAATCT GATGTCCAG CTACCTCCC CGGAATATG GGTAGCACC ATGTCCCAA 540  
 CTTCCACAG CCCCCACGC TGACTAGTCT TTTGTCTAAA CATCAGCTC ATCACTGCA 600  
 50 GCTAATGAG CTGCTACCT CCCATGCATA TGTACAACAG ATTTGCTAC TCCAATAGCC 660  
 CAGTTCTGAA GTCTGTTC TTACGTTGG CCTCTCCCC TTGGCAATN TATCTTGTN 720  
 NNAAAACCN AACCCNGTT CCGTGTGCC NGAAATTTCTA CTTTACCGT CCGTTATTC 780  
 55 NTAAATCATA ACCCGGTCA ANAACCTTT CTTGACNAT ATCNCAATTG GCNANCCNT 840

C

841

## (2) INFORMATION FOR SEQ ID NO:312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1253UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

GATCGAAGAG TTGATGTTG AGAAGTCAA GAAGCTGTTT GCGAAGTCCA TTGCAAGGA      60
TGTGGATGTTG CCGAGGTTG TOGCGGAGTA CCGACTGATA GTGCGGTGTG AGGAGCGGG      120
TGGGGTGGG CCGCGGGGG CCGGTGAGC GCGGAGGGG GAAACGGAAC CGTTTTCGCA      180
GGAAGAGAGC AAAGAGATTA GGATCATTCT GCTCCAAAG CCAATTGCGA TTGAGTTTGT      240
AAAGAATGTTG TGGGAGAACT GCTGTGTGCT GTACCGTTTC TATCAAGGC CCGACTTTCAT      300
CAGGAAGCTG GACGACCTGT ATGAGACAGA CCGCGTGAG TACAAGCAGC AGCAGCTACG      360
CTTCTTGGCG TTGTGCTACG CTGTCAATGC AGTGGGTGGC CTGTCTCTTA GCTCATGCT      420
CCCTGGTGGG GGAAGCGAAG ATGCGGGCTC TCGAGCAGA ATAACAGCGG CTACATTGGC      480
GGATACGGAC ACACGGCAGC CTTATCTGCA CGACGAGGC TACCGGTACT ATGTGGCTGC      540
GAAAAAGCTA GTGATCTAC GAACGCGGT GACACGAGG CGAATCAAAC CTTGTTCGG      600
TTGTGTGTTT CCAAGTTCC GCGCGGTGNC CCGGCATCC GTTTTCTGTC CCGCTATNA      660
ATTCCNCCN CTTNAGANT CCACCCACC CCCCCGANA ANTAAAAAA TTTCCCCCCC      720
CAACCGGAAN TCCNCCCG NTTACCCC CTANAAANG AGGTTTTTTA AACAAACGG      780
GGNGCCCCNC NCCCCGNN CNNACATCC CCCCCTAAA TCGGAANATT NNCCGAAACC      840
GC                                                                 842

```

## (2) INFORMATION FOR SEQ ID NO:313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1254RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GATCGGCCAC ATTGTCCCTG AGGCTTATGA AGGGGGCCCA ATTGGGCTGG TGCAAGACGG 60  
 TGACGACATT GTCATCGACG CCGAGAACAA TGCCATCAAC CTCCTTGTGC CAAAAGAAGA 120  
 5 AATTGAGTGG CGCGCGGCTC GCTGGACCCA GCGGGCTCCA CGCTACAAGA GGGGCAAGCT 180  
 CGCCACCTAT TCTAAGTTAG TCTCCAACGC CTCCAAGGGT TGTGTCTTGG ACAGCGACGA 240  
 CTAGCACCTC GACGCAAGTC ACTATTATT AACAAGATTA TGTATATAAG CACCCCGCCA 300  
 10 TGTCATTGA ATGGACGGCA TATGTAACAA AAATCGAGGA TGCTTCCCTA TCGTCTACAA 360  
 ATCTCAGGAT GTTGAGTACC TTTTCAGTGT CTGACTGAAA TAAATGTTGA ACTTTGATAG 420  
 TACTTTTATG TTTGAAAAAT TTTAAAAATT TATTGTATGG CTGTCAACAC GAGTACTCAT 480  
 15 CTTCAACCGA CATTACGGGT ACGTGAAGAG CTTATCTATC GATAACATGG CGACTCAGGA 540  
 GCGGTATTTT ATCGGGCGCA ATAGGCAGAC GAAGGTTGGG GACTTCTATT TGCCGACCAA 600  
 GACTGTCCAT TCGACTGGAA AGTGCATCCT CTATGGAATC CGTTGGACGA ACNCATGCG 660  
 20 GNGTTTNGC CATTGAAGGC CACAACCGA GNTACTCGG AATTATATGG GCNAAAAACT 720  
 TTTGGTCACN CTGNCGAAG CACAATNCTT CGCAAGNAA NAAAAANGGA ATTGNCNAT 780  
 TTGGAGCCCN AAACCTNTAC NTGNCNTGGN GNGGGTANC TCNNNTCCN ANGTEN 836

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1254UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GATCTCTGGT ACCCCAGCAG CCTGGCGGG GACGTGGCAT TGGTGAATC TCCCCAGGT 60  
 AACCGGGTGT GCTCTCAGC CCTTCCCAC ATTGAAGTTA AGCTTGTTAG CGGTACTCCG 120  
 CTTCAATTTT TGTGCCCCGT CGACCGGTAG CGTCATAGTC CCGCGGTGTG GCGACCGGG 180  
 45 GCGCGCCATC ACAGGTATCT ACAGTTCAAC GCGCGGCTGG CGATCCCAAG CGCAGTCTGG 240  
 AATCTCGAAC GGTGCTACAA AGAACGGATG CGTGGCAGAT CGAAGCTATC GAGAAGGTGG 300  
 TGGGGGAATT GAGTGAAAGT ACACGAAGGC AGGGTGTGAG ATCTCGTACC TCTCGCATA 360  
 50 AGTACGAGAA GGAGTGGCG ACGGTGTTC GAAATCAGCG CAGTGTCCAG TGCGGGGAAG 420  
 CGTGCAAACG GAACCTGGAA ACAATCGAC GGACCTACTG CCAGGTCCAA GCCCTTTCCA 480  
 CGGTGTCACA GCTAAGATGG TGAATGCCA ATAATTGTG ATGCTGGTAT TCGTGTGTGG 540  
 55 ACGATTATCT ATTCGGTTCA GCGTTTCATA TTAGGTGG CTGCAACGT GGTGACATCA 600



CGATTGCACT GTATATATGA TGGAGTAATT CGCATACACT GAAAATCNTA ATAATCAATA 660  
 ACCCATGCCN CNACTCGNCA ACTTCNCNC TTCTGCTCCN GGTGAAATCC CCTTCACTAN 720  
 5 TTTTTTTCAT TGOCCATTNN ACCGAACTTT ACNAATNATG CAATGANAAC CCCCCCTCCC 780  
 AAACCTANAT CCTTTTINTIN NGGGTCCCN ACNGTTCNCN TTCNGNCNA NCCCNCTTIN 840  
 ATTCCAANAC 850

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1255RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

25 GATCGTGTG TCAGGGTGCA TTGCACTGGG CCTGAAGACG GTGGGGACTG ATCGGGGGCC 60  
 GAAGAAGCTG TCGCAGCTAC AGCGGATTGC GCGTGTGGGT CAGGGCCGGC TTATTGCGCG 120  
 GTGGGACTCC CTCTTCAGAC CGTTCAACGA GAAGATTGCG CAGATTTTGT TGACACGGAA 180  
 30 CGACATAGTT GACTGTGTCG AGTATAAGAA CGCGCAGAAT ACGTCCACG AACTGCTGGC 240  
 GATGGGGGTG ACGCCGATTG TGAACGAGAA CGACACGCTC TCAATCAGCG GAGTGAAGTT 300  
 TGGGGACAAC GACACGCTGA GTGCGATCAC AGGGGGCTG ATCGGGCGAG ACTAAGTGT 360  
 35 CCTGATGACG GACGTGGACT GCGTATACAC CGACAACCG CGGAAGAAC CGGATGCAAA 420  
 GCGATCTTG GTGGTGCCGG ATCTGTACA GGGACTGCC GCGGTGAACA CCTCTAGTGG 480  
 GTCGGTTCA GGTGTGGGCA CCGGGGGCAT GCGCAGAG ATCCTTGCTG CAGACCTGGC 540  
 40 AACGAACGCC GGGTGCTAC GATTATTATG AAGAGTGAGC GCGCGTCGAC ATGGTGCGGA 600  
 TCGTGGAGTT CATGGAATGG CGCAGCAGTG CACTGCAGTT TCTGCTGACG CGAGACTTGC 660  
 AGACGGACGA GCTGAATTTG TTGCAGAGCA CGGGTCCCA CTACACAGC NCTTCTGCA 720  
 45 ACTTTGCACC TCCTGAACNA CNGATTCTG ATCCNCGTC TGTGACNCG NCGTATCTAA 780  
 CAGGGGCTNA GCGCCCCCA AACAACTGNT CCCACGTINT CCGTCAG 827

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: 1256RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

	GATCTAATGG CATTCTCCCT ACCAAATGGG CCCAATTGTA TATTGCCGAT CTTCCTACAG	60
10	GGNACTGGTT TACGGATCCA GCGAAGATCG GGAGAGTTCA GCTCTTGGTA TTGCCGACAT	120
	TGTGTGAGAA ACACCAGCTG CAAACTTGAG GCCATATGTC ACTGTCATCA CAGGTCCACT	180
	TATCGTGTGT GTTGGCGAAA GGTCTAGCAG TGATATTAG GCTGCTATCC TATATGCOCT	240
15	AAATGTTCTC TTTTCGAAGG TTCCACAATT CCTGCGGCGA TTCATACCTC AACTACAGAG	300
	AACATTTGTT AAATCTCTTT CGACTCAAC CAATGAGACC TTAAGATTGC GGGCGGCGAA	360
	GGCACTAGGT ACTTTGATAC AATATCAACC AAGAAATGAC CCTCTGGTGG TCGAGCTAGT	420
20	AACAGGCGCT CAGCAGGCGA CTGAAAGGGG AGTAAGGACG GCTATCTTGA AGGCATTGTT	480
	GGAGTTGTC TCCAAAGCTG GCAGCAAGAT AAGCGAAGCT TCCAAAGCTA ACATCATTAG	540
	ACTTGTGGAG CAAGAGATGG CATCCACAGA CAGCAAGTTT GCAGTCGCTT ACGCCAAGCT	600
25	TCTAGGTGCA CTTTCTGAAA TCATGTCTCC GGAGGAGGCG CAGACCATAC TTCACGAAAA	660
	GTGCTTGATC CAATTTTGAA GAGCAGCTGT AAATTGCCGT CAGACCCAC TCTATCTTNC	720
	TACCCCTGTA CTTTCTCCCG CCAATACCCN ATTTTGAATN TTTTGGTGC ACGGATCNCN	780
30	ATCCTTCCNN CACAGGTTTN CCCNNGNAT TCCCCCNAA NGAAAGTNAN CCCCCC	836

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 841 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1256UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

45	GATCAACTGG TCGGGCGGGC TGCACCAAGC CAAGAAGAGC AATCCTTCGG GGTTCGTGTA	60
	CGTGAACGAC ATTGTTCTGG CGATTCTGAA TCTGCTGCGC TACCACCCAC GCGTTCGTGA	120
50	CATTGACATT GATCTGCAAC ACGGAGACGG TGTCGAAGAA GCATTCTACA CTACTGACCG	180
	CGTGTTCACG GTCTCGTTC ACAAGTACAA TGGTGAGTTT TTTCCGGGAA CGGGGGATT	240
	GGATGAGATC GGATGCTCCG GCGGCAAGCA CTTTTCGCTG AATGTGCCG TCAATGACGG	300
55	CATCGATGAT GATTGCTACA TCAACTTATT TAAGAGCATC ATAGACCCGC TAGTTACATC	360

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ATACAAGCCA ACAGTAATTA TTCAGCAATG TGGAGCAGAC TCTTTGGGGC ATGACAGACT 420  
GGGGTGTTC AATCTAAATA TCAGAGCCCA CGGCGAGTGC GTCAATTTGT GAAGTCGTTT 480  
5 GGGATACCTA TGCTATGTGT CGGTGGTGGA GGTACACCC CCAGGAATGT GTGCGGGCTA 540  
TGAAGTACG AGACAGGCAT CCTTAATGAT GTGCTCTTAC CTTACAGATAT CCCAGAAGAT 600  
ATTCCGTTCC GCGAATGGTT CGGTCCAGAC TATCTCTGCA CCGGTCTCTT GGATGANTTN 660  
10 TCCAAAATAA ACNCCCAAT TACTGGANAA NATACGTCG GNTTTAAAN NTAAATTNIG 720  
CNGGGGCCAT TTTGNCNIGA NNCGAATATC CTCAGATTT CGTTTAAACN AAAAAAAT 780  
GATCGGAANA ACCAAAANAT NCCTTGNTAA CANTNAAGAA NTTTGCCGNN ACTTNTTANT 840  
15 C 841

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 841 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1257RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

30 GATCACTGGT GTCACCAAGG GCTACAAGTA CAAGATGAGA TATGTGTACG CGCATTTTCC 60  
CATCAACGTC AACGTTGTGC AGAAGGACGG CGAGAAGTTC ATTGAGATCA GAAACTACTT 120  
GGGTGACAAG AGAGTTAGAG CTGTGCTGT CAGAGAGGGC GTCAGCGTCG AGTTCTCCAC 180  
35 CAACGAGAAG GACGAGATTG TTTTGTCCGG TACCTCCATC GAAAACGTTT CTCAGAACGC 240  
TGCTGACATC CAGCAATCT GCCGTGCCAG AAACAAGGAT ATCAGAAAGT TCTTGGACGG 300  
TATCTACGTT TCTGAGAAGG GTGTCAATGC CGAGGAAGCC TAAGTCCCTT ACTGACCGTA 360  
40 TCTTGATAAA TAATATGAGT ATTATGTAAT CAAAGAACTC ACTGCTTTTT ATTGGTGGTG 420  
TTTTGTCAA ACGCTCTTAT TAGCGCCGGG GTTAGAGTGT GGAATACTG GCGTTATATG 480  
CTTTAGAAGT TATGTTAAGT AAATTTAATG TCCTATCAGG GCCACAGCCT TAGCAACTAG 540  
45 GTGCAGGTAC TCCTTTAGCT TGCCACTGTT CTGGAACAGA AGATATATTT TATCTGTCTC 600  
GTTGSCACCA TCGTAGACAG GTTCACCGCT TCCTTGACAG AACGATGGAA CGCCAGCTTT 660  
CCGGGTGGA AGTTATAGGA ATTATGGATT OCAATGACAG TTGGTGTGTT AACNANCTG 720  
50 ATTTGTCCAN TTTCCCGTCT CNGAAGCTNC ANTGNITCCN TGACCNANCA AACCCGGAN 780  
ACCCCTAGGG CTGNAGGCT TGAATGCNTT AAAANANITT CNITGANAAA NCATTGNTAA 840  
55 T 841

## (2) INFORMATION FOR SEQ ID NO:319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1257UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GATCGGGCCG CTCACACACT CAGGTACCTC AAAGGAATAC GAGTTTGTGG CAAGCTTCCC 60  
 GTGTCCAGAT GCACAGAAAA TCGATATGTA CATCAAGGAG CCGCAAAACA AGTACCTCTT 120  
 TTGGGGAACA GAGTACACTT TCCAAATCAT CTGCAGCCCT GCAGACGGCC TCACTCAOGA 180  
 TCCATACGAC GCGCAAGCCG CTGCGCCAAA TGTGATAGTC GTCCAGTCCC CATCCGGCAA 240  
 GATCTACCGT CTGAAAAAGG CCGAATCCGA TGTGGAATTT GGGTATGCG AAGCTAGGCT 300  
 AAAAGTGCAC GAGCCAGGCG TCTGGCTGGC CCTAATTACC TCTGAGGCAG GTGCTGGTTG 360  
 GTGCACTTTC GCGAAGTGA TCTGTGTTTA ACACCTAGAT GCTACACAGT CATCCACCCC 420  
 ACGAAATTAA TAGATAGTAC GGGTACATAC AAGCCCTATA GTTCTTTAAT ACACTTGCCC 480  
 TATATTGAAT ATGTCTACGA AGTATATGGG CGAGGCACTT TCAAAATCGG TGAAAAAANA 540  
 TGCACCACTT CGAAATCCAT GTTTTATGAG CTTAACAAC AGTGGTTGTT GAAGAACAAT 600  
 ACCCTGCCAA GGAATGTCA GGTACTCGAA CCAGCTCTCA ACAGATTCTT AAAGATTGCC 660  
 AGTGTGTGTA CCGAATCCAC GTTGGCTGAA TGCTGGGACC GACATCAGAC CTTGCGATTG 720  
 GTACAAAATC AGTCTATAAG GAGAGCGCCT GTNTGCCNA AAAANAAANA CCACGGAAGG 780  
 ACNCATTGTC ACTTGAACNG AGNCAATGTG TNCNGTACG CGGVNTTTC GNTTCAAGCC 840  
 CCAAGGACAA NAAAGC 856

## (2) INFORMATION FOR SEQ ID NO:320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1258RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GATCCAACT TCTACTAGG TATTTTTC TACCTCAGC TGCAATTCCA TGCCATCGCT 60

# EP 0 866 129 A2

AACCAAGATA ATATTCCTCT CCAGTAGATC CATATTCCTCT CCGACTTCG CACTAATCGG 120  
 GATGACTGGC ACGTTTCAC CCAGATCTTC AGCATGTATT TCATGCTGTA GCAAATCATT 180  
 5 CATTATTTTG TTGATCACAG TTTCCTTTTC TTTTGCCGAC CGGAGTTTGT CCACCTTGGT 240  
 TATGGCGACA ATCAGCTCAT TCCCTGATTT TTTGACATGC TTAATCGCTT CAATGGTCTG 300  
 GGGTTTAATT GAGTCTTCGG CAGATACTAC CAAGACAAAG ATATCGGTAA TATTGCGGCC 360  
 10 CCGTTCCCTC ATCTTCAAAA ATGCTTCGTG CCCGGCGGTA TCCAAAAAG TGATCTTCGG 420  
 CTTCGAAACA GGTGTGACAA CCTGGAAAGC ACCAATGTGT TGTGTAATGC CACCAAACTC 480  
 CTGCGAAAGC ATGCTCGACT TCCGAGATA GTCCAATATG GTGGTTTTGC CGTGATCAAC 540  
 15 GTGACCCATA ATGCTCACAA CAGGTGGGCG GTCCCTCAGG GCGTTGGGT CTGCAGGCTG 600  
 CTTCAATTCA TGTAAACGT TCTCCGAGT GACAATTCCC TGCCGAGGG CAGTTGGTAG 660  
 CTATCTCCTC CCAATATAGC TCGATGTAGT CTCCTGGAAA TATGTAGTCC GCGTGGCTTT 720  
 20 TCAA 724

## (2) INFORMATION FOR SEQ ID NO:321:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 853 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1258UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GATCCTGTTT ACAACTAAGT TCGCATCCCT ACCAGGGGAA AATATGAAAT ACCAAGTGTT 60  
 GTATTCCGAA CGCTAGAATT CTTGTACAAA AACCGCGGCA TTCAGGAAGA AGGTATATTT 120  
 40 AGGTTAAGCG GATCCAGTTC TCTCATAAAA TCTTTGCAGG AGCAATTIGA CAAAGAATAT 180  
 GACGTGGATT TGTGCAATTA CAACGATAAA GTTCTGTGTA CACCAGGAAA CGAAAATCAG 240  
 GCGGGTCTCT ACGTCGATGT GAATACCGTT TCAGGTTTAT TAAACTATA CCTAAGAAAG 300  
 45 CTTCCTCATA TGATCTTTGG GGATGCTGCA TATATGGATT TTAAGAGAAT CGTGGAAAGA 360  
 AACGGAGATG ATAGCAAAC AATAGCACTC GAGTTCAGGG CATTGGTTAA TTCCGGAAGA 420  
 ATTGCCAAAG AATAATGTGC CTTAATGTAT GCATTGTTTC AGTTATTGGT GAAGATCACC 480  
 50 GAGAACAGCA AATATAACAA GATGAATCTG CGGAATTTGT GTATCGTATT TTGCCAACG 540  
 TTGAACATAC CCGTGAATAT ACTACATCG TTTATCACTG ACTTTGGCTG TATATTCCAA 600  
 GATAAGGCGC CGATGGAGAA CGGACCGGT CAACATACAC ATCCCGCAAT TTAGTTCATA 660  
 55 CTAAGTAAAA TACTATTAAC TTAGAATATG TGATAAGTGT TTTAATTACN TAACTTGGTA 720

TTAGTCNAT TGINTAATAA TTGAATATGA ATGCNITATT NITCTINANT CAAINTGTCA 780  
 CGATTGGATT TACACCGCG TCTGTAANGA CNTCTAGCTT GGTCATCCCA NITCTCANIT 840  
 5 NCTCCCGCTT NCA 853

## (2) INFORMATION FOR SEQ ID NO:322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1259RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GATCACACGA ATATTGCGGG AGTATTTCTC CATGTTGCG CGCAAGGGG CCTGCGCATC 60  
 GCGGTTGAGC GATTGCGGCT CGTTGATGAT CACACTCTTG TACCTCGCG CTAGCCCCTC 120  
 25 CGATCCGCTC TGGAAATCCA CCTGCTCCAT CTGCGCAATC TCCTTCAACA ACTOCTGAAT 180  
 CACGATCCGG TCATGTGTGC CCATGTGCT CGGCGTGATC TCGATGTGGT ATGGGCTGCT 240  
 GACGACGTTG AGCTGAGCT TCTTGTAGA TGGGTAACA AATTGCGCA CATCAATCTT 300  
 30 TAATTTGTAT ACACCTGCTC CAAAGATACT TGCAAGGAGC CCCATGCACC GTGTCTTCTT 360  
 CCCACTTCCA TTGGGCGCGT AAAGTAAAT ATGCGGCAGG TCCTTCGAG AACCTGCTAA 420  
 AGCTGAGC TGCTTGTAA GCGATGCGT ATGTGAAAGG CTGGTCAACG ACTCGGTCT 480  
 35 ATGCTTGTC ACCCAAAGTG ACATATTCCT GTGTATCTG AGATGGGCTT TTGTGTGTG 540  
 TAGGGAAGGT GAGCAATTCA GTGCAATTA AATTCATTA GATTGCGTT TTAGCAGAA 600  
 ACGATATGCC CTCAGTAAG CCAGAATACA TACAGTACT TGGCTACTA CTTTGTACAG 660  
 40 AAGTAAAGCT CTCAGAGAT CGCTGAGGA GATGGCATGT ATATAAOCN CAATTACTCT 720  
 GATGCNAAAA ATGTTGCACC CNTGCTTTT TANTCTGTC GACAACTANN AGAGCCTNTA 780  
 TCNAGTCCAA ATTTTNCNAA ANCTGGGAAA ACCTTNTNCC GTGGTNTATN AACACA 836

## (2) INFORMATION FOR SEQ ID NO:323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1259UP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

5	GATCACCOC CAAATCAGCA ATAACGCGAA AACTGTGCCC AGTACCTTTC AACGCGCATG	60
	AACCTAAGG CGCGCAGGG TCATGGGTAC TCGACTGCCT TTGTATCCCT CACACTGCGC	120
	CTCTTCGTGT GCGCAGGTG CTTGTGTGATG GTAGCGCGC GCGCCGCTG ATCTAAGCGC	180
10	ACGTCTCTTT GTACGTGGGT CTCACGTGCA CATGTCATC CATCCGCTTG CGAATGAGTA	240
	GATCAGCACG GAGACCATGC TAGGCAGGGC GGTGGGCGA GGTGGAAAGG TTGCAGCATT	300
	GAGGTGGAGC AGCAAGATGA CATCAGAGG TAGTAGTCGG AAGAAAGAGC TATGTGCAGC	360
15	GTACAGCGTA GTGGATGAGC GGGTTTCGG CAGCATGGAA GAATGCGGAC GTAGAAGGTC	420
	GGAGTTCTTA TTGCTTGGC TTTCTAAACT GAAACCTCG TOGGATGTGG CGATACTGTA	480
	CGAAGAAATG GGGCTGCGC ACTTTGGAGA GAACTACGTG CAGGAGCTGG TGGGGAAGGC	540
20	AGCAGAGCTG CCGGCGGATA TCCAGTGGCA CTTTATCGGG GCGCTGCAGA GTAACAAGTG	600
	CAAGGACCTG CGAAGGTAG TGAACGTCAT GCGGTGCGA CCATCGACTC GCTAAGAAGG	660
	CGCGAAGCT GAGGAGGCG TCGAAGTTC CAGCGAGCC CCGCATCTG TGTTACATTG	720
25	AGTGAACNCT CTGGCAACNC AAAGNNGTIN CNGATGAGC NACNGTGCAC TGTGATTCTT	780
	CTNCCAAAAC AAACCTTCCC TGCCCGACGA TAAATGGTCC TGGACCCCTC CCGCGAAGGG	840
	AACCGATCCC C	851

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1260RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

45	GATCCTCAGA GGGCCCGCAA GAAGCTTCG CGGAGACAGT AACGATGTTT GGCGAGGTTG	60
	TGCTGTATCA CAGTTGAGCT CTAGGTTGCA CTTTCGGAAA GAGCGTACC GTAGCTGCAT	120
	GAAAAAAAG TAAGGCTCAT CAGTTTATGC AGAGGCAAGA ATAAGTTTGG TAGAGCCTTA	180
50	CTTCACAAGC GTGCTCTAG CGAGCCATAT TATTCTATGG CCGGCAAGAG AAGACCGAAG	240
	AAGCCAGAG CTCATATCG AAAGTACGTG GCGGTCAAG GGTTTGTGCA TACCTACGGG	300
	GTTCACGTA CTGAGAGTTC AGCACAGAT GAAAGGGTT TGTTCGCGC AGACAGTGGG	360
55	GTGCAGGTAT CTGACGATGA TATTGCGAGA CGACTTGTG ATATGACACT TTCGCAAGC	420

GCAGCGTTTG CCGGTGGAGC GGCACCCATA CGGTATCCCG GACACTCAAT GGTGCTTCCC 480  
 TGGGAGCTGC AGTTTITGGT TCTGTCCAAA TGCAAACTA TTGAAACACA CTTCATGCAA 540  
 5 GTGTGCAGGC GGTGGTATAT CATGTGTCTG CCATTGATCT AOCGAGCACC AAGGCTCTCC 600  
 AGCAAGACTT CTACAAGTTT GTGGAGACAC TGGTGGCAGC CCGTAAACAG AATTACCGGC 660  
 AATATTCCTC GATCTCGACC GTCCATGAAT ACCNNANCGC AAACCTTTTC CAAGGTCTCT 720  
 10 CCGTGTCTCC CACCCCTGAC ATTCCGGGCC CAAACACTCG TATCCCCNIG AATCTTACGG 780  
 CNCCCCNNTT GCAACCGATT TGTCTNTTCC CAACGTTANC GAACNCTITG AG 832

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 846 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1060UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GATGACCGG CCGCCCCAGC CCGTGCCGTG GGTGAAGTGG CCGCCCTGGA TCATGAAGTT 60  
 CCGGATGACG CCGTGGAAAG TGGAGTTGAT GTAGCCCCGG GAGGCGTCTT GGCTCTTTTC 120  
 30 GAGCGTGAAG AAGTTGGOGA CCGTCCCGGG AGCGACGTGG CCGAACAGCC CGAGCAGGAC 180  
 ACGGCCCACT GGCTCGTGGC CGTCTGTCAG ATCGAAGAAG ACACGGTGTG TGAOGGTGGG 240  
 GTCTGCGAGC GCGAACCGGC AGAGCAGCGC CTGTGCGAGA ACGAAGAGGA CCTGCATTGG 300  
 35 GGGTGGCTGC GGGAGGCGCG GGACGCGCGG GGAAAACGCC CGCTTTTATA CCGGAAAAG 360  
 CTGCTTCGGC TACGTAGCTA GAGATACAGA GCGGTGGAAT TGAGGCTCTG CAGCATCAGG 420  
 CCGTCCATCA TCTCGGGCGT CAGCACGTCC GAGTAGCCCG CCGTCCCGCC GTCCAGCGCC 480  
 40 GCGGTACAGC CTGGCGCAGT GCGGCTAGAC GCGGTCTGTC CACTGGCCCG CTGCACGGAG 540  
 TTCTGCTCCA CCGGCACGAA GCGCGCGCCC TGGCCAGGCT GGAAGCGCGC CAGACGCTGA 600  
 TCGCGCCCGC CCGCGCCGAC AGGTGGAAGC CCGTCCGACG CAGGCGGTTT TGCAACACGC 660  
 45 TGTACGCGGT GCGCGCTGTA CCTTCCCNNA ANANGTNTAT CTTGACGCAT CACCGTTCCG 720  
 CCCCCTCTGC TTCCGAACCA AATCCGTCC NCTTAACAC CNITTCANGC CNITCACTTC 780  
 ACNCTGNCCA CACNCTTNC GGTACGTCC CAATGCCGTC TCCCCGGGC GCTTAGCNGG 840  
 50 GCTCGT 846

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 835 base pairs



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1261RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GATCATAAAC GAAGAATTCC TAATTAACAA TTTGTCTGTC ATGTACTTCC TCAGTGAGAA	60
ATAGCGATAT AATCATTAGA AAGCTTCCCC GAGCACTTTA GCAGCACCGC ATGCCAGCAT	120
AACCCOCTGG ACTCAGGGCA GTATGCGGCG TGGCACCTCG GCACCTCATC GCAGGCGAGA	180
CAGTCCACCA CTGCGAGCAC CGTAGTATTT ATACTTTTCC AGGTTGAAAA ATTTTCCACC	240
GCCCCACGCC GCAGAGGGCT GGAACGCGAT TAGGGCTCAC AGCGGTGAC TGGCACTGCT	300
GCCCCAACAG CGCGCGCAT GTAAAGTGAA ATGATATATT ATACCTTCTG ACTACAATGT	360
GAAATATACA AAGGTGGCTC ATAGGCGCAT TGCATTTATT CAGACGCGT AGCTCTGGTG	420
TAGATAGCCT GCTTGGAGTG CTTGGAGATT GGCTTGATGA TGCCCTCGGT CTCCAAGTGT	480
CTCAAAGCAA CTCTGGCCAT GGAACGCGG ATCTTCAATC TGTCGACCAA CACGGACACA	540
GAGACGTATC TGTAGGTTGG GACCTCCTTT AGGATTCTGT CAAGCTTGTC CTGGTCCAAG	600
ATGACGGGGT GCTGGGCCTT GTCCTTGTTG GACTTCTTGG ACCACTTCTC TTGGACTTCT	660
TACCACGGGC CATGGGCGGC GGCCTTCTG GGCCTTAAAN ATNTTGTTTT TGGTGCATAT	720
ACNGTGTGCC CNTATACTGT CGCACCACT GGCNTCTCTG CGNAGGGTGG TGAGCTTCCG	780
TACTCCNCCC CCTAACCNC CCCCCNNGT TGTCNPTTC NNCNNNOCTA ANICT	835

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1261UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GATCTGCAAC AACACCATTC CATCGCGAAG TCCTTCCAAT TTCTGTTCTG GAATATTATG	60
AGGAAGTTTG AGAACGATAT TGGGAGCGAT GATGAGGAAG ATCCCTTCCA GATCAACGAT	120
TTGGACGAGG AGAAGACCTT GCGCATGCTT TCTAACCAAG CCTGTTTCTT CCGCTACCTG	180
ATGGCCGAAG GTCAGGTAAA GTTAGATGTT TTAACCATG TATCCATTAT GGGGTGAAC	240

TCTGACGGGA GACTTTTCTT AGAGAATCTT CTATTTTCAGT TTCTGTTGGC CTCAGCCAAA 300  
 AAAGCAGAAA CTAAAAAGAA GGTGGGGAAT ATCAAGGAAT GGTCTTACAG AGATGACTTG 360  
 5 TTGCAGGGCG CCTGTGCGA TGGGATCCAG GCGGAAAATA AAAAGATAAT CTGCAATCG 420  
 CTCAGGATGT TTATGAGGAA TTTTAGATAC ACGAACTATA TTCTGTTGTC GCTTGGCTCG 480  
 AAGGAGTATC AACGTGACAT GAGAAGGTTG GACTGGGCGG TTAAGCGTTT TTTGGAACCTT 540  
 10 ATAGATGAAG AACTGGATAG TGCAGATTGT GAAGAGCTTC TTGTCACTAG TCTGAATGCA 600  
 TATTACGIGT AACATTGAAC ATACGTACTC TATATTAAAG TGGTGAAAGT GATGAGAGTA 660  
 TGACGTCCNT GCTTTTATTG CATACTACTT NIGAAITACA GTTATTGGT GAATGACNAC 720  
 15 AAACANGTTC CATTACTTAC TTGTGTGACNT CCGCNCGACC ACCACCCGCG CCACACCTTT 780  
 GTTACCTTA TAAAAATCTC CACNCCGNC GTATANAGCC TNAANAATTC NTTCGCTCAT 840  
 GCGGTTTTGA CN 852

## (2) INFORMATION FOR SEQ ID NO:328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1262RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

35 GATCTTTTGA CACGCTGGTA ATGTTTCCCA CTAAGTGGTA TTTTCTCTTG TCTAGATAGT 60  
 CTGCGGTAAA GACTCCCGAC GTGATCGGCC GGGCAAGGAC GCGCATCTGC TCCAAGGCCG 120  
 TCACAAGTTT CAGGTTCTGT TCCAGAAAGC ACTCGCGAAC TACTGTCAATG GTCACAGGAT 180  
 40 CAGTTACGGG AATTCTCTCT ATATATGAAG GCTCGATACC CTGAGCCTCC AATTGTGTTAT 240  
 TCACCTGCGG ACCCGTGGCA TGCAGCAGAA TCGGATAGAG CCCCACATGG TACAGGAACG 300  
 CCAGGCATGA AGCCAGTTCC GGCAAGTTGT CGCTGATGAT GGCACCTCCA ACTTTGATAA 360  
 45 CCGCGAATTG CTGCTCCGAG ACGGAAGTAA AGTACTTTCAG GTACTGTCTT ACTTCACGCT 420  
 TAGAGCCAAT ACTGTTGAGA AGCTGGATCA CGGTGGACCG TGCTCTGAGA GACCCAACGC 480  
 CCTCGTTGTT CCGGTTCTCT GCATAGTTCA GCTTCTTTAT AGCGGCAGTG CTGAACAATT 540  
 50 CCGGCTTGTA TCGGCGACGG ACAGCCCATG GCGTCCGGTT TTAGATCTTG CTACCAGCGA 600  
 AGCTCTACTA AACAGTAGAG AGTGCTCGCA AGCATCTTGG TACTCCGTTT ATCCAGTCG 660  
 CCGGAGTTCT AGCTCTCGAA AGCAGTCGGT GTGGCTTATA GCTTAANTTC TCTTGGGTTT 720  
 55 CATAACCACA AACCGTCTCN TTGNCNTTCC TGANTTTCAA GACCCCNANA TTTTCACAAT 780

TTTGTGATTT TTTGNGNGNA AGGGTGCNAT TTATTNTTGC ATNNTTTAA A

831

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1262UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GATCACAAGC TTGTTGAAGC CAACTGCTGA AAATGTCTCC TACGAGAAGA AACGATTCTC	60
TCCACTAGGA GACGTGTGGC AAATTTTAAA AGGAGCCAGT AAGACGCAGA CTAGCCCCAG	120
CAGAAGCGCC AGTAGTTGTT AGGAAGCATT CCAGAGCGTA TACGACACTT TGAAGACGGA	180
CAGCGTTCAG AGAAGACAGA GACAATCAAC ACCAAACAAA CATGGAGAAT CCTCACGTAC	240
ATGATAATTT ACAACACATC CAGGCGGTGT TATCGAACTA CGACACATCG TTTCTCTCGG	300
ACGATGAAGA GGACTACTGT CCGCTCTGCA TGGAGCCTTT GGACATCACC GATAAGAACT	360
TTAAGCCGTG TCGTGCGGG TATCAAATCT GTCAGTCTG CTACAACAAC ATCAGACAGA	420
ACCCGGAGCT AAATGGCGGG TGTCCTGGT GTCGCGGAAA TATGATGATG AGTCGGTGA	480
GTACATTGTT TTGAGCCCCG AGGAGCTGAA ACTTGAGCGA GCGAAGCAGG CGCGAAGGA	540
GCGCGAGCGC AAGCAGCGCG AGAAGGAGCG AAAGGAAAAC GAATATGCCA CCGCAACATC	600
TGCGCGGCAT GCGCGTTATC CAGAAGATTG GTATACGTTA TTGGCCTGAA CCACCCGTAC	660
CGTACGAGGA GGTGTGTGCG CTGTTGCGCT CGGACAGTTA CTTTGGCNGT TNCGGGANAT	720
TTACNNATCN TCCGTGAACC GCAAAGGCC CCATGACCCC NACGGTNTGG ATNNTTTTCC	780
TTCCCGGAAA AAGAGCGGCC CNNTTNCGGC GTGGATGINT TTNTGANGG CNGGTGAGG	840
GGGTACGACC NATNTGCCIN TTTTG	865

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1263RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

	GATCGGCGCA TTGCTTCTG AATGGTTCCT CACAGAAGGA TTGCTTACC AATGGCATTA	60
5	GTTCAGGAG GTCTCGCTA CTAACAGAAT CGTCTGTGG AACTCTCTT AGGAAGGTGA	120
	ACAGTTCATC TATCCTTTCA AAATTGATAC TCTGAAAGG TTCATTGCG GGGTTAAACA	180
	TACTAGATGC AGTCATTAGG GCGGCACCTT CTGGTTAAT ATGTCAGCT ATCCTTTTTA	240
10	GTGCTTCTTC CTCATTTTCA TTGGGCTTGA ATAAACCTCT AGCTATCAA AACTCAATTA	300
	GTATCTTCCT GACCTTAGTA GTGGTTCGT CTGGGGGCT AGTCATACTC ATTAAGTGAT	360
	GACGGAGCTT TTGCACACCT TTGCCAGAAA ACACACAAA TATTTGACGT TGGTTAAAGG	420
15	TAAATTCATC AGGAGGAGGT CTGCAAAAT GTGTGATATC TGGCTGAGA AAAGAAGTAC	480
	CGCAGTCAAT GACAAATGAG AGAGCTTTGG ACAAGCCATT ACCAACTCAT ATATTGGATA	540
	AATAGTCAAA TTAGTACAAT ATGATAGGTG AACTCTTTC AATGTGTCAT TCCTACCAG	600
20	CAAAGCAATC ATATTTAATA ACCTCATCTG TCATCTGAGA ACATTCACCA ACCCTATCTT	660
	TTTAGTTTGT TAATTCCCCA ATCATATAAG TATGAATTGT CCATTTTGT CACAACNATC	720
	CNCTCTGAT CNNGGANATC CTGATTCAAC CTTATCCCN CCNGAATGA ACNTGGCCAA	780
25	NGANATTNIN GTTTTTCN CTGAAANCT CNAATNCAT ACCCGCTTA CC	832

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1263UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

	GATCTTAAAA GCTGGCTCC GCAGATAGAC CTCTGCGCA GAGGCTGGAA ACCTCAACTA	60
	GCAAGTGGC ACCCGAATCA GATAAGCACT AGAGTGTTC CAGTAACAGA GGAAGCGATC	120
45	AAGGAAGATA GTAGAAGAGG AACTGCTGC CAGGCTTGAT CGGACAGAGG GTTTAGCTTT	180
	CTGTTGAATT TTAGAGTTT GGGCTTTGT TTACTTCGTT TCATTCTTTC GTGTAAAGAA	240
	GCTGTTTGA GCTGCCATC ATTTGCCAGT CGCCAGGTAG GGTATTGCAG GCGACGGAG	300
50	TCGGTGAAC AGAGCAGGAC CGAGAAGCC GATAGACAGG CGTTTGTGTTG TAAGCGGTGA	360
	GAGCTGAAGC AGGTCAAGAG GCGGCTTGG CGAGGTGTG CCGCGCGGC AGAGCACAGC	420
	AGGGCATCCG AAGAAGCGG AGCGTGGGA CAGGAGCGCA GCGCGCGAA CAGCGGGGTG	480
55	TGATGACGAG CGAGACGAAC AACAACAACG CCGCGAGCTC GAACGCGGG CAGCTACCGC	540

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CATCGGGGCT TCCGGGAGC TGGTTTACGA CGCCATTCTT GCGGCTCGA CCACAGACAG 600  
 ACAGCAGTAC TCCAGAAAGT TTCGGGAGCG TGTTCGGCGG TGAAGCCAGC GCGCAGAAC 660  
 5 TATTTTTCCTA CTTACCAACC GCGCGNAATG CCCCCACTTT TMTGNCCAA ANACATTTT 720  
 TCCNCCAGCN CCCNCCCTNC TAAAACCAAT TCTTACNGGG NOGAATGAAA TGGGTGNTT 780  
 TTCCCGCCCC NGAGAACACA TTTTTCNCA CTGTGACCCG ANNNNTANT CTCCNAACA 840  
 10 TTATTTTTTTC C 851

## (2) INFORMATION FOR SEQ ID NO:332:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1364RP

### (>i) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GATCTCGTTT TTGTAATGCT CTAGCTCATA TTGTGTGAAG GAGAAGGGTG AAAACAGCTC 60  
 CGAGGCTGCA ACTACTGCAA AGAATAAGA GCAAAATATG GCACATAAGA TGCTTCCCA 120  
 30 ATTCATTGG TACAGCTCTA ATACTGTGAA CCTTAATCT CCGGTAGGCG CAACAGTTAT 180  
 GCGGCCAACC ACGTTAAGT GATAATGATG TAGGTACCCG GGTGAAAAA AGAGTATGTG 240  
 GAACCGCCCA GCTGAACCAA GCGATGAGA CATGCCAACC ATATCCAAGC ATACTTGACC 300  
 35 ATGATGACGC AAAACTATCT AGCATAGTGA GTCTTGACG TGAGACAGGC TTCAATCGTA 360  
 AACCTCCAC CTTCACTATT GTCACGTGAG AGGCAACATA ATTGATCTTG TGAATACCAC 420  
 CCATACATTT TGCTACCACC CATACATACT AATTAATGGG GAAAATAGCG GCTGGTACAG 480  
 40 ATTCTTGCACT CCGCTGCCC CAGAGGGGCG CCGGCTCTC GTTCCCCAGC GCGGCAGGC 540  
 GCGGCAGGC CGACTGTCTT ACTACGCTCT CCTGTGTGGC CCGTGGTTAC CGGCTCAA 600  
 ATTACCAANC CTCCAATTTT TGAATATCCC CGACAGTTNT GTNCTNTTT TTTACCCCAA 660  
 45 TTCCGGAAT TCCCTATTAA ANGTAAGAC CCNNNTTAC TTTTGTGGAN TAACCTNNGG 720  
 CGTNCCTNNG GGNVNCCTT TTTTACNGG CCCCNTTCA GGCCTTTTGG TTCCCTAAAA 780  
 CCGGINAAAA AAAAAAGAT T 801

## (2) INFORMATION FOR SEQ ID NO:333:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1264UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

10	GATCTCATGT ATCACAACCA GACTATGATG CGACTTGGGG TGACTATGTC TCCTTTGCCC	60
	AGCGGTTCAG AGAACGAGTG AAAGACAAGG ACCTTATTTT GATCGACTCT GGTGACAAAC	120
	GTACCGGTAA TGGTCTCAGT GATCTCACTA GTCGATGGG TTTGAAGTCA AGCGGTATCT	180
15	TTAACCTTCA GAAACTTGAC TTGTAACTC TCGGTAATCA TGAAGTAT ACCTGAAGATG	240
	TGGTTGCTTT GGAATACTAT GGAACAGCAA TGGAGCTGA GCTAAGTGAT AAATATGTCA	300
	CAAGCAATGT GGAATTTATC ACAGAAGATG GGGACGTGT ATCGGTTGCG CAATAAATAT	360
20	AGGTACTTTG AAACGCCAAA CCAGAATCTA CGTGTATGG CGTTGCAAT CATGTTGAT	420
	TTTCCCGTGG GCTGCTAAAA ATGTTAGGTT AACCCCTCTG GCCGAGAGG TTAAAAAGGA	480
	CTGGTTCACC CAAACTGTGG AAAAGTACCC GCTGACAAGC TTGATATTAT AGTTGTCTTC	540
25	CGTCATTTAC CAGTCACCGG TGGCGAAACG AGACTTCTG CAGTTACACC AACGACTAAG	600
	GGAATCTTAC CCGGACACTA TTATCCCGTA CTTCGAGTG NNTACTCAGT CNGAAANTCC	660
	CINGITTTTG ANAAAAAGAN TGCTTTACCA ACGGCGAAT TOCTGAAACA TGGAAATCNA	720
30	TCAANANNG TTTCNCAAGA AACCAAAATT TOCATTCNAT ATGACTTACC CAATTCCTTT	780
	TCCCTCTCNG NTINANACTC CAAATTCNT CCAAGGAAGA ANANTNACNC CC	832

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1265RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

45	GATCTTGCTC AGAAATAACT TGCAATGTCT CCACTATTTT CTCAGATTG GCATTTATGC	60
	ATGTCACCTAG GCATTCGGTT TCAGGTAATG CATTCOCAAC AAGTGGCTTA CGATCTGGAA	120
50	CAGATTGTGT TCTTTGTGAT TCTGGTGGAG CCGTACCTCC AAAAGTTGAA TCTTCGTTTT	180
	CCGCCGAGCA GGAATTGCAT GGACGAGACT TCTTGTCAGA CATAACTCA AGTGGGCGCG	240
	CTCTATCTGA CATATCTTCC TGAATCTCTT CTGCATACGT GCGTTACCT GGCCTAGTT	300
55	CGTCTCAGT CCTAGCTCT CTCTTGCAT GCATATCOCT TGTCGTCAGA TATGTTTCTC	360

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TCTTCGGGCT AGAAGGGTCC TCATTGTAG GATCTTGAAC AAAAAGTAGT TTGTTATTCT 420  
 CCAGCTGGC AGTCTCTTCC AGGTTTACT TCCGATGCTT ATTAATACTG GTTCTTTAGA 480  
 TGGTTCCCTG ACTTTGGCTA TAGGCCATTG GTTCCGGCGA CTTGTGAAGG TATGCATTGA 540  
 GAGTCTCTCT GGTAAAGCT GINGTCCCC CGTTATTTTA NCACGGCTTG GCCGGAATGG 600  
 TACACNGNTG AGTTAATCNC NGGGGGTTC NGTTCCATOC TGTGGGGGGC CCACCCAGAA 660  
 CCCNAACTTN GGCGCCACNA TTTCCCNCTN CCAAACNNTT TGGCCNAAAA AANAATINTT 720  
 CCCCCAAGN NGGANNACGC ATACCCCGAN ATGNNGTATN TTGTGGGGGN AACCCCNNA 780  
 ANCCCNCCC CCNNGGGAA 800

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1265UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GATCCGGTGG CCGCTGGTGA AGGCAGGAC GTGGTTGTAC CGGCAAGGCG GCCTGGGGCG 60  
 GTTCTACCTG GGCAACGGGC TCAACGTCAT CAAGGTGTTT CCGGAGTCGG CGATGAAGTT 120  
 CGGCTGGTTC GAGCTGGGGA AGGCGGTGCT GGCGGGCTTG GAGGGCTGGG GCGAGACGGG 180  
 CGAGCTCTCG CGCTGTGGA CGTACGTTGC GGGGGGGCTT GCGGGCATCA TGGGCGAGTT 240  
 CTGGTCTTAC CCAATOGACA CCTTGAAGTT TGGCATACAG TGTGGGGCCC TGGATACGGG 300  
 CTGCGGGGGT CTGCGGCTGC TAATCAAGAC GGCGAAGGAC ATGTACCGCG AGGGGGGTCT 360  
 GCGACTCTTC TACCGGGGCC TTGGGGTTGG CATTTTGGGC GTGTTCCCCG TACGCGGGCG 420  
 TGGACTCTCG CACCTTCTCG GCGCTCAAAC GCTGGTACAT TACCGTGGC GCAAATGCGC 480  
 TGGGCATCTC CCGAGAACGA AGTGGTCAAT AGCATCTCCG TGTGCTGCCG AATGGGCGCT 540  
 TCAGCGGTAC GTCCGGGCGA CGTGTCTACC CTATCAACCT TCTACNGANG CGNTCCAGC 600  
 CCCAGGAGT TNCNCCNCCC CCTCTTACA ANGNITCAAN TINTTCCGAA AACACCNCCN 660  
 AGGCCCCCCC GCTTTTACAA GGTGGTTC NACATGCGA GGTNNCCNC ATCCACNCT 720  
 NTTTTTTTNC NAAANTTAAA NNCCANCCCC CCNAATAAAG GCGGCTTNTC CCCCCNACCC 780  
 CNGGAATAAN GGTTCGCT NNAAAACCA NACNCCCCC 820

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: 1266RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GATCTTATCT	GGAACACCA	TTCAGAACGA	TTTATCTGAA	TATTTGGCCT	TACTAAATTT	60
TAGTAACCCCT	GGGCTTCTCG	GTACGGGGC	ACAATTTAGG	AAAAATTTGG	AAATACCCAT	120
TCTACGGGGT	CGGATGCTG	ATGCTACTGA	CAAGGAGATC	GCTGCTGGTG	AGGTGAAGTT	180
ACATGAGTTA	TCCAGATTG	TGTGAAATT	CATTATCOGG	AGAACCAATG	ATATCCTATC	240
GAAGTACTTA	CCTGTAAAGT	ACGAACATAT	TCTATTGGTC	AATCTCTCTC	CGATGCAAAA	300
GGCAATTTAC	GAACACTTGG	TGAGGTCACG	AGAGGTTGCC	AAGTTAATGA	AAGGTACAGG	360
GTGCGAGCCA	CTGAAGGGCA	TAGGTTTGCT	GAAAAAGTTA	TGTTACCACC	CTGACCTGCT	420
AGATCTCCCG	GATGAGATCG	CCGGTCTCTAC	AAATTTAATT	CCAGATGACT	ACCAGAAGTG	480
CTAGTGACAC	AACTCCGGC	GCCGAAGAA	TTCCCTTTT	GNATTOCAAC	GANACATTCC	540
ATCNAATTTT	GCNATTOCTA	GAACGTTTTC	NGTTTTAGAA	TCCAGCCNTG	ATTGNAATGA	600
AAAAAATGTC	CCNGATTTCT	ACNNCCCCC	ACCTTGGATT	TINTCCAAAA	AATNINNNCCN	660
CCCNCCCCCN	GGTTTNTTCC	CANCTGAANG	NNCCCGNAA	ATTAAANNAC	TTTNAACCTT	720
TTGAAAATTC	CAAAACCCCC	GGGAGAAATT	NICNTTNTT	TCCCCCGGN	CNGGGNNGGG	780
NTCCCCCTTT	NGGCCCCCGG	NGAANTTTGA	CCCCAAAGN			819

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1266UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GATCTGTCAG	CATTACAGA	AACCATCGCT	ACGAAAAGTT	TCCTACAAGT	AATCCAGCC	60
AGCCGAAGGA	CTCCCCGTTG	GGTCTGTAG	CCGTCTTGGC	AGGCACAGT	TTCCAGGACT	120
TGCTTCTGT	TGGTCAGAGT	ACTAGGCAGG	ATGCGTTTGC	TTATTCCAAT	CACAGTGTG	180



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5 TGGCTAATGA TCGCCAGCCC TCTTTACCGC GAAACCTGC CCCAGACTOC ACGTTCACCTG 240  
 CGGAGTTTAA CCAGCTGCTA TCTGAATCCA GCAACTGCOCT TGAGCTTGAT TCTATATTCT 300  
 CAGGCAACTC AGTTCCTCTGG AATGGGAGAG CCTTAACCTC TGAAGCAAGA GCTAACCTCG 360  
 AGGGCGATGT GCCATCTGTC TCGGAAGATG CCCGGAGCGA CAGCCAGGCA AATTCTGCAC 420  
 AGAATGGCOCT GAAGTATTGA GTCTAGCGGA CACTGAGTAT GCGGACCTGG ATAGTTTGAT 480  
 10 CACTAATTTC TACTTCTACC ATGCGAGGGT TCGTCCCGCG GGTCTGAACG TTTTGTATATA 540  
 ATGATCGATT TTAGAAAATA TAAGAACCCO CTTGAATATG AATACTGNCN NTTAACCCOC 600  
 GGGGGTTGCT GATACCCCCC CTNTCCCCCN CTNGGNTGAA TTNTTACCCC NOGGNGGGGN 660  
 15 GANAANAAT TCCTGCCNNC TTGGGTTCCN AANCCCCATT CCTTTTNNAA TNAAAANTGC 720  
 TTCCNNGNCN TTTTAAAAA AAAAACCGTG TTGCCCCNAT AACCAAATCC CCNCGCANGN 780  
 AATTTCCTGG GTTCAACANC CGCTCAC 807

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1267RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

35 GATCCATTCC ACCGGATTGC AGCAGCTAGT GCATTTGGCC ATACGCCCGA TTGCCCTTTC 60  
 TTATAATGAA TCCCGGCTTG TAGAGCATCA TCGGCACCTT CACGTGGTAT TGAATAGCTC 120  
 CTCATAACCG CACCGGAAGA TTTCAGGAAT ATATCTGGTT GTGTAGTGTA GAGGTATCA 180  
 40 CTGTGGATTG TGATATGGCT GTTGCAGCTT GAACATTCCA CTAACCTCGG TTGGAATCCG 240  
 AGCAGGAACA ATTTTGTGNC TNAANCCNA NATTTTNNCC CCTANAATAN TGGNCTNNCC 300  
 AAAATCNTCN NNTTTNAATT TTTTCCAAA CTTTGTCCGT GACCGGANIN GAAATGNGGG 360  
 45 NAAGTGAAT GTCCAAGNCG GGNCCGNA AATAGAAATC CAGGGAAAAT TCTACANTTA 420  
 NANAGGTGNC ACCNCCGNA ACCCCGGGNN GGNNNACTG GNOCTTTNA ACCTGNGAAT 480  
 GCGGTNTTCC AACCTTTTNC CGGNGGCTT GGGCCCCCN TTAATNCNAT TACCCNCCCC 540  
 50 TNCCTTTCCC NAAANNGATN CCCCCCNCG GAAAGGTTN TTNNNNANCN TAGGAGGCC 600  
 CTNGGTCGG GAATTGNNN CCTTTCTTNC TCCCCCCCCA AATCCNGGAC CCTGNAANNC 660  
 CCTTNNCCC CCNFTTTTAC NNFTTTCCNN GNAANINCTT CCTTGGGCC ATCCCCGGAC 720  
 55 NNNAATTGGG GNTTTAANGG CCCCCCGGNC CCCCNCNTGN AAAAAGNTNN GGNCCCCCCC 780

CCCCCCTTN GN

## (2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 824 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1267UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GATCCGCATC GTTTTGTGTA GTCATACTAC CTGGACGCCA TGTTCGCCGA GCTGGCGCCG 60  
 CCGGCGAGTC TCGGTCACCT GGTCCGCTTG TGCAACGCGG ACTGTGCCCC CTCCTACTGG 120  
 TTGGAGCTAC CCAAGGACCG TATCCTGTTC CTATGTGCGA TTGGGAACCT CGTAATCAGG 180  
 CACCTCGTGA ATGTAGACCC AGCAGCAAGG GACATGCACG CTTTCTGGGA GAAGGTGAAT 240  
 GCGCTCTTCT TGGAGAACGG CTCAGGGGCG ATGCTGCAGA AGGAGGCTTT GGTGCCGCAA 300  
 CCGAAGAGCT GCGAGAACGA TGGCGGCGAG GCGAACGTTC CTGGGTCCCC GATTTCCTGT 360  
 TGGCAGACAC AATACACATC GGACCAGGCG AGCAATTACA TGAACCCGCA CGCATTCGGC 420  
 ACGGGGCCCC ATGCGGCGCG CACAGGCGGC TCGTCTGTG CGCTAACAG CGACACCTC 480  
 TCTGTGGAC TGGCTTCACA CAACGCTGC GCGCCAGAAG CGTGGCGCAG ATTCCATACC 540  
 AGACTTGTCT ACGCAGGTC GAGGACGCCA TCAGACAGGG AGCTTGCTGC TTGACCAGA 600  
 AGGGCTTGAG CAGGATTCCC AGGACGACAC GACCGCCTG TAATGCAACT GTTGTCTTC 660  
 CNATTTCGCG CCTATCCCC AATGGAACGC CACTCCCCNG AAAAAAAAAA AATTTTCGCG 720  
 TGGATATTTG ATGAATGAA TTAGAAAAAT TACNTTTCIN NNATTCTTGC GGIGCCACAA 780  
 CAATTGCGAN TNCTAGACCC GCGNCCTGGC NTINGGTTTT AAAT 824

## (2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 787 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1268RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GATCCTGAGA ACACTTTTTC TGTGGAGGCT TATCAATGCT CTTTCTATCC GCAGCTTCTT 60

CCAGGCAGAT GAATACTGGC AGTGGCTGGA GCGTGGCAT GTTAAGGCGT TTGGATATGG 120  
 TGGGCTGACT TGGGAGTGGC AGCATGGGCT GCGCAGCTAT GCATTCCCGA TGCTCTTTGA 180  
 5 AATGTGGTAC TATGTGGCGT GGATACTGGG TGTGGCCACC CGGATGGGCG TCAGGGGGTT 240  
 GGCACATGCG ACGGGCGCTGT GTGGGGGCGT GGTGGCGAGC GCGCGGGCGG GCGTGGCGCG 300  
 GATGAAGGCC GTCTGGGAGC TGCCGGAGGC AGCGCAGGAA CTGGTGGAGT ACTACGGGGT 360  
 10 TATTGTACGG GCGCGAAGT GGTGATGGCG GCGGTAGCAG CGTTGGGGGA GTTCTACAGC 420  
 GTGCTGCTGG TTGGCAAGC TGTATCTGGG AGTGGCGGAT AAGGGGGACA CCAGAAGGGC 480  
 GACCGCGGCC GTGAGCGGTT GCGCTGATGC TGACCATGAC AACTTCTTCA ACTGTTTCTT 540  
 15 CGGACGGGA AGTTTCATCA CTCCTTCGAG ATGAAGCTCA CGGTGGGCGC TCTACCATG 600  
 ATTGAACGGG CCTCACTTGG TTCTCTGCT TGNCCCAACT TGCGGTGGCT CTTTGGCTG 660  
 CCTCACGCA NTACTTTTTA TCTGGCNCCT TGCTNTTCTT GGTGNGANCC TGTTCGCCCN 720  
 20 ANNGTGNCN CCTTTTAACC CGNCCCAAGT TGCCCCGAGC CCTGCGGTN TTTCAATCCA 780  
 ANNANNC 787

## (2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 840 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1268UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GATCCAGGTA TACCCGCCCTC CGTGGCGCAG CGAGCTGGC AGCGGCTTCA TGGCTGCAAC 60  
 40 TGAGAATGCC CTCGACCTGA TGTGGCGTAT GCTGAAGATG GACCGGCACA AACGGTGGGA 120  
 CACGACTCGT TGCCTGCTCA GTCAGTATTT TGTAGAGCTT CCGGAGGGGA CACCTCTAC 180  
 GGAAGTTCCA AAATAAATA AGTAATGACT ATGATAACCT AGATGGTATA CTCGGAGGTT 240  
 45 TTGTGTTTGT GCTTTGAGGC GATGACATTG GCTTTTATGG TATCGCAGAC GTTGCGTGAA 300  
 AAAGATTCAA CGTCTCGGTA ACAGATTGCG GCAGACTACT TGTGAAAGA ACAAGACCA 360  
 GAGCGCTGGG ATGCTCAACC CAATGACGAA CCGACTCCGC CTTATTGGCG CTGGCTGCAG 420  
 50 GTTCTTAGC ACCAACAATA GCGCGCCACT GCACAAGATC TTTCCCTCCC AAGAAGCTGG 480  
 TGAACAGGAT GCTGTTGAC CTGATAGCC GACTGACCTT CCGGAAATT ACTGCGTGTA 540  
 TACGAGCAGT TGTACACCC AATTAGACAG TAGTAGGGCG ATTTGTAGTA CCGCGCGGT 600  
 55 TGAGGGCGCC ACGACGTTTA TGATTATGA AAAGTGCTG AGAAGACTCG CCGCCAGAA 660

CGAGAGCTCC CATCGCCNTC TACTTGCNCC GGANAACAAC TGCTTTACTT GCTGCCCANT 720  
 GGANACNAAA ATGCACGNGC NCTNCCCTTG ANCCCGTGCA CCGNMTGGCC NAAGGNNOGA 780  
 AATGAATTTG CAATTTAGNT CNGATTTTAC NCTCTGGNVC CCCCCCCCCA CTGANNGANC 840

## (2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 787 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1269RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GATCCCACTC TTGGCAAGCT ATACGGTGAC ACTATCATAG CTCGCGGTGG CCTCTACGAG 60  
 ATGGAAGACA ACCTGGGGGA GTTCTTGAC AGAGAACCA ATAACGAGGC GTACCTCAGA 120  
 GATCAGGGCC TAGCCTAAAT GCTCCTTCTT TTGCGGGCT TCTGCCCCC CTATGTATAT 180  
 TCCAGCTAGA GAATCGCAAG CAAGCCATAC TTAGAAATAG GATATTGTTC CGGGAACACT 240  
 GATTTACTGT GGGTACTGC TCGGAAACT CACTGTGTC GTATCGAATA ATTAGGGTTC 300  
 GACTACGGCC AGTGTGATGC TTCTTTATA CCGCATACT AAAACAGGGT CCTCAGTCGA 360  
 ATCGTGTGTC ACTGAATATG AGCCCCCTCA TGAGTTCCTA TCGGTAGAG CGTCTATGT 420  
 GCAGACCATA TCAACACCT CTGTACAGC GTGGAGTTCA ATATACGGT ACGACGACA 480  
 TACAATAGTA CGTGTGCCA ACCGTATAC GAAGAGCTGC GTTCTGATTG CAGCAATTCC 540  
 CAAGCCCCGG AAATACAAA CCGCATTTTT AGCCAGTGC GATAGATGTC CTGAACCANG 600  
 GAATTACANC GAAGGNGAT TGCTACTACN ANCATCANCC AGGGCTCGNG TATTTCTCAT 660  
 CCATCCCCCT CNAACNAAA ATCCGGANTT TTAAATTTT CATGCAAACC ATNCANATCC 720  
 CCNTTTNGAT ATTNCCCAC TGGCCCCCCC NCCCCANNT ANCGTCGGG ATCCNGNATT 780  
 CCCCCGT 787

## (2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 820 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1269UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

5 GATCGAACTC CATGAAGGAG CGTAATGGCC TCGTGGAGCT GCACCGCACT GGGTGGGTAC 60  
 ATAGCGGGAT GTAGGAATGC GGGGATAAAG ATTGGGAAAA GCTGACTGGG CTGCGCCTCT 120  
 AGCTTCAGCT CAAGCTGGGG CAGCAGCGTT GCTATAGGCT GTTGTGGGGA CAAGGTGGAC 180  
 10 ACTTCAGTTG CAGTAGGAGC AGGTAGCATA CGACTAGTGA TATCGAACTG GTGCGGGTAA 240  
 TGAGGATGAG GGTCAATTTC TGGCTCGAG CGCTGGCTAG CACCACAATT ATCACCAGT 300  
 CCATACCTCC ATGCAATTCT GAGATCTTGG CTAAGTGGGA CCGTTTTCG ACCCCCTCCG 360  
 15 GCTAAGTTTT GCACCGTGAC CTGCGATCC TCCTGGGAAA TGCGAGATTT CTTTACCTCT 420  
 TTACGTGTGC CCTGGAATAT CCGCGGCAGC TCCTTCGCAT ACTGAGTGTG GAGCGTGATG 480  
 ACCACCATAT GCGTTATCCC CCGCGCTGNN GGGCGGNNAN TTTCCCCCCC GGTTATTTCT 540  
 20 GTCCCTGGGC CTGCAANAAC TTCCANTTAC GAGCAATCT GGTCCCCCTG TTCTTCCCCC 600  
 AAAACATCTG GCCCATTTGA NCCCATATGC CCTAGAACCN ATCCAATCTG CAGCCGNGA 660  
 NTTTTTGGAA ANNAATTACC GGNAGGANC AAGCCGGAAG NAAAGCCCGC CCGCCCTGTG 720  
 25 GAGCGNACTT CCCCCCCCCC NAAAGCNGA ANTTNNTTTT TNNTTTGGGC CNANCGNCCN 780  
 TTTTCNGCCC NGCGGGGANG GCCTTAAAN TTCTTCCCCC 820

## (2) INFORMATION FOR SEQ ID NO:344:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 806 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: DNA (genomic)  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1270RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:  
 GATCATATGG TGAAGTTGGC ACATACAGTT GAATCATCCC AATAGCAAAG AGAAGCTAAG 60  
 45 ATTTACCTAG CGCGGCATCA CCTGGAATAT CTAGCATTTG CAGCGCAGGT GAAAAGAATT 120  
 TCTCATGAAT TGATTGGAAA TGTGGTTCGG TGTGTTCAT TGCTAAGCCC GCTAGTACAC 180  
 GATAATCATC ATTAGACTCA CAGGTAGAT GGGCCTTCAC TGTTGCTTA TACCAGTCTA 240  
 50 ATAGAACCCTG CCTGTACGA GCATATTGAT CCTGAAGAAT AACCACCGAT GGTCAACCA 300  
 TOGAATTGAG CAACAATGTC GGTTCATTCA CGGTTTGAGT GATGTGACTT CCGGTGAAAT 360  
 TCTCAAAGGA ATTTAATTTC GGTATCAACC CCTTCAACAA GGAAGCTGTG AAGATATCAT 420  
 55 CAACATGCGA TTTGTAAAGT AAACCTTCCC GCATCATAG GAAATCAAAA GTGGCTGGGA 480

AAGCATAGTT TGGCTATTG GCTTTGACTA ACTGCGAAGT TAGAATACTA CTTGTGGGG 540  
 CCAGTTTGAA TAGCAGAGTT AGACATTCAA CGGATTCTNA GAATATAATC CTNGCGAATT 600  
 5 TATCCATCCN OCTANAAAAT TTTTCCNCC TTGATCCANA ACNANAAAAT TCCGTTGACC 660  
 NCTGAAGACC TATTCTCNCC TTINAAGAC CTGCNCATTC TTCNATTTC CNAANGNNTC 720  
 CCGTTCTACC NAGAAANTTC TTGCATGCCN NCATGGTTTN AACCNAAACN TCCTTTGANG 780  
 10 NPANTINACTT CCCCCNCCC AATTTA 806

## (2) INFORMATION FOR SEQ ID NO:345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1270UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

25 GATCCGATTG TCAAATTTTC TGAATGGTAT GGTAAGAAGT TTGGGGCTGG AAAGGCTAAC 60  
 AGTGGTGTTA TATCTTTGCG TGATATTTTA GCTTGGGTG AGTTCATTAA TAGTACCTAT 120  
 AAGGCATTGG CTTGCCCTTA TGCTTCATTA ATCCATGGG CGGCAATGGT ATTCAATTGAC 180  
 30 GCGCTTGAA CCAACAACAC AGGTACCTT GCGGAGAGTG AGGAACGATT AGAACACCAG 240  
 AAGCAAGAAT GTCTCAAATA TCTGTCTGAA CTAGCAGGAA AGGATTTAAA CAAATACATG 300  
 TCTGGTCCAT TGATGTTAA GATTGACGAT GAACTCTOC AATCCGGGCT TTTTAGCCTA 360  
 35 CCCAGAGTTT CTTCCTCATC TGTCCAACCG GTTTTCAATC TTGGGCGACT ACTACAGCCT 420  
 ACAATCTCAT GAAAGTTGTC AGAGCAATGC AAGTACAAA GCCATCTTAC TGAAGGATC 480  
 ACCTGGTGTT GGTAAACCA CATTAAATTC CGCATTTGGT GACTGTACCG TTACGAATTA 540  
 40 CCGNTTTTAA TTATCCGAAC CAACTGATTT GAATGAATTA TTIGGATCCG AAGCNCCCCG 600  
 AAAAAAAAAAN GNAATTTNT TTTGNGTGA TGCCCCCNIT TTINAACCTA TGCCAAAGTG 660  
 GATGGTTTIN TTAAATAAA ANNANATTC NCCCCANCN TTTTAAAGN CNNAACCTGT 720  
 45 TTGINNCCNT GGNGAACCA NCCCCAAAT TAANAAAAT TTTGCCCCC ATCCGCTTTT 780  
 TTGINNCCA AACCCANACA GGGNGGTGA AAAGGGNTGC CAANCTTCC TC 832

## (2) INFORMATION FOR SEQ ID NO:346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1271RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```

10 GATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT      60
ATTATATTAA TTCTCATTG GAGCAATTTG AGATTAGAGA TTTATTAGGT TTAACATCAC      120
CAATAATAGA TTTAGTMTT ATTAATATTA CTAATTTTGG TTTATATCTT ATAATCTTTT      180
15 TATTAGTAAT TTTACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTCTTA      240
ATTGATATTT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA      300
TTGGTGGTAA AGTTATGAGG TTATTATTTT CCATTAGTTT ATACATTTTT TATTCTTATT      360
20 TTTACTATAA ATTTAATTAG TATAATCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT      420
TTGTAGTATC AATAAGTATA ATTATTTGAT TAGGTCTAAC TATTATTGGT TTTTATACTC      480
ATGTTTAAAT CTTTGTTTAT TTTACCACTA GGTACACCAT TAATTTAGTA CCATTATTAG      540
25 TATCCATTGA ATTATATCCT ATTTGCTNNA ACTTATTCCA TAGGTTTTTA AAATACACTA      600
ATATATACCG GTCCATTTAT AATGGTTATT TAGNNGGTTT AATATINAAT TNAAAACCAN      660
AATATTTTACA TTTTATGGTN NCCNCCCAAN AAGGCATTGG TTTGGTINIT TAAAAAGGCN      720
30 ACCTATATCN CCTANITGAT NTTTTTTATN CCCCCTTTTA AANANCNATT TINNCTTAT      780
TAAANTAAAT C      791

```

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1271UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

```

50 GATCAATCTT TCGATCATTG TCCAATATTC CCCACTGCTG TATCATATAG ATATTGATTA      60
TAATTTCTAA ATCAACGTGA TTGTCTAAC TTAAATTAAC AATTATGAAT TTTTGGCTAG      120
TTATTATTTT TTAATTAAC TAACTTAAA TCATTATAAG CTGACTTAA AACAAATAAT      180
TATTACATTA TTCTTTATTT ATTATTTAAT ATTTAGTTAA ATTTAAGTT CATTATCTT      240
55 AATTTTACT CACGAGTACA CCACTTATTA ATACTATTAA TTAATAATAT TAACGTTTGA      300

```

TTGCGATGTG TAATGTCTT AGTTAGCGCT TAATCTGAAC CAACATCATG TTCTCATTAT 360  
 TATTAACATAT TTTTAATAT TTTAAATAAT TATTTAATAC GAAAGTTATA GGATTGGAAC 420  
 5 CTATGAAATC ATAAAGATTT ATAATAGCTC AAATATTACA CTTTAAACCA CTCAGTCAAA 480  
 CTTTCTTAAT ATATATACCT TATATATGGT TTGATAATTT ACTTATAATA TATAGTATAT 540  
 AATTTAATGA TAACTCTTAT CATTTAGGTG CGTAGGGTTC ACCCCCTAT TGCTAGTCAG 600  
 10 CATATGAGGT ACCTCCCCC AATGATAAAA GTTATAATAT ATAATATTAT ATTAAGTATT 660  
 TAAAGANAT AATATAATTA TTTAATAATA TTTTATTTTA GGNAATAAA AAAAANTTTC 720  
 ANNTTTGAAA NANGGTGNG AGAATTANAA AAAGCNAATA ATATGTTCAA TTGACCCAT 780  
 15 TAANAATGTA GINCCTGAC ATCNOCTATT TCCTATANAA ANITTANAAN AANA 834

## (2) INFORMATION FOR SEQ ID NO:348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1272RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GATCAAATCT AGGTTCTCG ACGCAACGG TGACGAGTTC GTGAACGGC TCAAGCTCTG 60  
 TGGCTTTTTC CATAAACACA CAGACAACAG CAATAAAATG TTCACGAAGT TTGAGTTCTT 120  
 35 CAAGCCTCCA AAGGAGATCC TAGAAGAACG CAAAGCCAAG CTCGAGGTA AGCAGAAGTT 180  
 CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG CGGTGGGAAA ATCCAGAAGG 240  
 AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCTAGTC TCCTCTCAGC 300  
 40 ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT 360  
 CAACCGTTCC TAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG 420  
 AATGTAGGCA TTTGTGGCCA TATGCTGCTT GTCTCGAGC TTTTCTTGTT GGGCTCCCAT 480  
 45 CTGTGCCAG GAGCGGAATC CGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC 540  
 AGAAGAGGCT GATAATTGTA GTNCAGCAC ACCATAGACG CGAACAATG CCCCAGGCGC 600  
 AGTCTGCGT TAGTTTGAAA TCCAAAACA CTTGGAATCA TCGGTTCGCC GGAGGCCCAA 660  
 50 TTATCOGAN TTGGCTTTTA AANCCNAAT ACAANGANTG CGCCCNVGT CCCCCTGTACA 720  
 TTGTGCCCCN CCTAGGNGC CCACTCCCN CNGAANITT TTATTCATTT AATCTCNG 780  
 NCCCNCTTT GTGANAATG AATCANITT TIN 813

## (2) INFORMATION FOR SEQ ID NO:349:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 844 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1272UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

15  GATCGACCCC GCGGCGCATCG GGCCCTCCGG CCTGCTGCGC CCCTCGGGCC TCGGCTGGCA      60
    GCTGCTCTAC ATCCTCACCG TCGCCATCTT CACCAAGAC TTCTTCATGT CCGGCTTCTG      120
    GCTGCGCACC TTGCGCGCGC GCTCCAACCG CGAAGCTGCTG CTGGGCTGCT CGCTGGCGCG      180
20  CGTGCTGCTC GCGGTGCTGC TGCTGCTGCT CGGGGTCACC GGCTGCTCG CGGTGTGGGC      240
    CGGCTACGGG CCGGTGCGAG ACCTGACAG CGCCAGTTTC TTCTGCTGC TCGCGGGCT      300
    GCGCGCTGG GCCAAGCGCG TGCTGCTGCG CCTGCTGCTG GTGCTATCCA CCTGCACGCT      360
25  CGACTCCTTC CAGAGCGCAC TGCTCTCCAC CATTTCCAAC GACCTCTTCC CGCAACCGCC      420
    TGCCCCCGCT CTAGCGGGCG GCGCGGCTCG CCGTGTGCTG GTTCCCCGTC GTGCTGCTCG      480
    GCGTGTGGC CACCGACAT CCTGGCCATC TACCTCATCG TGAAGCTGCT GTCCGCGCGC      540
30  GTGCTCCCCG TCATGCTGCT GGCTTCTGGC CGCGCGCCCG CGCGCCCTGT TCTGCTTGG      600
    AGCTGATCGG CGCGGGCTCC GNGGGCTGT CTGGGTCTTC NCTTTCCGG CCATCTATAA      660
    CGCTNINCCN CNANGGGGNC GCTGCTATT TATTGNAANG NCCCTACTIN AATAANGGGG      720
35  NNCTTNGGN GCTNGTCTNT TCCCCCNIN GGGAACTGTT TTTCCCGNA NAANTCNGC      780
    CTGGGNCCC GTTGGNCCN CCGGANANT CANGTAACC NCAGGGGAAN TCCAAANTTT      840
    CTNC      844
  
```

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 792 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1273RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

```

    GATCCAATA CAAGCAATAT TGTCGCTACC AGAATGCCCC ATTTGCGACC CATATAATCA      60
55  CAAGCGAATC CCATCCCCAC CTGCCCTATG ATAGTCCTTA TGAGTGATGC ATTTGAAACC      120
  
```

CTGTAGATA CATCTGCACT ATATTCTATC TCACCGTACT GATTTCGTAA TACACGGTTT 180  
AACATCGACA TGACATTATT TTGGTAACCA TCTGAAATAA GCGCAAATCC TGCCGCCAGG 240  
5 ATACTGAATA GATGTAGCCA TTGGCCCTTC TTCCCCACAG CAAAACGTGC TTTCGGAGCC 300  
TCCGGGTCAT ACTTTAGTAA CCTGTGCTG GACATCGTAT TTCTGCAAGC CCGGCTATC 360  
CGAATAATAT CTAGCGGGTC AAGCGTTAGG TTGCTGCATT CTATATTATA TATTTCTCT 420  
10 CTCTACCACG TGCAAATTTA CCTGTATGAT TATGCTGCAA TCTCCGGT CTACTTCCTT 480  
TCTTGAGAC CGCTACCGAC TGCTTTATGA TTATCGGTGC ACCATATGGC GTCAAGCAGC 540  
ACTAGCTTTT ACCTGTGATA CCTTCCTTTA CTAAGTGNAT TCCGAAGTAN TTGNNCCA 600  
15 TACTATATCC TTCCCTAGA GTGAAATAAC CTTCCATTTA GGTNNTOCC ATTCCNGAA 660  
ACAGTTTTTA AANAANACA ACCTTTATCC TTNAACCCCA AACGCCCAA AAANAAAATT 720  
TCCCATTIN CTAGGTTTTT TNGCCNGGA GGAAGAAC CCCCCCTAAC CCGCTAANA 780  
20 ATTCTCTNC CC 792

## (2) INFORMATION FOR SEQ ID NO:351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1273UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GATCGGGCTA TAAAACTGAA AGTTCATGTA TGTGCTCTG AATGCAGAGA CGCGGCGCAC 60  
TTTACACATC GGCAAGCCTT GTGTGCGAA TGAAACATTA AGCTTATGTC AATACCATG 120  
40 AACTGTATGC CAAATTTAGT AAAACTCGTA CGTGTGGCA GCATAGATAG AGCTGTTACC 180  
GATATCTOCC TTGAGGCTAA AGCAGCAT TGGGTATTAA CTTCCTGGA CTATTCCGAA 240  
TCAGAGCTTT CAGATTGCTC TTATCATGG TCAGTCATCA AAGTGTGGA TGTAGGATG 300  
45 TCTATTTTCC CACCGCAATA AAGTGCAGTA TTATGCACT ATTCAATAAG CTTACCTCTC 360  
ACCTGATAT CTAGCACATC AGCTGGAGCG GAACCTAACC AGACCGAAG TTTAGTGGCC 420  
AGCTCTTGA GGAGTGAAA TATTTCTTGG TCCGCAATG ATCTCATGC GCATTATAT 480  
50 GCGTAAAGT TAGGTACATA CCTGTGACAC CCAACAAAGT ACAGTTGCTA AGTCCCAAT 540  
ATCTTAAAG ANCGTTTAA ACCNCATATT AAGGTGAAGT TTATGAACCT TTGANAGTAA 600  
CTGNTCTMT ATAGCGGAAT ACCANANNA TAACGNCCT GTTANGGAT CTATCGAAG 660  
55 NTTACTTCN NTTOGANCAT TTTATAGTTC NNTTATTAC CCGGANAAA TTGAACAAC 720

CNTGAGAAAA GTTNTNNCCN CNGGAAANG AAAANTVINC TTNIGANTCC CCCCCTTTAC 780

5 CTTGAAGNTT CTCCATTNC GAGATTCAAA TTTTNTAAN AAGGANTTN TAA 833

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1274RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

20 GATCAGAAC AAAAAGCAGT TOGAGTATAT CAGTAAGCAC TGGGAAGTTT GGGAAATAGC 60  
AGTGCTGAGA GTTACGGGAC AGATTGGCAA AGACACATTT GCGATGGAAT TTAATTGCCC 120  
25 GCAGCCAGAG CACGCACAAT TACACATTCA CCTTAAAGGT GCAGCCCGGC TGCTGGGAAA 180  
ACTGCACGG GAGGGTGGC TGATGCACCA CGAAGATAAC CAAGAAAACC GGGGCCGGGA 240  
AGGACCGCTG ATTCGGTCAC CGCGCTGTC ACCACGAATC GGGCCGGGAG AGAACCGGG 300  
30 CGCGTINGGA ACGGAATCCC CGAACCCITT TTNITACCCC AACTTGGNTC CCNGOCTPAN 360  
TTTCAAACCG NTINCAAACC CCNCCCTGG GTTNTINGC CCNNINCCCA NTANTTGGGC 420  
TNGGGGGGG GGGGCCNGN CCAAAAAAA ANGGGGTNTN CCNGGGNGC CCGNGTTTT 480  
35 ANCAAAANAT TTNCCCCCGG GTTCNCCCC CNVAAAAGGT TTTTCCCCC CCGGGGTTT 540  
ACCAAAAANC CNGCCCCCCC TTGGGANGGT TTCCNNITC CCATGGGGGG TTTTCNCGG 600  
GCTCCCCCN GGGGAACCCC AAAAAAGGC CCCCCCTTTT NTGGGCCCC NAAANCCCC 660  
40 CNTNNTTTT CAGANGGTT NCCNCCCCC TTTTPTTTCC CCATTANNCG GGAANTCCCN 720  
NTNTTCCCC CTTTNCCCC CCCCCAAA ANNAATTTTT TNNATTAAAA GAGGGCCCCN 780  
NGAAAAANAA NACCCNCCC CAC 803

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1274UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

5 GATCAATTGC GGATACACGA GGCACAGGC GATAGGCCAA GCTTCCAAGA ATGGGAAGAG 60  
 TACCTAGTCA GGGTCGTCTT GGTAAAGCTG AACCGCTGCA AGCAGCTCTA TACACAAAAT 120  
 GTAGAGATTC TATTGGATAT ATATCCGCAG ATAGACCGCC CATAAACACT AATGATACGC 180  
 TAATTCATAC AACTACAGCG TGTACATCAA ACACACACAC AAGTTTGATG CACACGCTTT 240  
 10 ATTGTTCTCT TGCACACACT TGATTTAGAC GGTCACACCC CTCAAGGTGT TAGAGTGGCC 300  
 AACACCAGAC GCGAAACCTT GAATAGTGAC AATAGTGTCA CCTTCGCTCA GGATACCAAG 360  
 CTCCTTGGAC TTCTCCACAC CGAAGTTCAA TCTGGCTCG ACGTCATCG TCCACTCATC 420  
 15 AGCTGCTTCC TGTTCGTAGA CGAATGGGAA GACACCTCTG TGCAAGTGGC AGTATCTGGC 480  
 CGCTCTTGGT TTTCTGGTCA CCATAACGAT TGGAAAGTTT GGCTTGTACT TGGAGACCAT 540  
 CTGTGGTGTT CACCCGAGGT TGATACACGA ANATGCTTGG GCTTCTGCTC GAANTNCCGC 600  
 20 GAAAGCAGCA CACAAGNCCC CGAGGTGAA TTGGCTTGNT CATTCTCTGA GTCACCGTAT 660  
 TTGAACGTTT GGAAGGCTTG CAGGACATAT AAAATCTGCG CAGNCTTAAA CGTNAATGGT 720  
 TGANACCTTG GGGTCCCGN AAAAATAANA TCNCCCGCN GAAAAGTTCC ACTTCGAACN 780  
 25 CCCCNGTNGT CTGGTTTGTN TGGTANCCCA ACGG 814

## (2) INFORMATION FOR SEQ ID NO:354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1275RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

40 TGACTCGGCT TCGTGAGGAA CTGACGCTTT TACTACATGT AGATTGAAAC CGTTTTCCT 60  
 GGATCGCCTC GTCTCGTTGC TTGGTATCTT TGCCAATCCT CCGAGTGA CGCTGCCTGT 120  
 45 AGAGGATCTT CCGATGGGC CAAACAAGCC CCACAGCCC AAAGAAGTGT GAGAGAGGC 180  
 TGAAGAAGGT TCATTGACCT CCTTTATGCG TTCAAATGCT GACGGAAGTG ACAAATCGTT 240  
 CCAAGACGC ATGTCGACA ATTCTCTGAC GGTGGACTCC AAGACCTGGA TGGCTCTGC 300  
 50 CCTGGTCTTT GATATCTAT GGATAGTGGC AATGTCTTT GAGAGTGCA TGTCTCGTT 360  
 TGTGAGGTTT AGGTTATCAA GTTGGCAAT AGGAGCTGC TCTGCAAGTT GGTGGTTTTC 420  
 TOCACCAGCT GTGCTCTGT GTGTTTCAGG TCTGTATCA GTTCTTTAA GCCTCTCTT 480  
 55 ATCGGCCGAT CGTCCACTG GACTGNTATN TTTTINCCAC NCCATINNN CCATAATTG 540

NTNAAGNAGG TNCCCCNCCG GAATTTINGNT CCGTTTCCA NAGNTOGGNC CGGGGATAAT 600  
 TTAAACNITT AAAAATTANC CCGGCCCTA NTTCCTTTTN CCNAATNNNN GNNCCCCCN 660  
 5 GNAANNITTT NCAANNCTTN TGNVCCNTAN CCTTTTINNC CCCACGGTTT TTNNTCCCC 720  
 CCGNTCCCN ATTNNGGANT TCCCCNTTN CCCC 754

## (2) INFORMATION FOR SEQ ID NO:355:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 842 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1275UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GATGCCCCAC ATTATGTC TC AGGTACTTT GTACGTTAAG AAGACCTGOC GCTCGATGCT 60  
 25 GCCTCAGAGC ATGTCGAGC ACTACAAC TT GGACGTCCT ATTGTGATG CCGACAAGAA 120  
 CGAGGAGTTC GAGAAGAAGT TCCATTGAA GCGCGCTCCA GCGTTTTCCT GTGCGGCTGG 180  
 AAATCTAACT GAGACCATGG CCATCACTA TTACTGTAAG TTGCCACCGA CTACACACCG 240  
 30 AAGCATGGAG CCTAGTGTG ATGAGAAAAC CTTTCGAAAA AACAGTTATC CCTGTCTGAA 300  
 TGGGCATAAT ATCTGGTTC ACATGTGTG AGAGACCATA CTCTGATTTA GAGCTACATG 360  
 CGAGGTTCG AGGAACACGT ACTAACCGAA CAACAGTGGT CAACCTAATC CAGGACGAGA 420  
 35 AGGCCAAGGC TGCTCTGCTT GGCTCCAGC TAGAGGAGCA GGCACAGGTG TTGCGCTGGG 480  
 AGTCTTTGAC CAACACCAAC TTCAITGACG ACGTTGGCTC TGCTCTCTAT ACCTAGAGAG 540  
 GGTGTGTTCC CMTINACCA ANNCNACATG GAAAACGNCN TTCCGNGG CGAAACNTIN 600  
 40 CCGNAGTIT TINNAAAAAA GAAATAACCN CTTCCTCC TTACCCCGG AAANTTTTNT 660  
 TINCCGGAN NCCNTGNCN TNGGGGGT GAACNNANT CCCACANTT NGGGGNCNN 720  
 NTGGGNCNG GCGCCCCCCC CCGNNNANG GTTACCCCTT GGGTANCCCC NNNINAAAAA 780  
 45 CNCCNCCCC CCTTNGGTC GGACCNAAAG GGGGGNCCC CAAANGAAAA AAAAAAAAAA 840  
 AA 842

## (2) INFORMATION FOR SEQ ID NO:356:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1276RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GATCGTATTT GTTGTGACC AGTAGCACTT TTTTCATCTT CCTTGGACG ACCAOCCTCG 60  
CCACGTTACC GAGGATC 77

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1276UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GATCCTCGGT AACGTGGGG AGGTGCTGT CGAAGGGAAG ATGAAAAAAG TGCTACTGGT 60  
CAACAACAAA TACGATC 77

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 822 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1277RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

GATCGGTCAC GGACAGACTG AATGGTCAAA ATCAGGTCAA TACACAGGCT TGACAGACCT 60  
TCCGCTGACC GAATATGGTG TCGGCCAGAT GCGGCGCACT GGTGCTGCGA TATTTAGCGC 120  
AAAATACATT GATCCTGGGC ACATAACATA CGTATTTACT TCTCCAGGCC AACGGGGGCG 180  
GAAGACTGTG GACCTGGTTT TGGAAAGCCT CAGTGAAGAT GAACGTGCAC GCATCCAGGT 240  
GGTGGTGGAC GAGGACCTAC GGGAGTGGGA GTACGGTGAC TACGAAGGTC TGCTGACAAG 300  
CCAGATTATC GAATTCGGTC GTAGCGGTGG CTTGGACTGC AAGCGCCCAT GGAATATATG 360  
GGCGAGCGGC TCGGAGAAGC GCGAGAGCAC CCAGCAGGTG GGCTGAGGC TATCACGAGT 420  
GATTGCCCGG ATCCAGGCAT TACACGGGCA GCACCAAGCT GAGGGACGGC CGAGCGATAT 480

TCTGGTGTTC GGCATGGCC ATGCTCTCCG TTATTTTCTT GCGCTCTGGA TGAAGATGGG 540  
 CGTCGAAGCG CCGACGCCAG ACTGCGCCAT GCGCTCGAGT AACCGGAATG ACGATCCGTG 600  
 5 CCGTTGGTGC GGCTGGAGCA ATCCGTACCT GCAGGACACC CCACTTCTTG CTAGACGCAG 660  
 GTGGCATCGG TGTGTTGTCC TACCCCNCCN ATTTGAGACC ANCTACTCN CCTGGCCNTT 720  
 CNTTGGCCCC CCGAGATCCC CCCACGGTNA GTCCACCGA AAATTTTAT ATCTACAAGN 780  
 10 GNGTCCCCC ATGAATATAC CNTATCTTCT TAATGGTCN CN 822

## (2) INFORMATION FOR SEQ ID NO:359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1277UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GCGTCTTC TGCGGCAGC GCGAGTCCAG GTGCGCAGC ACGCCCCAG AGCGGACCT 60  
 GCGCAGCGA TAGTAAGGT ATGCGACCAG GCGCGCGCC AGCAAGTTC TTGCGCGAA 120  
 30 GAACCAGAG AACCGGAGC GGCTAACAG CTGCACAGC TGTCGTAT ATGTGCGCAG 180  
 CGGTCCCCG GACGCCAGC CCATGGTGT GCGCACAGT CCGAGCATCA GCGCGCCCC 240  
 GCAGATCAGC ACGTCCCCA CGCAGTAAG CATACAAAC GGCTCTGGA GCAGCAACA 300  
 35 CGAAAACAG CTGTTGAACA GCAGTCCGA CGCTGCAGC GGGGCCAGCA TCACAGTGG 360  
 TAGGTGGCA ATCTGCATG TGCTTCGAA CAGTTCGCT AGAATGAATA GGTGAGAC 420  
 CATCTGCCAT AGCGGCTAC GTTACACCAC CTGCACAGT CCGGTGCCA CTGCGAGGC 480  
 40 AGCTTGCGC TGAAAGTACC AGGCCAAAA GACTGCATAC GCTTGAACT ACCGCCACA 540  
 CGACCCATAA TAACAGTTG ATGACCAAT CGCTTGATA CCGTCACCC TTGCTGCAG 600  
 AGTACTCTAC TGTGGGCGC TTTTGGCTCT AGGTCTCTAC GCTATGCCAA ACATACTGC 660  
 45 TCCGGTGGT CATGTTGAT GCTGTATGTC ACGTGACCGA TGACAGGGTA CCTGTGGTT 720  
 CTCTCCGGT TCAGGATAT GATACGAAA NCGGAATTA NCGGATGAA TTCCCGACC 780  
 CTGCGATAC GACNCCAACN GGAGAGCGG TTTTNGT 818

## (2) INFORMATION FOR SEQ ID NO:360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1278RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

10	GATCTTCAAC CTGCTTCOGC CTATGAACAT TCIGTTGTGA TTGAGAGGCG ATACCGCCTC	60
	CACCTTTCTT CGAGCCTGCC CGGTTTGGT AATOCATAAG TTCTTCCCA TTCTTTTGGT	120
	ATTGGTATAA GCGATGCAA TGAAAACAGC CTCTTGAATA CAAATOGACT TGCTTACGTA	180
15	TAAAATTATA TTTTATCAG AAACITGGCG AGCATCAAGC TCGGCTTCAT TGATTCATAT	240
	ACTAAACAGA ATACACTACA TGCTACCGTC CGAAAACGAA TAATCTATTT CCAATATATA	300
	TATATATATA TATATATATA TTATAGTGT ACTTTATAAA TCTGAACTAG GTCATACAAC	360
20	TCTCAAATCA AACGATATTT ATCTACATA TAGCACGGC GACGCACCAA TTGAAGACTC	420
	TAGGGCGCCT GAACTTGGCG CTGCCCCTGA TCTTTAGCCT GTTCTTTTAC AGGGTCATAA	480
	ACATAGTACA TACCGCGCTC TAGTTGCTCA TACTGGATGT TCCTCTGTTT CAGCTGCGGC	540
25	CAATTTTGTG GAGGGATATC CCACCCACAT TTCTGAGCTA TGAAAGCTGC AACGTCTGCG	600
	CACAGCCCCA GTAACCTAGG TCAATTCGCG TGCTTAACGG GTCTCTATG ATAGTACTTG	660
	TGGTACGTGA GCTGGACCTT GTTTACATCN CGGAAACTGC GGNCTTCAN CTNITCNATC	720
30	ANCNCAATCG CATNCANNTT CTGGCNANTT TTTTIGANTC CATGACCCCC CCNAAANNT	780
	TTCCGGTNG ACCCACACCC CTTGAAATN NCTGATNIGN AGANGCN	828

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1278UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

45	GATCTTGGAT GTACTGGGGG CTCATACTTC GGCTTCGTGT TCCTGTCTT TTTGCCCCTC	60
	TGGCCCTTGC CATACGTGGA TGCTCTTGG CCCATCTTAG AGATATCTGC TGTGCGGCTA	120
50	TGGAGTAAAG CTCTGCTTG CGAACTCTAA GTAGTGTAT CAACTGTGT GTATCATTTT	180
	TGCCACTGG AATCCATCAA TTTCACCTAG CCAACCCAA GCTGCGAECT ATCAAAAAAC	240
	AGGAGCAGGA AGCTGCCTGA AGAAGCGCTC CAGGGGCTA CCGACGGGA AACTACGAG	300
55	GACTGGTGCT ATGACATCTT TCCCGGATC CATCCCGAGT TCAGTGTCTT CGAGCTGTAC	360



EP 0 866 129 A2

AATTGGGTCC GAGGGGTGG AGCGCAAGCG TGTGACAAC ATCAACGACC GTATOCAGGA 420  
 GCTGCTCAAC GTGATTCCAG AGGAGTTCCTT CCAGGACTAC TACCAGAAGA AGAAGGAOCA 480  
 5 GGAGTCCGAG AGCGGGAGCG CGGGGCTCTT GOCCAAAAAC AAGGGAACTG GGACGGGOGA 540  
 CGGCAAGCCC AACAAAGGCA GATTCTCACG CAGGCGCTCG AATATGTGAC CTATCTGCAA 600  
 ACCAGTGGAT CTGCGCACCG CGAAGAGGTG GAGCTGATCC TGAAGGTCAG GAGCTGTGTC 660  
 10 GGCAGACGGG CAGCATCGTG AACGACGTGA ACTAGAAACA CCATTGCCGA CTCGGCTGG 720  
 GAAATGGGT TGGGCTCTG AGCGTCTCC GGAATTNTGC GGCNCAGGG CAGCACACCC 780  
 NGGCAGCACA CGCCCCAGA CCACACACTC ATTTGGGTCC CATTOGGACG CNTAGATTTT 840  
 15 CNOCTGGNCT GTTTT 855

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1279RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GATCCTTCCTG GATGCTGGTA GCTCCGATGA GGAAGTCGTA CTTTGGTAA TGTCACTGCT 60  
 GCTTAAGCAT CTACTTTCAA AGCGTGATAT ACAGAGAGCG TTTGCTAAAA GTGGTGGATA 120  
 35 TAGGTTACTG TTCTOCATAT TAAAAGATAT CCAATCCGGG CTTACAGGAA AAGTCACGAA 180  
 TCTATTGTGC ACCTATGCAT TTGGAAATCA TATGTGCCA ACACACAGCG AAAGCACGTC 240  
 CCTTCTTATT AGACCGCAAG GCGATGGCT ACAAGGATA GTTTTGAAC TTCATTATTT 300  
 40 GGCATTGCA TTGTTAGAGA TAGCGGTGAT AAAAGCCCCA AAGGAGGATC AACAAGAGTT 360  
 GAGTAAAAAC ATTATTACGT ATATCAACGA GTTGGCGTTA CTTCATAGTA CTCACTCTCG 420  
 AATATOGCTT TTTGATOCOA GCGTATGCCA ACTTCATGAG AGATTGTTAA CTTTGTATT 480  
 45 AACTTTGACA GATCCCAAAT ATCAGGGTTT CTATATACAG GCTATTCTGG ACATTGAACT 540  
 TCTATTGAGT AACACATAT CTTTCACTTA AAGAATGATG ATOCACCACC TTTTGAAC 600  
 ACTTGCAAAA TATTTTGGTA ATGAAAGGGA CATCCGATTA GTCCTAGCAG ATTACAGTTA 660  
 50 GTAACAAAGG TCCAATTATA TTGAGACCAC TATATNTTAA AATTGTCCCC NIGTTATTGA 720  
 AAACCTNTGC CCNGGTACA CTTATTGCTN TTCNACACCG TCCTGNAAAA ANTGTGNTTT 780  
 GTTACGATTA ACTCGTTTC TTGATTGAGC AACTTTTGT TTTTATCATA G 831

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 841 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1279UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GATCAAGAGT ACAGTTGATG AAAAGGAGTT CCATGATGAA ATATGTAAGA TGGACTTGCT	60
TAAGAAATTG ATAATATAAA AGGCTACGAG CTTCATATT ATAATACGCA TTGCATAATT	120
TATTACATTA AATTGATATA GGTATATTTT TCTTGAAGA ATTAATTCTA ATCATTTCOA	180
TGTGAAGATA TGGCCCTCTG TGTTACCTGC GGATATTTTC ACTCTTAGTA TATCTACATA	240
TTTTGGGCGAG CCATTATTTA AACTGGCCAG CTTGACTCTG GACCCAAGAG CCGTAATGGC	300
AGCAGCTCTT CCTGAGCGCA ATTTCTTCAA GCAATTGAGG CACCATGTGC CGTCTTTTAA	360
TTCAAGCACA TATAAACAGA CCGTCCCGTC AATAAACCCCT AGCACAATTA TATCCTTTTC	420
TTTCCAATAC ATGTGCGGAT ACGTGGACAT TTCTGAGAT GCAAAGTTAA CAAAGCTTAT	480
AGCAGTGATA TCTTGCGTTA GAGACATGCT TGCAAATTTC GAACCGTTGA GGTCAATAAC	540
ATGAACGTTA TTTGAGAATA TCAACCACCC ATTAAATGAA CTGTACCTGT TTGAAACCGC	600
AATGCACTGG NNINNCTINGA AATATTNCC AACCCNCCCT TAAAAGNGTC CCCCCTTATT	660
NNGNCTINGC TATTCCCAAA AACNTACCCG NTTCTNTGIG NNCCAAGGN NTTTTNNCT	720
TNTTGGCAGC CTTTTAGAGN TTAAANATN TTCCAANCCC CAAATCCANT TTTTAAAGGN	780
CTCCCCINAA AANNVCNIGA ATGANCAGGN GAATTGTTT GCGNTTAAAC TTCCAGINA	840
G	841

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 826 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1280RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GATCATCAGA CCTGTGGGAG GGTTCGGTAG TGGAACTCT TGTAGGGGG GAGCCGCTGT	60
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TGTGAGCCTT GAGCGCTCT GGAGACGGCG GCTCGAGTG AAACGGAGCT CGTATCGGGG 120  
 ATCGCGAGAT GTACTGGGGC GACCTTAATG CAATTTTCTT CTCGAAGGAC TTGTGCGGGA 180  
 5 CGGAGGAAAG TCTTTCAAAT ATTGACGCAG AGCGGCGCTT TGAGATTGTG CTCTGGAAAG 240  
 ACGTCTTTTC CAAGGCGGCC GGCAGCTTTT CTCCCGTGCT TGCAGCGCTT GCGCAGGTG 300  
 CAAGCACGGC CGCCTTCGCA AGAACGGGAC TCTGCTTCAG TAGGCTTGTC TTGGTCATCA 360  
 10 TCGGCTGCAC CACCAGCGGA TCTTTGTGTG GCAGGGGCAC AAACATGTTG GACCGCGGGA 420  
 GGTGCGGTG ACGGCTGGC GGAATCAAGG CTGCGGTCCG AAAGTGAAC GTGTCTCGG 480  
 GGCTCTTGA CATCGAAACC TTGCTCTGT TGATGGGACT TCTCCGAGTC CACCTCTGT 540  
 15 ACCGTGTCT GCTCCCGCTC CTGCGTGGC TCGGCTCCN GNCNCCNGT TCCTGCCCTC 600  
 CTGACTNTTC CCCCCCTTT AGGGGAACAC GGAAGAAAA NAANINCCCT TTCINNCCG 660  
 GCGCTTGTG TCGCCCCCN NNNNCCCCN CCCNNNNN NNNNNNNN NNCNNNNN 720  
 20 NNNNAAAAT NTAGGGGNGG GAAAAATNG GTTAGNGTC CCACCGAA CCCCCAAAA 780  
 AACNCCCAT GTNCCAGGG NCTTATGAN CANCTTCNN NTGGGA 826

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 840 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1280UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GATCATAATG CGACTATGCG CCATAAGCAG GGCAATACG CTATOCACAT CAAAGTCCCT 60  
 40 GACCGTCCA TTCTCCGCGA CCGTACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGCG 120  
 CGCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAAT ATTTCACTGT GAATCCTGT 180  
 GAAACACTAA CACTTCCTGT GTATGAACG GAGTTAAACA TCCAAGGCAA CATTGTGAG 240  
 45 GGGGGCAGA TTACCAATTT AACTCAGGT GTACCAGGCG ATGTCCGAT TTCTATCTA 300  
 GACGGGAACA ACTATACCA CTGGCAGCG TTGACAACT CTGAGAGGGC ACTCTGTGTG 360  
 ATTGATTGG GTTCCGAAGA GGAGTACGAG ATCACAACG GTTAAATTT TGTGGGGCGC 420  
 50 TGTCCCGCG AAGAACTTCT CCATCTCTAT TCTCCCCAAC TCAAAGCACA TCACAGAGAT 480  
 ATTGACAAA CTGACGGCCA TGATGGACG CCGGAATAC GACTTGTCTC CTGCTCAAAG 540  
 TGCCAGCGG TCTCTTCTC GCAGCATCTG CTCGGGGGGC TGGCGAATGT CACCGATTCC 600  
 55 AGGGAACCTG CGGCCATTGA TGAAAACGTG GANNVTGTTT TAAAAAATTT CNGTTGGACT 660

TTCANCTCCN NNNNTTCACN TTTCOCNAGG CGCCAATNCN GANCTOCTNA GGCCTGNAA 720  
 CACCATTNAN CNCTGACCTA CTCAAAGATN TTCTATCCCC CAATNTCNMTT TCCAACACAA 780  
 5 CGATCTGCTA ATTGNGGNC CAACCATCAC TTNNVGCATC ATTTTGCCAC AACAATGNGA 840

## (2) INFORMATION FOR SEQ ID NO:366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1281RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GATCCGACGT TCAGTGGACT CTTCOCATTT AAGGTTTTCA ACAAATTOCA AACTCATGTG 60  
 TTAAATGCOCT TGTACCATAC CGATGAAAAT GTATTTTATG GAGCTTGTA GGGCTCGGGT 120  
 25 AAAACTGCAA TGGCAGAAAT AGCTTTTATG AGTCACTGGA GAGATGGTAA GGGACGTGCC 180  
 GTCTATATAT GTCCATCTCA GGAGAAAATT GATTTTCTGG TGAAGGATTG GCGAAACAGA 240  
 TTTTAAATG TGGCAGGTGG AAAGGTTATT AATAAACTCA CATTGGAATT AACTAACAAT 300  
 30 CTTCGAACGC TAGCCCACTC GCATTTAATC TTAGOGACTC CAGAGCAGTT TGACCTGCTT 360  
 TCTCGTCGCT GGAAAAGAAG AAAAAACATT CAGACATTAG AGCTGTTGAT TCTAGATGAT 420  
 CTTCATATGA TCAGTAGTGA CTTCGCTGGC GCAAGGTATG AAAATATAAT ATCCAGAATG 480  
 35 CTGTTTATTC GGGGTCAACT TGAAACGGCC TTGGGTATAG TGGTTTATC TACCTCCCTC 540  
 GCTAATGGTC GCGACTTTGG AGAGTTGGCT CCGAGCTAAA AAGCTACATT TTTATTTCTC 600  
 CTTTCACGAA GGGTTATGCC CTTACAGATC CNCTTACATC CGTTCCTAGA NGCATGAAAN 660  
 40 TCTTTAATTG AACTATGGCC AATCGCTTCC TGACGNACAA CTCGTGATA CTGCCANINT 720  
 TANCTTTTGT TCATTAGAA ATGTTTCAAT TCTGTCTCTG CACGCCGCCG GGANGAAATC 780  
 45 CTGGTCNCCN ATTAGTTGGA ACCATTCTAG GNNAAAAGAC TCTTATCTTA ACN 833

## (2) INFORMATION FOR SEQ ID NO:367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1281UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

5 GATCTGAACG TATGAGAGCG GGTITTTTACT AATTATAGAA CCATATGAGA TAGAAAATGC 60  
 GGCAGTTTCCA AATCCAATAA TGCGATTTCAC GTGCGCTTGAT GOCTCCATTG CAATCAAACC 120  
 AGTGTITGAG AAGTTTTTGT CAGTTATTAT TACATOGGGG ACCATTTCTC CGCTTGACAT 180  
 GTACCGTCCA ATGCTGAATT TTGAGACAGT TCTTCAAAAA TCTTACTCCA TGAAGCTGGC 240  
 10 GCAGAAGTCC TTCTCTCCAA TGATTATAAC CAAGGGGTCA GACCAGGTAG CCATCTCTTC 300  
 TCGGTTTGAG ATCAGGAATG ATCCCTCAAT TGTCAGGAAT TATGGTTCCA TATTGGTTGA 360  
 ATTTGCCAAG ATTACTCCTG ATGGTATGGT AGTGTCTCTC CCTCATATT TATATATGGA 420  
 15 ATCCATTATT TCAACTTGGC AGACAATGGG GATCTAGACG AGGTTTGGA ATACAAGCTC 480  
 ATCCCTCGTG GAAACACCAG ACGCCACAGG AAACCTCTC TACCTTTTAA AACINACNA 540  
 AGGCCNGCC NNAAATGGGNC GGGCCANITA ATTCNGTGG COGNGGAAA ATTCINAGGA 600  
 20 ATGGATTING ACNCCCTCGG NGGAGTGTG TGAAAATGGA TCCCTCCCTT NACCGANAAC 660  
 GPTINTTTAG GGAGGGTINT NCCNINANA AAANATCCAA ACCGGGAATA CTTTTCTCTT 720  
 NNAGCATGAA NCCCCCCCCT TTTGGGAAA TTCAAGGGTG AGGAANATAT GGTTAATGIN 780  
 25 CCCCCANCN GNINCCNNA AAAAANCACT CCAATGTCC CAGGNCCTIN NGNACCACTT 840  
 CTNNNAITG GAT 853

## (2) INFORMATION FOR SEQ ID NO:368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1282RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

45 GATCCGGAAT TATAGAATCG ATGAGCATTT CATTTAGCAA CCTTCTTCCA ATTGTAAATG 60  
 GTTCATATAT AAACCTCCCTA GCTTCTCTTT GATAAATCCT TTCAAGAACA GCACCGTOGC 120  
 AGTCTGGGTT TATCTTTTATA TTATTCTTG TTATGCAACT CGCATGGTCT ATGAGGTCCC 180  
 TACATACATT TAGGTGCGCC ATCAGTACCA CCTCTTCCC CAGATTCTCT ATGTTCTCTCA 240  
 50 CACGTTTGAA TAGAGTTTTT AGGAAACGCA GCTTAAAAC TTCACCTTCC TCAGTGTTC 300  
 TAGAATTAGC AGGCAGTAT ACGGAAATGA CCACCACTT ACAGGCCAAT TCGACTAGAA 360  
 55 GGCATCTCCC CTCCTGTCT AGTTCCTGTG CATTAGCATC ACTCCCATAG GGCAAGCCAT 420

CATAACCACC AATAACCAATG GTCGGGTCTT CGCAATATGC TACCAAGGCG CCATCTTTTT 480  
 TTAATTTTTT AGTCTGCTTG TAATACCTCC TCCCGCCTTC AATACTTGTA ATGATTATOG 540  
 CAACGATOGG CTGCTTCAGG GATTCTGTTC CACNCCACN CCNATACCT TCTCTGN 598

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 622 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1282UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GATCTGGCA AACACCCCA CTCGTGTAC CTCTOGATG CTGTCAATG AGTCTTGTG 60  
 CATGCTTCTA TCCTTCAGCA GGAACGGGC TAGGTACGG ATGTTCCGC GCAGCAGCC 120  
 GCAGATAGCT TCGATGACG CGGGGTGTA CACGGTCACC GACTTGTAGT ACCCGGGAA 180  
 GAGCGCCGG TTGTCATCG GTAGCACCAT CAGCTCTCG TACTTGCGG GCACCTCGCC 240  
 CTGCTGGG GGGTTCGACC GGC CGCGCC GCGCGCGAA GACGCGAAC CGCGCTGCC 300  
 CCGGAAGAA CTAGCTCCG ACGACCGATT CGCTGCTCT TCCGTGGCT GCGCTCGC 360  
 CTCTCGTGG CGCACCGCTT CCTCGTGGG CCGCTCTCC GCGCGGGG GCACCTTTTT 420  
 GTGCTGCTC TGGTCCGCT CCGCGTCTT GCTTCAGTAT GCAACTGCCC GCGCGTGTA 480  
 TCCCGACTG CTGCGCAAG GCGACTCTT TTGGGGGGG GGGGGGNNN NNNNCCCN 540  
 CCGCGCGCG GCGCGTTCN CCGCGCGGC CGTTTGTG TMTTCAGCC GCGCNVTGG 600  
 CCATCCCCC CTNNTTTTT CT 622

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 798 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1283RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GATCAGGAAA TCGACGGGAC TGGCTGATTG TCTTTATAGT CAAGCATATT AAACACAGT 60  
 GACTTAACT AGATTTACAC GTGACATGCA ATTGTGTGTT TCTTTTTT TTTGAAAAC 120

CTGCATCGAG CTATTAGATG CTCATCGACA CTAGTGTACA AACAGTCAA GGCTTAAAAG 180  
 CTCTGCAGCA TGGACCAAGT GAATAAGGAG CATCGTCTTA AAAAGGAGAA GCGACAGCT 240  
 AAAAAGAAGC TGCCTCCCA GGGCCACAAT GCGAAGGCAT TCGGGGTGGC CGCTCCGGGA 300  
 AAGATGGCCA AGCAGATGCA GCGCAGCAGC GATAAGGGG AGGGGGGGCT GCAGTTTCG 360  
 ATGGTGGACC GGACGGCGGA CGACGACCG CGGCCACTCA TTGTGGCGT TGTAGGTCC 420  
 CCGGGGACGG GTAAGACAAC NCTGATCAAT CGCTGGTGG GGGGTGACC AAGACGACCC 480  
 TCGGGAGAT TAACGGTCC ATCAGGTG TCTCCGGCAA GCGCGCGCT CTGACGTTCA 540  
 TTGAGACGCC CGCGACGAT CTGAATCCG ATGTGGACAT TGGGAAGGTT GCAGATTGG 600  
 TGCTGCTGCT GATGGACGGT ACTTTGGTTC GAGATGAGAC ATGAGTTCC TGACCTGGCN 660  
 CACNCCAGG ATNCCCTTTT NCTGGATTAC AANNCNCAT TTTTCATNC NAGGCCNCTC 720  
 CNGCTCNAAA ACTTTTNACC TCGTCTGAC NATTTTNCN GGGGNNCNT CCGCTCGTN 780  
 TTTTITATGN NNNNCNT 798

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 829 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1283UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GATCGCTGG CCATCGCG AGAGCTATGT GCATCGCTC ATAGTGGCT TGATAAGTGT 60  
 CTCAACCAAG ATTGTGAAG ACACGTGCA CTCCACGAG TATTTCAGCA AGGTCTGGG 120  
 CATATCGAAG AAGCTCTGA TCGCCTCGA GCTAGCCCTC ATACTGTCC TCCGGGCGA 180  
 GGGTTTGATG GTCACGGCTG CAGCTCTAAA CGCTGCTCA AACGCACTG CTGGCTTCG 240  
 CGAGCAGTCT GCGCTGCCAG CCGCTGCTG TCAGTGATAA TCGCCACTTC TAGGCCACA 300  
 ATTGGGTAT TTAATAAGCA ATAAATCTC CAACACTAAT AGTATACACC GTTTGCGAGA 360  
 GTAAGCAAGC AGCAGGAGT GGCAGCTTT CTGGTACCAC CTCAAGCCCC TTGCCATTGC 420  
 TGCTATCTG GTTAGGCAT GAGCAACCTT AGTCAGTTTC GAACCGTGA TATATGTTTC 480  
 GAACAGTGA CCTTTTCGT GAAAGAAAA AGCCTAAAGG CGAAATGTTT TCCATGTTAA 540  
 CACAGCAGAT TAGAGGTACC TTGTACTGGA TATTCTGTAG GATCAGGGC TACGAGCATT 600  
 CATCCAGAAG CTTTGAACCT ANGTTGTTT NGGATGCCAG TINGGACTT ATNCCGTGCN 660  
 TTTAAANAA TACTTCGTCC TAGTCTTTG AACAAACNIG CATTGTGTGT TCITNGTTTG 720

GANVATCGGN AAGACANCTT TTGCOCTGCT AANAAGACNG TTGGGAACNG NNGCCNNTGN 780  
CCCNCTCCGA GNCNNGAACN GGCCCNNTTN CNNTTCNNCN GGGGNNNC 829

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 817 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1284RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GATCGATCTG GTCAGGTCTA TTTGTGGCAC CGATGACAAA AACATTTTTC TTTCATTCA 60  
TACCATCCAT TTCAGTTAAC AATTGGTTAA CGACTCTATC AGAGGCGCCA CCAGCATCAC 120  
CCAFTGAGCC ACCTCTAGCC TTTGCAATGG AATCTAGTTC ATCCAAAAAG ACAACGGTTG 180  
GGGCTGCGGC TCTAGCTTTA TCAAAAATAT CACGAATGTT GGA CTGAGAC TCACCATAAC 240  
ACATGCTTAG CAACTCTGGA CCTTCACAG AAATGAAATT AGCAGATACT TCAGTTGCGA 300  
CTGCOCTTTC CAACAACGTC TTACCACTAC CTGGAGGACC GTAAACAAC ACACCTTTTC 360  
ATGGCGATAG ACCAAACTTA ATGTATTGGT CAGGATGCAA GACGGGATAC TCAACGGTTT 420  
CCTTCAACTC CCGCTTTATG TCATCCAACC CACCAACATC GTCCCAAGTA ACGTTAACCG 480  
ATTCAACCAC GGTTTCACGT AGCGGGATG GATTGGAGTT CCAAGTGCG AATCTAAAGT 540  
TATCCATTGT AACTCCTAAG GAATCCAAGC ACTTCAGGT CGATTTCATC CCTCGTCCCA 600  
ATCAATTAGA CTCATCTTCT CICTAATCTG TTGCATTGCA GCOCTCTGAC ACAAGAGGC 660  
ATATCAGCAC CCACATACCA TGGTTTCAGC AGCTAGCACT TCCAATCAG TCATCAGCCA 720  
TCTCANTTCT TGNVTGGAT GTTTAAATTC CCACCTCCA GTGCTCTGGA NACCANTTTA 780  
TTNNGTCAA TTTACCAACT TTTAGNCGN TNNATG 817

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 831 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1284UP



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

5 GATCAAGCTG ATATGTATTC TCGGCTACT GGTCGTATCC GTGGTAATCT TCTTCGGCGG 60  
 CGCTCCCAAC CACGACCGTA CTGGCTTCOG CTACTGGAAG AACCGGGGC CCTTTGCGAT 120  
 GAGCCTCGCG CCAGGAAGCA CGGCGCGTTT CTTGGAAGTG TGGCGCGCGG TGATCAAGTC 180  
 GGCTTCGCC TTCATCCTAT CACCAGAACT TATAGGCAIT GCATGCGTGC AGGCGCAGGA 240  
 10 CACCGGGCGG AACACTGAGA AGGCATCGAG ACGTTTCATA TACCGTATTA TCTTTTCTTA 300  
 TGTGAGCTGC GCGTCATGA TCGGCGTCAT CTTATCAAGA ACTGATCOGA AACTCATAGA 360  
 GCGCTGAGAG ACAGGGCGCG CAGGCGCTGC CTCTTCTCOG TTGCTGCAGG GGATTGCCAA 420  
 15 CCGAGGGATT CCGGTGCTCG ACCAAGTCAT CAACGTGCGG ATCTTGTCCTT CTGCGTGGTC 480  
 GGCAGGCAAC TCCTTCATGT ATGCATCCAC GCGCATGGTG CTAGCGCTTG CGCGCGAGGG 540  
 AAATCGGCCA AAGTTCTCTA CCAAGATCAA CAGATATGTG TGCCCTACAA CGGGTCATC 600  
 20 GTCTGCACGC TGTTCGCTG TCTTGCTAC CTGAACGTCA AGACGACTCC GCAATGTGTT 660  
 CCAGTGGCTG TCGAACATAT GCACCATCTC CGCTTCATCC GCTTGTTGCG CATGGCTCCC 720  
 TTATATCCGT TCCCGGGCGT TCTTTTCACA CTCNNANCN TNCCTNCCA GTTCCCTGCA 780  
 25 CCNTTTCNCC ACTATTCNT TMTAATGINT CTTTTINGAC AATGTTCCCT C 831

## (2) INFORMATION FOR SEQ ID NO:374:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 817 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1285RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

40 GATCCGGGTC CGCCACAAGC TGCTGGTCCA CATCGTGCTG CTGCGCGGCC CCCCCGACGC 60  
 GCGCGGAAAG AAAACCGAAA TCAAGGCCAG CATTCGGTT ATGCTCTACA TATCGCGCT 120  
 45 CGTACCTGTG CAGGGCGCA CGTCTGGT TGATAACGCT GCGCGCTTCC ACATCGTCC 180  
 CCGGTGCTG ACAGACCTAT TCCGACCGG GAGCGGGAC TCACTTCGA GCTGGGACG 240  
 GCGCGGTCC TACGAGTGC GGTGCACGA TGGCTGTAC GATGGGACG TAGGCTGCT 300  
 50 TGCTTCGGC AGGGGGGCC CGCCGATTC GGCGCGGCC CGCCCCCGC CCGAGATTC 360  
 GCCACTGGGT CTCTTCGCG CCCTTCACG CTTGTGTTG GATGATCTAA GCAGGGTCCC 420  
 CACGTACCAA CAGCAGCAG ATGGACACTC CCTGCCATTG CATCACTCT CCCCCGGTA 480  
 55 TGCGGCCACC GCGCAACNG CCGGGGGCA ACAGGCACN TGACAATCAC TTNTGGGTG 540

CGTCGGGGCC CCCCAGACCC CCTTGGGCCC TTATCTGCCC CCCCCCAAAC CNACCNITGCN 600  
 CCCAATAGGG TCAAACCGCG GNGTTGGNAA TTINCTTGNT CINGNNNNG NGNGGGTTTT 660  
 5 GGGCCCCCCC GGTINCCCCC CNANTTNGC CCAANCGGAA NCCGGGGAGG GTINNINGTN 720  
 NNNGTAAAA ACTINTACCC CCCCNTTTG GGTNCCNGGC CGNGGGTTT TTTTTTTOCC 780  
 CGGGGNGCCC CCCCNGGG ACCNTTNGG NACNATT 817

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 831 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1285UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GATCTTCTTC ATGACGCTAC TGTAGACAGT TTCACAACCG ATAGCCTGAA GACACAGTAC 60  
 25 AACCAGAGCA AAAGATATCA ACTGTTTCGG ATTCGGTATT CGGAGCATTC CAGCTTTAAG 120  
 GACCTAAGTA TTTTGCACAC CACGATCCAG ATGAACGCCA TTCGATCTAC AGTGAACCTG 180  
 30 GCGTCFTTGG AGATGCATCG CATGTGGTTC GACACTTGGT CTGTTATTAG AAACGAAAAA 240  
 TACCTGGGTA AATTATGATT ACATGTTATA TATAGTAAAA GATAACAGCC CACTCAGTGT 300  
 TAAATGGTCC ATCATGCTC TAGGACTCGT TGTGTTGCT CGACAGAACT GCAGTCCCCA 360  
 35 TTTCCTGGT AGGTTTTTGT GAGGCTTTTT TCTAATTGTC TAATTTAAAG TCCTGAATAT 420  
 TATCTCCAA TTGTGGAATG AAAGACACAT GTACCACTAG AGGTTCAGCC CGATGGCTGC 480  
 AAAACGGCAT ATTTGTCATC CAAATCATGC CGCTGGTCCA ACAGTTTAAT AATGTCTCTG 540  
 GAACTTCGAC TACGTCCGGA ACTGCTCTAT CATCTGGAAT ACCNCTCCT GTTATGCNTT 600  
 40 ACCATANTCC CCTCCCTTGG TGGCCNAATT CTTAANCAAT TTTTGNITAA AINCCCCNT 660  
 GCTTNNTAA GTTNAATTCC NNTTGGCCCC CCCCCTCGGG TTINTCCGTT CTTTGGGAATG 720  
 45 GAGGAAGGCC AGGCTTGACC CCAATACNC GCGCTCCGGG AAGNGTCTC CTINGCCTTN 780  
 CCCANIGGNN TNCCTGGGTT NGNGCAAAN CNACNNNGG CCTCCTTNCN C 831

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 802 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1286RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GATCGCACCT ATAATGAAGA CCGTTTITTT TTTATGAGAA ATAGCAGCCC TCCAGGGGTT 60  
 ACTTATTAAA TAGCTACAGT AAGATTAGGT TATTGGTTTG CAAATTCATT GGTAGATCAA 120  
 CTTGTACACT TCAAATAATG CTTCGCTGGC ACGTCATAA AACATGTTAT GCGCGGTGTT 180  
 GACAACTACT CTGAAGCTAT AGTCAGGTA GTGGTGCCA TTAGCTGGAC ACACCTTATC 240  
 TTCCTGCGG ACCAAGACAT GCGCTGTGCA CCGCTGTGAG AGCAAAGGTG GCGCGTTAAT 300  
 TAGGTCITGC CAGCCTAGAA GATACTAGT GATGGATTG GTGAAACTG CTACACCGTC 360  
 GTAGAAGTGA TTTAGCTTCC TGTACTTGT CCGCATGTTG GAGAAAAGA ACTTAATTCC 420  
 GGAGCTGTC AACCTTCAT CTGGTCGAAA TTGGTCTTA TGAATTTGAG AAGCATGATC 480  
 AAGAAGGGCT TGAAGAATGT TAGTGAAAGG TTTAGATATG GCTCGACGAT ATCCAACTTT 540  
 GATTGTAGAG TTCTAGGTGG CCGCGCGCC AATAGAATGA TCTTCTGCG TTCAATTGTT 600  
 GACGCGTAT CCTGAAGGCT AATGCCAAGC CAAATGCACC CCATCNATTG CCAAAACTC 660  
 CCACNGACAT TATTATGGTT GGCNCGTAGA CCATGAATCT AAACCCCTA TCACNCACCC 720  
 CCCCCACANG GTTACCATGG CCGATGTCC TTCCCCANCC TGAGNTCNAC CCGATTNTCC 780  
 CCTATTTC CACATATCT CC 802

## (2) INFORMATION FOR SEQ ID NO:377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1286UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GATCTTCGCA GCCAGCGCGT AGTCCACCG CGTCAGTCC TCGCAGAAG CCGCGCGTG 60  
 CACGTACAGC ACCACCGGTT GTCTGGGTG CCGCTGTGCG GCGCGGACA CATACACCGC 120  
 GCGCGCAGTC CGCTCGCGG CCGCAGCGC CGGCCCCCG AGCTGGAACA GGTGCTATC 180  
 CTGCACAACG TAGTCTCTCT CCAGCCTTC GCGCGCGCG TCGAACGAC GCGCGCGTG 240  
 CCACCAAGGC ACGCAGTCC CGACGACGC CCGCAGCGG GCGCGCGCG CCGGTCCGC 300  
 GTGCGCGCG GCTCTACGC CCAGCAGTCC CAGCAGCGT CCGCGCCCC CCGCGCGCAC 360  
 CACCGAGTAT ACCAGCGCG CCGCGCTGC CCGCAGGCC AACCCATAGA ACTTCAGCAG 420

AAACGGAGT ACGCTCCAG TTTTGTITGG AGATCCCATG ATGCGCGGCC GAGGGACGTC 480  
 GACGCCCCGC ACCTGACGGG GCGGCTACTT ATACACCACA AGATTCTATA GAAAAGGAAT 540  
 5 GCGACCAACG ACGAACGGTG TATCGITTTGG GAAAAAAGG AGTCCCCCAA CTAAAGCTTG 600  
 CTGCTGGCT ACGAGITTTGT GTTTCAGGTT TCTTCATAGC ATCCAGTTG TTTTGTITGT 660  
 TTGGCAAATC GCATATGAAC CATAAANAT CAAANNITGT ACAATTGCTG CGACCGTTG 720  
 10 CCCATCCNC CGCGGAAANA TCCAGAAATC GAGANAATTT CAGACGCGG GTTTGCCAAA 780  
 NTCCGAAAC CCCAAANTOC CAACATTOCT GNCACATTTG ATTCTGNNNC NNCA 835

## (2) INFORMATION FOR SEQ ID NO:378:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1287RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GATCCCACTG GTATTAGGTG TCTGAACACG GCCAAATAAA ATACGCAAAA TGAAGGCGAT 60  
 30 TAATAATCTT TCATCAGTGT TGACAATAAC CCTTGACTCA TTCTGAGCAA ATAACITTTG 120  
 TACTTCGTGG TTGAATAACG TGTATCTAA TAAGTTCITC AGATTGTCCC TATAITTCAC 180  
 AGCTACTGGA TCCTTGTATG CTAACAACGC ATCTAGGGCC AGTTTCTGCA CTTCAGCGT 240  
 35 TCGACTACCC AATAATTCCA TCAACCTTTG GCGGACATCT TOGGATTTGT AAATAGCTTT 300  
 GATATTTCTG AACTTGCCCA ATAATTTCAA AATTAGATTC CTATCGTCT CAGACCATGT 360  
 ATCCGCAGAG TGCCTGCTA ACTCACCAG ATGGTCTTCA TCTTGGTTGG CATCGAATTG 420  
 40 ATCATTCGGT TTAAAGACAA AAGGTACAAT GAATCTGCTA TTTTGCTOCC GCGAGCTGTN 480  
 GCAGCGGAT TAATATCTTC AATGCTTGTT TCTAATCATA CGGATATCC GAGTGAACCG 540  
 CGANCCCTT TAAGGTTTTC CAACCAAGGA TTTTTCGAAA NCAACATNCN TTNGAACNT 600  
 45 TCCNAANNCA AATAATTNAT CCTAAAAAAT TINTGCCNA NTCCAAAAAN TCCCNAGGG 660  
 GTNNAAGAG TGGCCCCAAA TTCNAAATNA GNGVTTTTIN GGNVTTINOC NAAAAAAAT 720  
 CCCNCCNAC CNGNNTTTA ANAATTTTIG GGAANCCAT TCCCCCCCCA AGGGGAAAAA 780  
 50 AGNGTGNNCC CNATTTTNA 799

## (2) INFORMATION FOR SEQ ID NO:379:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1287UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GATCAGGTGG	TGTGGCCGA	TACCGTGACG	GAAATGGATG	TCCTGGCCAT	GCCCGAGATA	60
GATTTCTCTG	ACACAACGTC	CTCTCGAAG	GGCTGATGC	GGCGAGAGCG	CTCAATGGAG	120
AGGCACGTAC	AGGCGCGGAA	CACCGTCACA	GACCATGGG	ACATGTCTTT	GGAAGTGGGG	180
AGAAGATACG	CCCTGACGA	CGACCTGGAG	CAACAGACGT	CGCTACTGGA	CCTCAACTTT	240
GAACTCAGTG	ACATGCAGAA	CTCCAAATCT	TGGGTGAAG	GGACGCACAA	TTCCGAAGAG	300
ATCAGTGOCA	ATGTGCTTGC	AGAGTCGCAA	CGCCAGGAGC	TGCCCCGGAA	CGAGGCATT	360
GAGCGTGAAG	AGGATCTTGA	TTGGAATCTG	GGATTCACGG	AACCAGCAAT	TGTAGTCCCT	420
TCAAGCGATT	TTGAACACGA	TAACAGCATA	GAAGTGGGCC	GGAGAGCAGT	CCCCGAATGC	480
GGACCTTCAG	GAAACTGTGG	ATTTGGGATT	CGACTTGGAT	ATTGCCAGGG	TTGACATTGA	540
GGCTACAGCC	GGCGAGCAGA	TGCTGGCAGT	TTGCATCTGA	GCTTTCCGGA	AGTATAGTAC	600
GTCCTCTCTG	AACACTGTC	ACANCCAAAA	CAAGAAAGGC	ACCTGGTTAT	CAATCTTACA	660
TTCAACCCCA	CCGATTACT	GAAAGGTGNT	CNAAAACCCC	CCCNACANTG	CTCCNTGANT	720
ACCCATCCCN	NCCCATTCN	NCCCNAAAAC	GGNINTGAC	CCTTTNAAAT	GATCCINCAA	780
TTTTGCNTGA	CATCTGCTC	NITTOCAACG	AGNCCCA			817

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 787 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1289RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GATCGGGATT	GACCGTAATA	TTTCAGCTTT	TTGATGTGAA	TTGCCAAGAG	GACCAGCGAT	60
TTGAATCTCG	CTGACTCTGT	TGTGAGTAAT	TAGTACAAGA	ACCTGTGGCC	TGTCACAAIT	120
AAGCCCTGGG	AATAGGACTT	CAACTTCAGA	AGCCACAGAT	CGTCAAGCGA	TGATACAAGT	180
GCCTACCAAC	ATTGACTTAA	CATGAAAATT	GATAGCATTT	TTATAACAAT	GGAAGCAAAG	240

GACTAAGTCC TTCAAGTGGT GCGCAATGCA GCGTGTTAGC AGGTTTGGC ATATTCCTGG 300  
 AAGATGTCAA CCTTCCAAAA ATATTCCTCA GAGCATTAAAT TATCATTACA CAAGCCCTTG 360  
 5 GGTGAGACA GAATCTTGAG AGGTGCTGCG ATAAACTCA AAATGCGAGT GCTTGGATT 420  
 TAGGGCTTAT ATACTGATTT AAGTGGTGGT GGTTATCTAT TCAGGGTTGT ATAAATTAAA 480  
 ATATCACAGT CGGTATACTC TTACACACTA ATTATAATCA CGTGATATTT GACTATTTAT 540  
 10 TACACCAGGA CACCTGCTA TGAAAATAGC AACAGGCTGA TGGTATTAAAC ATCTGAAGAT 600  
 ATCGCCAACA TTAGAACACA CTACTGACAC AACGGCCAGC CATTGAGAC TATGGCTGCT 660  
 ACTACTGCAN TACTGTCATG CTTATCTGAC NOCTGACCNC TGATTGTTGC GGAAATCCT 720  
 15 TTGATCNGCA AAATCATNCT GNTGACCNCA ANTTCTACTN TATTAACCCC CCCACCGCCA 780  
 ACCCTTG 787

## (2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 788 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1289UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GATCCAGGC TGCCCCAGGA TGACGGAAAG TTGCATGTC TTTCGGGCGC TACAGGCTCG 60  
 35 CTTTCGGTAC TGAAGATTAA ATCGATGATC AAAAACTCG AAGAGATTTA TGGTTGGGAC 120  
 CATATATCCA TTCAAGTCAT ATTAAC TCA GCGCTGCGC AATTCCTTTC TAATAAAAAC 180  
 CCAAGAAGA AGAACCTTTA CGTGTCTAGC GAAACAACT CATTCTCAA CTCCGTGGCT 240  
 40 CACCAGGGGA AACTTGCAAC AGAACAACTC AGACGCATCC TACACTGCGG TAAATAGGCT 300  
 CTCCAATACC CCTGCACTTG GGGGGCGCAC ACCAACGCCA GCAGATCTTC TCAGGGGCGC 360  
 AGCGCCGCAA GCGCGGGCT CCGGTCTAAG CCAGGGCGCA GCTGCGGCGA AGATTGAGCT 420  
 45 CCTCCACAC ATACAAGTCT GGACGGATCA AGACGAGTGG GACGTGTGGA AGCAAAGAAC 480  
 AGATCGTAC TGCATATTGA ATTACGCAGG TGGGCGATAT CCTTGTGCTC GCGCCACTTA 540  
 CGCGAATACA CTTCCAAATT GCGCTGGGCG TTGTTAAAC CGCGAACAT GTTCNTCGG 600  
 50 NVTGNAACCA NTTTTCCAAT TCCTNCNCCA NCGNGTTT NENINNTNA ACCCCCCCCC 660  
 TACCCCCCN AAAANAANAA NAAAAACCC GTTNTCTGTG TTTCACCNCC CANAAAAAG 720  
 GGTNCCCCCG GAAAAACGAC TGGGGGAGA GAGAGGNANN AAATTNCNAN AATCCTTTTA 780  
 55 NCCNGGG 788

## (2) INFORMATION FOR SEQ ID NO:382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1290RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

GATCGCTAGA TGCCAGGAT GAGACTGTTT AGGTTAGGCA GGTGTTGTAT GCGCGGCAG      60
AGGGAAACCC AATGACTTTG CATAGAACAA ACCCGGCATC ACCCATGTCT TGCGCTGTAT      120
AGAGACTAAG GTATCTGACG ATCCCTTAGC GACTCTCTCC ACCGCTGAC GAGGCATTTG      180
AGCTCTTAGC AACTGCACAA ACGTACTCGA ACTCTGTTTC CAGACTTCTT TCTGTTGTTC      240
TTCAACTGCT TTGCATGAA GTACCCCGCA GGCTATTTTT CTTACCGGCC TGGTGTGTGT      300
CTATATACCC GGTGTATTTT TTGATAAAAA ACTCAGCTCT TCTCTACGG CAGAAATATA      360
TATCCAGTCC TTAGCGCCAT GCGAAATCT GCCTTTTTC ACCTGTTTCT CCAGTCTTA      420
GCACTGGCAG AAAAAAGATG TATGGGTAT AGCGCTGGC CCGCGGAAA AAAAAAAAAA      480
ATAGAAAAAT AGAAAAATAA AAAGAAGTGG GCGGCCCCG GGCAGACGA AGAAAAATA      540
GGGCGCCACC CCTCCAAGCA GACGACAGC GAGACATAAT AAATCCACA CCAAGGGAAG      600
AAGTCTTGIG CACGCTCCCG GCTCATACG CTGCAATCT GTTCCATCC GCTTGCAACC      660
CAGTATGCAT GTCAAGCATG NTCGAGCTC CGCTGCTTGG AGTGAATCT CTTCTACCC      720
AGCCGAATCC CATACTTGCC TTCACATACA TACCTTTCAT T      761

```

## (2) INFORMATION FOR SEQ ID NO:383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1290UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

GATCAGACAT GGTGTTTTTC GGCCTCGCT CCTTGTGGT GGGTCACCG CAGTTCACTG      60
GGCCAGCATC AGTTTTGGTG GCAGCAGAAA CCTTAGGAA TGTGACTTTC TCTTCGGAGG      120
AAGTGTATTA GCCTAAGGTT ATACTGCCAA CCGGACTGA GGACTGGGC TTGGCCAG      180

```

EP 0 866 129 A2

GATGCTGGCA TAATGGTTAA ATGCCGCCCG TCTTGAAACA CGGACCAAGG AGTCTAACGT 240  
 CTATGCGAGT GTTTGGGGTGT AAAACCGGTA CGCGTAATGA AAGTGAACTG AGGTGAGGGC 300  
 5 CTCTTTAGAG GTGCATCATC GACCGATCCT GATGTCCTTG GATGGATTIG AGTAAGAGCA 360  
 TAGCTGTGTG GACCCGAAAG ATGGTGAAGT ATGCGTGAAT AGGGTGAAGC CCNANGAAC 420  
 TCTGGTGGAG GCTCGTAGCG GTTCTGACGT GCAAATCGAT CGTCGAATTT GGGTATAGGG 480  
 10 GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTCCTGCCG AAGTTCCTTC CAGATACAGA 540  
 ACTCCTATCA TTTTATGAGT TAAACNAATG ATAAGTTACC GGGTTGAAAT GACCTGACTA 600  
 TCCCCACTTT AATAGTTAGA ATCCCTGTTG CTTATTGAC 639

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1291UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GATCGTGCAC GGCAAGACGT CGGAGCTGCG TCACGACGGG CGCGGGCTCT TCAGGGGGT 60  
 ACCCCAGGCC GTGGCAGTGA CACGGTACCA CTCGCTGGCT GGACTGGGCT CAACGTTGOC 120  
 GCGCGAGCTG GAGGTGACCG CGCGCACGGA GACAGGCGTG GTTATGGGCG TGCGGCACCG 180  
 35 CAAGTACACC GTGGAGGGTG TGCAGTTCCA CCGGAGTCC ATTCTGACCG ACCACGGGCA 240  
 GCTAATGGTG CGCAACATGC TAGCGCTGGA AGGCGGTACG TGGGCTGAGA ACGACAAGCT 300  
 CCAGCTGCCG GCAGCGCGCG GCTCTGTGCT GAGCGAGATA TACGCTCAAC GACAGGAGGA 360  
 40 CATGGCAGCG CAGATGGCTA TGCCGGGAAC TGGTATGGCG GACCTGGAGG CGAGCTTTTCG 420  
 APTGGGGGTT CTGCCGGCGG TGGTGGACTT CCATGAGCGG CTGCGCGCGG ACGCCCGCGG 480  
 CTGGCTGTGG TAGCCGAGAT AAAAGTGGT CTCCGTGCGG TGGCAATATT AGCGAGGCGC 540  
 45 TTGGCNCCAN AANANGCGCT TNCNINTTGC CGAAGGCGGA ATTTTCGGCC ATCTCCGGTG 600  
 CTTTACCGAA CCCACTGTTT TAAAGGGACC CGCNAGANCN NAATTATTNC CCGACCCNCC 660  
 CTTTGANAAA AACNANACTG CCCAANACC GCGCGGTTTG CTNCTTTANG ANATCTTTAT 720  
 50 TNCNNTTCC AATNTTTGAA GCGCGNTTNC GGCNACAAT TTCCCTTATT TTNAATTTT 780  
 NAACCACCCC CCCCAGACC NTTTTTTTTIN CCC 813

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 773 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1292RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GATCCGTGTA TTTTATTATT ACATTATTTA ATTAAAAATA ATGATTTAAA TAAATATTTT	60
TTATAAAAAA TAATTAGTGC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAAACC	120
ATCAACTAAT TGTATATAT TTAATAAATA TTAATTTTAC TTAATTAAGA ATTAGGAAC	180
TTATCTATTA GTCGGGGCTG TTTCCCTTTT GATTATTAAC CTATCGCTA ATAATCTGAA	240
ATATTTAATT TTAGATTAAT AATATATTCT GAGATTTAAT ATTTTAAATA AAATAAATAA	300
TTATTCCTTA AATAATATTA ATAACIATAC CATATATATC TAATATTTAA ATAATCATA	360
TAACATATGT TTCGTAGAAA ACCAGCTATT TGCAAATCAG ATTGACTTTT CTCTACTTAC	420
CATTATTCAT CAGATAATAT TGCTACATTA ACCTGTTCAA TCGTTTTTAT ATTTTATTAT	480
ATTTTAAATA TAATAAATAT ATATTTTAAT CATTTGATAA TAGTAAGATC ATCTGCTTTC	540
GGTTTAATTA ATATTAACIA AATTTAATTT ATTTTAATTA ATTTTACATN GTTAAANATT	600
TAAATTAATT TTAAACCAN TTTTATTTTN AAATTTTGN AAATTAATAC TGGGGGNCCC	660
CTTCCAAGG GGCTNNNNN NATTTTNTA AAAAAATAA AAAGGGCNN ANAAACCTTT	720
TAAANTTCC CCNGGGCCCC NNAANANINA AANATTTNAC CCNAAAGGTC CCN	773

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 798 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1292UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGTTAA	60
CAATAAAATT CAATAATTTA TTTAAATAAT GATTAAATAA TCTCAATATA AAATTATTTA	120
TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAATTTG	180
TGCCAGCAGC TGCGGTAAGA CAAAGGGGGT TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240

GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA 300  
 GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA 360  
 5 TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTGATAC CCGAGTAGTT 420  
 TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA 480  
 AATTAAAGTA TTCCGCTGA TGACTIONT TGCAATAATA AAAATCAAAA CAATAGACGG 540  
 10 TTCCGACTTA AGCAGTGGAA CATGTTTTTT AATTGATAA CCCCCANAA ACCTTACCAN 600  
 TTTTNGAATA TTTAATTATA ATAATTINIA ATTATTACGG NGTGCATATT NTCTTCCCTC 660  
 CCGCCGCCNA GTTTTTINAAT TATCNINAAC GAACAAACNC CCATTTTTTT TTINANAAAA 720  
 15 ATTATTTATT TTTTGAATAT TNAAAAAAA TAAANATCCT TTNTCCTTTT TAATGGNGA 780  
 GTNTTTTTTT TTNTCN 798

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 762 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1293RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

GATCACCGAG CAGCTGGTTC GCTCGGCAT AAGCGGCTT GGTCCTGCC CACTGTTCTC 60  
 CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTTAT 120  
 35 GTTGTACAC CTCTGGGTGG GGGCCCTTGA GTTCGCTTC GAAGCATGAG TACAACAGTC 180  
 TCATCTCCGC CCAGTATGCG TCTAGTTTGA TCGCATGATC GGGTCTTACA CCGTCCGGA 240  
 TATCGCCACC CAATGAGGCC TGCAAAGCG TAATGGAGGG CTGGGAGGTT AAGCCAGACA 300  
 40 TOGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCGATTGG ACCATTGATG 360  
 CGACACCTGT GCCTGCAGAA TCATGTGTAT GCACATGAAT TGGGAGGTCT GGATACTTTG 420  
 CCTGATCGA GCCAATCAGT AGCTTTGCTG CACCGGCTT CATGGTGGC GCCATATCTT 480  
 45 TAATACCCAA GATATGTGTG CCCCATGGCA ACAATCTTTT CAGTCAATCC AGTAGTAATC 540  
 AAGGTTGTAC TTCTTGCTG CTGTAGCATA TCACCTGAGT TACAGATAGT GCTCAACCAC 600  
 CCTCCGCTT TCTTCACGGG TNAAACCCA CTTCAGTGT CTAGTCTTCA CCNTCNAN 660  
 50 CTCTGAAATN TCANNCATCC CTTGCTGTT TGACAAATGT CATCCNTTT CCGCNAAAGA 720  
 ATTAACACCC GTGGCCCCAA CNOCTGAAN GATTTTGCCC NG 762

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 805 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1293UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

GATCTTACAT CTGACAACAA TACGCTGGCG GCAGATGAGC TGCATTGATG GAAATTTTAA	60
CACAGCTCGG GCAACCAGCT ACACGGGATA TATAAACTCA ATGCACGCGC CTCCTTACTG	120
ACACAGTCCA TCAGCATCAG CACCACCCCC AAAAATGAAG ACTACACACA TCCTATCCCT	180
AGCAACACTT GCGCGCTGCG CACCTGTTC A GCGCACCT GTTCAGCCCA CGGACCTCGC	240
CGCAGCGGCA AACGTCCCCG AGAAAGCTGT TCTCGGCTTC TTCCAAGTGT ACAATGTGGG	300
CGATGTGGAG CTGCTCCAG TGGACGACGG CGCACACTCC GGGATCCTTT TCGTGAACCG	360
CACACTAGCG GACGTGGACT ACTCCTCCGA GCATGTGGTT CAAAAATGGT TCCGTCTGTC	420
TCTCCACCAT GGGCAAAGTA TGTAAGGCCG GACCAGAGAC AGTTTGGGTT GAGATATGTA	480
AGTTTACTTG GTGTCTTACA CCATGCATTA TGACACGGGC TTACGTACCT GCTTCTATAA	540
GCTAGTTTAA ATGTTTTCTA TGGTATTTAT ATGGTTTTACC CGCGCCGATA GTTCGCAGAG	600
GCTGCTGINT TAAGGCCNAA CTTTATTCCT AANANGGTGG ATTACCCGGT NGAAANAATG	660
AATCTGAATT GCGGAAATTC CGCTGGNCT ATTANCTCCC CTTCCCGTCC NAATAAATGG	720
AANATGGTGG GGTTTAATAC AAAANGNCC GVTGCGGCA ATGNACTGGA TTAATTTCAA	780
AAACCTCCAA NTACCCCCAA NTGGN	805

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 764 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1294RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GATCCGAAT GTGCTCAAG CTCGCTGCT TTCGGCTGGC CTCGCTGTC TCTGTGGAAT	60
CGTTTCTGGT GGTCTCTTC TCCCATGTTG ACCTTGGGTT CAGCGTCTTC AGCTGGTACA	120
OCTCGAGAAG CTTGAGTTA TCGAATGCAA ATGGGTTTAG CATCTCGACC ATATTGCTG	180

CGCCACCTGC CTGCCCCCTTT GGCCCTACAT CGGGAGTCCA ACTTCAAAGT AATGCTATAG 240  
 AAAACGCCAT TGGCCTGGCC GTCTTATCAC GTGACTGTTC ATTGAGCTCG ACAGCTACTC 300  
 5 GACTAGCACT GCTGCTGCTT TAACTGGGCT ATACACTTTA TATCGTTACA TTACTTTCTC 360  
 CGTGGTCCGC GGATGGGTGG TGGTGGCTTG TGTGCAGACT CACTCTTGAA CAGAGGAGCG 420  
 TTCTTAAACA TGCTGTGTAC GACAAAGAAC CTTACGTGG AGCCTCGCA CGAATACATG 480  
 10 GTCCATATGT GTCACCTGGC CGTTCGGTGC CGTGGCTGTC ACGTCTCTTA GCTGGCAGTC 540  
 ATGTGTGCTT CGCTGCCAC CAACTTGCCC CGATAGTTTC GCGGTGCTT ACTCCAGCAN 600  
 ACCGTGTCG TINGGCTTC TTCACACTTA CAGGAATCG GAANTGCCAG ATCNTACTTT 660  
 15 TTGTTTGGC CGTTTCCTT CCGTACANAA ANTGGTTTAT ATTTTGGCG AAAAGNITTA 720  
 ATTTTACATT TTCNAAACAA CATANGTTC NTTTTTACNN AACC 764

## (2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 800 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAGL294UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GATCTGGAAC TCCAAGTTC TGATGTCTG CTTACGCTTC TCTGGCTGCT CATGAATCGA 60  
 CTGCTGCTTC CACCGAATGA ACGACCGCTT GTCCACATTA GGATGTACCT CGATGTCCGA 120  
 35 GTCATCCGAG ATTCTATCTT TGTCCACTT TGAGTAATCG ATTGCCATTG CACTACCTTG 180  
 TTTGTTCTG GCTTCACTAC TGTGTCTCTT AGATCTTCTG GATOCACCAA TAACTGATAT 240  
 CAAAGATTCA TATATGCAA CGTCCAATA AATAATGTTA CACATAAGGA AGGACCAAGG 300  
 CAACGCTGC CCAGTCTAG CAACTTCTGT GTGTACTCT CAACGATAGA AGTCTGTCT 360  
 CGAGATGTTG AGACGTAAT CGGCCACAGC GCTGCTGAGG TGGTGTACGG TCAAGGTGAC 420  
 CTGTGTGCA TTGGTCTTTT CGTTTGTGTG GTGCTGCTGC TGGCTGATCT GCTGTGTGCC 480  
 45 GGGCTGCTGC TGACCGAGCA TCAGTGTGTC GGGCGGGGC TGGCGTTGT TGGAGTTATG 540  
 GACGCGAATG AGGAGCGAT ACGGAATACT CGTAGCGTT CCGCCGCTAT GTCGCTAAG 600  
 AACTCTGTTT GCCAACGCA AGAAGGCTT GACCGANAT CNGTGCACNC CGAACCGTCC 660  
 50 TGTTCANITA TTATCCATCA CACNTCGGA AAAAGGGGG GGTCTCTCT AAGTCNAAA 720  
 CNGTGANGT CTGTCTTGC GTGGAATCG ATTTCCAAA CTCTTTTCT NCGGTTTGGC 780  
 CCNGCGGCC CCNGGGNGA 800

## (2) INFORMATION FOR SEQ ID NO:391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1295RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

GATCTTTTCT TCAAATTTGGG ACCAGGTGCT TAAGTCATCC TGATCCTGCA CAATCACGTC      60
CATATTGGCG GAGATCAGTG CCGTTTGGC ACCAGAATCG CTGCCCGGCC AGGTGACTAG      120
CAATCCGAGC TCGTTGACAG TTTCACCTT TAGCTTACAC CAAACCAGAG GAAAGTCCCG      180
CGACAGCTGC TCGTGCAACC GTTTGAACTG CTTGTATGTC TCCGTGTGG ACTTCACCGC      240
TGTCGAGCAG TCCGCTGCAT CCACCAACCA TGCCGAGGGG ATCTGCACTG CACGCTGTAG      300
CTTCTCGACA GTGAGATTGC TGAGCGTCGA GTTGTGCAGA ATTTGCTGGA GGTGGTCTCC      360
AAAGCCCCCC TGAGGTTTGG ACACGTCCCA GCACGATGGC AGTGACGCC CAGTCACTC      420
CGAAGAAACA ACAGCACTCC GCGCTGTCTG AGCAGAAAAG CAGGCCAGCA ACGCCAGGCG      480
CGTTGCAAAG GATATCGGTT GCCCCAAAG CCAAGCTGCA AACATCATTC TGGTGGTCAG      540
CGACTGCTTT TCCACGAGA TCCGTGGGGA CCATGCGCCA GATGGGGGCC TTAATATAAG      600
CCCCCTCTCG CCAGCATGAC TTCTGCCAAC TCCGAACAT TCTAAATGGC CAGCTGCTGC      660
TTTGATGGTA CCTNCCGCG CTNGCGCAA AATTNATATA CCATAATCCC CNTCCTAAAT      720
ATNCTTACAT ACCACGCCCC AAAGCGCTCC CGNAGCNEN CCGAGCCCC CACTTTNCC      780
NNAAGNANCC GNTGNG                                          796

```

## (2) INFORMATION FOR SEQ ID NO:392:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1295UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

```

GATCAACTTC AGTTCTGCGC GTTGTGCGCA TGGAGGCCCG CCAACGGCAG ATAGCTTCTC      60

```

AACTGTGGCG GTACCCCTGCA CGGGCTCCAC GACCGCTGTG CAGTGGAAAC GCTCGTAATT 120  
 GTTCTGTGGTG TAGTGTCTGA AGTACTOCOA AGAACCACAG AATGCGAGGC CTGCGAGGAT 180  
 5 ATAGAAAACC AGCGTCCCGT ACCTACCGAT TGCCATGGTT GAAGCAAGGA TTCCACTGOC 240  
 GTAAGTACTC AATTATTGAG TGCTAGCAAG CTGATGTTGA TTGTGTGATA TCAACGGTAA 300  
 TCGGTGCTTA AGGAACCTTT TCAAGAAACG CAAAGAAAT GCGTGGTAG GTGCGAGCAGG 360  
 10 TGACAACCTC ATATTACTCA TAACAGTTAT CTATCTAAGA AGCGGCACTA TCGATATACT 420  
 ATCAGCTTCG TATACACATA TATATCGGAG GTTTATAATC GCAAGTTAGC TATAATTGCC 480  
 ATCGAGGTGT AATACATCGA AGATTGTCTA CGAACTACT CTGTACCAA CACATCAGCG 540  
 15 TATGAACAAT AACAGCAATA TTATGACAGG CAATTGCATA AAGTATTCA AAGAGGGTTA 600  
 AACAGTTAAA TTCGTAAAG GTTCAGNGAN TATTCCTGA CACCCATAC CGAATCGCCC 660  
 TGCACCAATT GTTCACATGT TCANAGATTC TCGGGACTT CATATGNACC ATGTTGCGGC 720  
 20 CCGNAACTCN CATTATGTNA ATGCTTGINT TCTGACTCC CCGCTTGTG CCAAATGCCA 780  
 TCCAGGGTG ANAGGTGCTC GTGATCTC 808

## (2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 779 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1296RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GATCATTGT GCGTTTGAG GTCAAGCCAC GGACGTGGAC ATGTAAGTGA TGAGCTTCGA 60  
 CGGGCAGCTC TTCATTGTG CGGCACGCAA GAAGCTTGAG TTCCCGAGCT CTCCGCGGGA 120  
 40 GAGTTGGGCG TACCTTGCGT ATTACAGCGG ATACAAATTC GAGCGCATGG CGCTCCTGGA 180  
 CCGTCCGGTG GCCGAACTC CGCGCGAGGT TCTGGAGAGC CGCGGCAAAC AGGTGCTCCG 240  
 CAACGGTCCG CAATACAGGA CTGTGATGAG AACCGGCGTC GGGGAGCACA AGCTGGTGCT 300  
 45 CGGAGCTGAG ATCGACGGCA TCATTGACTT CCGGAGGCT ACGGGGACA AACTGAAGCA 360  
 CTAAGTGGAG CTGAAGGTGT GTCAGAAGAA CCGGAATTC TCAGAGAAAC TTTTCTCTTC 420  
 TTGGCTGCAA TGCTTTCTGG TGGGCATAAA CAGGTTTATT ATTGGATTCC GGGATGAGAA 480  
 ATTCTCTCTG AAGAGCGTCG AGGAGTTTCA TACGTCAGAG ATCCACACC TGTTTAAAGG 540  
 GCACGGAATA TTCCATGTAT GTTGTGGACG CCATAGATTG TATGGTGCTC CTTACAAATT 600  
 55 GCTATNTGAC TCCCCCGGGC CCGTGAANA NITCAACTGT TACAGTCTCC TGCNNCATGG 660

TGCTTACTTT TGCCCCACTG CCCAACAAAA ACCCCCAATG GGANAAATTN TCCCTNGTTG 720  
 GTCCCCAATT GGNNGNCCC CCANATANAA AATTCGGNAT TATTCCTTG TTCTCTAN 779

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 815 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1296UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GATCGTACGG TTGCTGCTG CGGTTTACCG ATATGGATCG GTTGTTTGCA GTTGGCGAGA 60  
 GCACGGTGGT CGGIGTCTCT GCGAGCTCT CGGACATGCA ATACCTACAG CGCCTGCTCC 120  
 AGGACATGGA GATGAGAAC AACTACGACA ACAGCCACGC AGACGGCGCG GAAGCGCTCA 180  
 AGCGGAGCTA TATTTTIGAG TACCTTGCC TCGTCATGTA CCAGCGCCGC TCAAAGCTGA 240  
 ACCCGCTCTG GAACGCCATC ATCGTCGCG GGTGCGAGGA CGGCGAGGCG TTCTGCGTT 300  
 ATGTGGACCT CAAGGGCGTC AAGTACTCCG CCCCAGCTT GGCTACTGGC TTGCGCGCC 360  
 ATATGGCCAT TCCTCTCATG CGTAAAGTGG CAGATGCCGA AAAAGACTGG CCGCGCTCGA 420  
 CCTCTCAATT GCGGAGGGA CTATCTGGA GTCCATGAAG GTGTTATTCT ACCGCGATGC 480  
 GCGTAGTTCC CGTGCCTTCT CGCTTGCCAT CATGACAAT GATGCGGTG TTCAGCATGG 540  
 AGCAACTGGA AGTGGAAAC ATGACCTGGG GTTTCGCCCA AGGATATTCC GGGCTATGGC 600  
 NCCCAAATNT TTTGAATTAC CNGGGCGCA ACGCGCACC CTGTTTACTA TCTTGTTCCG 660  
 GGNVTGNCC CAACCGCTNG GNEATCCCAT ACNTTCAAAA NGCNTAATCA TCTGCGCTGA 720  
 ACCCNCCTGT TTTINGINGAN ACCTTCNCCC CTTTTCNGA TTTCGCCGAT TGNCAAAAAC 780  
 CCTTTGAAAA AACATTNCCC NITGGNAAAT CGATG 815

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 766 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1297RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

EP 0 866 129 A2

GATCTOCTCG ACGCTGGTGA CCTTGCCGGC CTTCACAAGA CGGCCCAACT TGGTCACTGG 60  
 CACCCAGGCC TTCTOCTCGA CCTCTCTTCT GCGCTTGGG CCGTGAGGC CCTTGTTTCT 120  
 5 GCGGCCGAAG CCGCTCTTTC TTTGTTCTGG AGCTGACATC TTGCTATCGT CGGAATGGAA 180  
 CACCGAAAGC TGGGGGAGTA ACTTTGATC GAGCTGCTG ATGTAGTTAC GATACAGCTC 240  
 CGGCCGGGG CCTTGGGTGCT GAAAACTGC CCACGGTCTG CGTCAACAGA AAGGAGTCT 300  
 10 GGGTGCTACC GCTGTTTCCG GCTCAAGAC GTGCTGGGT TTCACACTGA AACCCACACA 360  
 TCAGACAAAC GCAGTCCCGG ACGGCTOGAA AGCAAAACC GCGTGAAGGA GCAACGGGA 420  
 AGCTGCGGG TCGGTGCGA ATCTGTCAA AACAGGGGT CACAAAGGA TTGGCGCTGG 480  
 15 CGCCAGGACT GCTACGGGG CATTTGGCCC GCGGCAGCC CCGAGCAATG GAGCAACCC 540  
 CTTCGGGAGG TACGGCTCAC ACTGCGGTAT AAAGCGGGC AGAGCGGTGG AAGCAGACAG 600  
 TGACACACAG GAGAGGACAG ATGTGGACN NCAAAATGAC AATCTATCA ANAGNGCGT 660  
 20 CCGGGCCAAA CTATCAANAG NITOGAAGTT CCAAACTNGC CAGATCAAAA GCGCCCAAAG 720  
 GGAAAAACT TCCCCCCAC GACCTTTGN CATTTTTAAC CGCNG 766

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 795 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1297UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GATCCAAAA CAATGAAGT TTTACAATGT GGAAGCGTG ACACAAGTGA ATGGCGCTCA 60  
 40 GGACCGCTAG GAAGGAAGTC TATGTGCAAT GCATGCGGTA TCTGGTACAT GAAATTAAAG 120  
 CAGCGGTTTG GGGAGGAGGA TGCTGCGGTG ATTATGGAAT ACCGGAGATT AACTAATAGG 180  
 CACGATGATC GCAGGGTGCC CAAGAAATTT GAGGTCCAT TGCTGAGGT CGAAAAAGTG 240  
 45 AAGAGAGCCA TAAGAGCTCG TGTGTGGAG TATTTGAATG ATGTTGAAAT CCGGTTAAA 300  
 ACGAGGAGGC GGGGTTATT ACATAAAGGC AAGCGGGCA GTGGTTAAA AACAGAGATG 360  
 AAAACCCCTG CCGCATGAAG CACTGGAAGG ATGAAACCAG TTTGTCAGCC GGAAGGACAA 420  
 50 TACCGGGGG TAGGAAGTA GAGACTATGC TGTGGCATGT AAGGAACGTA CTTTATTTA 480  
 TCTAACATAA CTAGGGTTCT TTTGACCTGN TACCTTTGTA TTATCCTTTG AANAAGTAA 540  
 CCCCCNCTT TTAAAAANTT TTCNNNTGN AAATAAATCC CTTTAAAGA ACCCCCCCN 600  
 55 NAANCAAAAC CTTTNNCCCT TNGCCAAAC CCACCCAGAA ATTTTCCNC CNTTNCAN 660



ACANNGTITN CGAGATTCCC CCMTTTNGGC CNAAAAAANC TCCCCCGAN TMTVINOCCAN 720  
 5 AGNGCCCTTT TNCNCTCCCC NCCNANAATC CCCAAATTAG AAGGGGINTT CNCCCNNGCT 780  
 CCCCAGATC CAAAA 795

## (2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1298UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GATCTTCTTA CTGGACTGGC TGCTAGAAGA TAAACGATTA TGGCTACGTC AACTGCGGAA 60  
 CTGTGGGCC GCGTTGGAGG AAGGCGAGGT GGCACCTTTT CCAGGTGGCG CTGTGGTGGT 120  
 25 GGTCCTCAAC CCGAGTCACG TGACACAACT GGAGCGAAAC ACGATGGTTT GGAATCCCG  
 CCGTCTGGAC CTGGTACACC AGACACTGGC AGCTGCATGC CTCAACACCG GCTCGGCGCT 240  
 AGTTACACTT GATCCTAATA CTGGCGCGGA AGACGTCATG CACATATGTG CGCTGCTTGC 300  
 30 GGGGCTGCCT ACATCCCGTC CCGTCGGGAT GCTAAGCCTG CAAAGTCTAT TCATCCCCCA  
 CCGTGCAGAT TCCATCGGCA AGATCTGCAC CATCGGCCCC GAGTTCCCTG TTTGCTAAGG 420  
 TGTTGACAA CGATTTTGTG GAGCTOGACA TTGAGGCGG CAATTGCTCC AGAACTTACT 480  
 35 CCAAGAACAC TTGTGCCATC TGACCACCCC ATGGCTAACA GACCTAACAA CCCCCCTTCN  
 GAAGCAACCG CTGTGATTTC NATCTCCNAG GTCNCTCCCT ACCTATAACG CTCTTGTGAN 600  
 A 601

## (2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1299RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GATCTCCAC ATTGAGACGG TAGCAGCCA CATATTGGC TTGAACGCC TTAACGGCG 60

CCATTGCTCC CATAGAGCTT TCAGATTTCG TGTTAGGCTC CAACTCAACG TCATACTGGA 120  
 GTTTAAATCG AGTGGGTGCT GTTGATATCC AACTTGGAGG CGTCTTTTTT GTCCTGTAT 180  
 5 CGCTTGAATA GCGGCCAGG TCCCGTGGCG AAAATCCATA TATATCCATA TTGGCCACCC 240  
 AGCTTGTAC ACATAGAGGC AATAGTGCCA GTAATGCTC GAGCGAAAC CATGCAGCTC 300  
 CCCGCGGAGG AGGCGCCCCG CAGCGTCGGG TTCCATAGAC GCGAAGCCCG GCGAGTGGG 360  
 10 CGCAAGCTCA GCACGCAGTT CCTCCTGTC ACGGTATGTC CCCAGCCCGC GGTGCGCACA 420  
 CCCAGATACT AACACAGCAC AGACGCTGTA TCAGCTGATT GTCCAACCGG CGTACTATTT 480  
 CACGTTTCTG GCGAATGTGC TAGTGCAAGC GTTGGGCGAG GCGCGGCGAG TCGCCATAGC 540  
 15 AGTGGCGTTC TGGATGTGA CCGTGGGCTT GGGCAITCC GCGCGGCTG CCATTGTGTC 600  
 TCGCGCAAGC GGTGTGGCAG GGTGTCTGG TGGGTGGGT GTGCTGGGC AACTACACC 660  
 TGGAGTACAT GGAGACCTAC ATTGGAGCC TGCTGTGAC GGGAGAGGGG GAGTCTGTT 720  
 20 TTCNCGATG GGTCCCGGC GGTGGGGT TCC 753

## (2) INFORMATION FOR SEQ ID NO:399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1299UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

ACGCTTTTGG TTTTGGGGT GATGGTGGT GGTGGTATAG ACGATGTGAT CTCGGCTGC 60  
 AATTGTAAGC CTCTCTCTCC GGAGATATCC CGCAGGAGA AGTCGTCTAA ATTTAACATT 120  
 ACGTTCATGT AATCACAGG CACCTTTTCA AAGACACAGA CGATCATGCC ATTCTTACGC 180  
 40 TTTGCCACA TGGACGCCA AATGAATTTC TGTGTATGCG AGGATGCTGA CGATGCAGCT 240  
 GAAGCAGGAG ACGACAGCGA TGTGAGGCT GGTGTATGA CGCTACTAT TTCACCTGTG 300  
 AATACTTGTT CTGGGCCCTC TGTAGACATA ATCTGTGTTA GGACAAAGCT CCGCTGTGCG 360  
 45 GTGTGTATCA GGTCAAGTAA AGTAAGCGC TTAAATGCCA ATTGGAGAT ACGAAGATT 420  
 AAGCATGCCN AATCGTTAGC CGCCTAAAC TGCCATGGGT GATGCTGGGA ACAGGTAAAT 480  
 ATGGCCTGAG GTGCTGTGTA CTTACCTGAT ATAAAAGTAT GCAGTATGCG GGGGCTTCC 540  
 50 TACGTTCTGC TGTAGTCTAT CGGATCTGG ATAGATGTTA GTTCATGGT AAATGGTTGG 600  
 AGATAATTTT CGTCTGCGA GGCCTGTATA GTAGTTCTG TGTGAATAT TCATGAAATG 660  
 GTTGGGCTAA GCTTCAAGC AGCTGCTTCT TTAGTCTTG CTCATTACTG ACTTCTTCC 720

CAGGATCTAC GCCATCOGCG TTGGTGCTGA C

751

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1300RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GATCTCTCTG CGCGGTGCAC AAATGACGCA GAAACAGGCA TTCAOOGAAT TGAAGAGGCC	60
TCAACTGCGG CGGATCGCTA CAGGCGCAGT GGGACGACAT CCTTTCTTTG GTGGGTATGA	120
GGATACCTAA ATAAGCACAT ACAAACGTT AAATATGCAT AAGGAGATAT ATGCGAAAGT	180
TAAAGTGTTT TTAGTGCCCC TCGGCCACAG TTGGGTGTTT CAGCGATAAT GGGAGACCAG	240
CCCGGCAGT GATCAGATAC GGTGTAGTG GCCATAOOGG CTTCGGGACG AATCTACGGG	300
GTATGGTGCC TGACGCTGCG CCGGCGCGT CTTACGCTGA GTTCCCCACA GCGTTCCTC	360
GTACTGGTTG ACGTCTTGGT CGTGACAGC CCTCGTTTG CGTAGOOGG CCGACTGCC	420
CCCCGCCCTC TCGGCCTCGA GATCGTAAGA CTGTTGCTG CTGCTOGAAA AGCCCTTCTT	480
GCGCTGCTG TAGTACTGGT CCTTGCGTA GTACCGOGG GCCTOOGGCG TTAATAOOGG	540
CTGGTATACC ACTTGTGGCG CGGAGCATAT ACTTGTGCAC GCTGCTTCTC CTGCGGCGG	600
CGCTGGCGG TCGGCTCTAT AGCAGCAGCA CGGCCAGCAC AAGAGTGC AATTCCNCTC	660
ACCCCCCAT AAACNCGAN TTACACCCCC TATCCNATAC CCAATTGACG CTACNCATCC	720
CNCTATACCC CATCNITGCA CNOGGTACCT ACTTTTCCCN AANTGACCCC CACNTNC	777

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 812 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1300UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GATGAGGAG TTTCCACTGG AGGTGGGCG CTACATGACG CTGCTGOGCG AGATAGACGC	60
CAAGTGCGTG CACACGGTGC CGGAGCTTAA CGCGCAGATA GGGGCTTCC TGGCTGGCTC	120

5 GGGCAGGCG GGAAGCCCGC AGCTGCAGAC CATCAACCGG CTCTTCCAGG ACCTGATGCC 180  
 GTGCTGGAG GAGAAGATGC ACGTCTCGTC CATTGCGTTC GAGAAGCTCG ACCGGCTCGT 240  
 CGGCGCGGTC GAGCTCGGCT ACGAGGTGCG GCTCAAGAAC CAGGAGATCC CCGACAAGCT 300  
 GCGCCTGGGC AACGACAACC AOCCTGCCAT GCACCTGCAC CACGAGCTTA TGAAGAAGAT 360  
 CGAGTCCAAG CAGCAGAGCA AGTCGCAGCA GCGCTGCGC TCCGAGTCCC GCGCGAGGC 420  
 10 GATGGCGGCC AAGAAAATGC ACGTGGACCC GCGGGGCGG CGCTGCTCT CAAAGGCCCC 480  
 CGCTCCCGNT GGGCCCCGGG CGCCCTTGG CGGCAAGCG CCGGCGCAA CTTCCTCCCC 540  
 CGCCCGCGCG GCNAGCGCAA GAAGCCGAGG AACAACTACT CGGCGCGGCC CCNAAACAAC 600  
 15 AATTTGCGGA AGGCTCTTA CTGCTACTGC AACCATTCNC CCTACGGGAA AATGTGGT 660  
 GCGAANGGGA AAAATGCCNC TCNATGGTCC CTCCTCGGA TCACTCNAAA CCTTACCGAN 720  
 GGGAAATGTT CTGCAANAAT GCAAAAAAAC CCTACATACA GNCGGTTAC TANNCCCCC 780  
 20 CCNCCCTNCN TGCTTNCNA TGGGTTCNC NT 812

## (2) INFORMATION FOR SEQ ID NO:402:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 786 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1301RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GATCCGCGAG ATTATCGTG GACCGCCAC AGGCAATTAC TATAACAACA TCCTGGGGTG 60  
 TTAAAGGACC TAACTCAAGC TCAAGTATTT CAGGATGATA TCCTAGATGA AGAGCTGGCG 120  
 40 CACAGCTGG TTCGGTTACA ATATTGCTCT CTTCGCGAAA ATTTAAACAT GTCTGTACTA 180  
 CAGCGAGCTG GTCAAGCACA ACAGATTTTG TCCTGTATTT TTGGCGGTAA CTCAGAGTAA 240  
 GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGGATTC ATCGAAACGT 300  
 45 TCCTGCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACC CTCTGTTCC ACTGCTACAA 360  
 CAGGATAGA GTCTGOCAAA CCATGTTTCT CCAGCCATA TACAATCCCA TTATATAACC 420  
 CCGCGCCACC TACGCTGAG ACGATACCTT TCACGCTCTC CAATTGCACG CCTTGGAGAT 480  
 50 GCAGTCTTC TACTACTTCA TCTACCATTG TTGCATGCC TTCCAGATG AGTGGTTGTC 540  
 GAATGGATGT GCATATATCG GACCGACTTT TTCTAATCA CATTCOCCAT CAACTCCGA 600  
 CCGTAAGTIA TCATCGCTCT CTTCATAC ACTTCCCAT GANATCAT CNGCCCCCGT 660  
 55 TGANCGGTTT CGCTCTACCT CCNCGCCAA TTNTTCNGN CCTACNCGG CAGGINTCCT 720

NTTNNCGTGA CCGTGGTGC TGCACCCNTG CNTGNCNCGA CTCCNAAAC NTTTGGNTGC 780  
GNGAAG 786

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1301UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GATCATCTGC GTGCGATACT GGCAAAAAT GAGAGACAGC ATGATGAAAA TATAGTTAAT 60  
AAGATATTGC ATGATATAAG CACAGGCGGG TTTCGTGAA GAGGAAAGGG TGCATTGAT 120  
CTGGAAATGA GTGAAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA 180  
CTTTTGAAAC AAAAGATATT GGAAAATGGT GATACTAGCA AGCTCGTATC TAACCCCAAG 240  
TCATACGCTT TTTTTCAGAC GATGGTGGAC GATGTTACTG AAGCATCATT TGGAAATACA 300  
TTTGATGCCA ATATAGATGA AAAAACAGAT CCATCTGCTG CAGGTGGGAA AATTGTCATA 360  
TCAGAACAAT TTGTAAAGGA AACCTGTCA TTCTTGTOGA GCAAGAGTGG CGACTCAGAA 420  
ATCCCTGCGA AAATAAATC TATTTTCATC AGCACAGTTG AACGTGAAGA AATTCAAGAC 480  
TTCATACATT GAAGCAAAAT AGTAACATTA ACATTTGAAA GGAGTCTAGA CTTCCTGCTC 540  
AGATGGCTGA CTCAGCAGTG AGATAGAGGT GATTACNGCT TTCTTTANAT ANATTCCNEN 600  
GCGCNAAAT TTTTATATGA ACTACTTCAC AANANITTTA AAGTTGGGCC CAGGGGGGCN 660  
ATCTTAAGGG AATAAANATN GGTCCAAGC CCAATACTTT TTINGGAAAN NGTINGNGGC 720  
CCCCNAAAG GATTTAAATT CNACCAACTT NTCNCCANN ACCCCCCCCC TTNTTTTCNG 780  
NG 782

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1302RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

	GATCGAAGAG CTCTCGCTG ACTTCGAACG GCACAAGGTA CCCAAGCTCC TGTAAAGAGT	60
5	TATGAAACTC CGTAGCGGAA AGCGTGAACG AACCGTTAAT ATCATTGTCC ACATATATCA	120
	TGCGCCACTT CTTCACGGC TTGTATAACG AAGTAACTC AGACAAGTTT ACGGTACCAA	180
	AGCGCGTGGC GOCAAACAGG CTAATTAGCG CGTCCACCGA ACTCATGCAG AACTGOGAAT	240
10	TGTCATCATT CTGTAGCAGA TGCTGTAGCT CCTCTGCTGT GAGACGCTCC ATCTTCGGGA	300
	CGTCGTGATT CATGAATAAT TTCTTTGCTG TTATAGCATC GGGGTCCTCA TTAGGAACGG	360
	TGGCGGGCTT GGCTTGGGTA TGGTTCGGGT GAGGCTGCTG AGCTGGCTGC GGCTTGCAG	420
15	GCAAATTATA GCTCTGTGGC CTCGGTGGTA TTGGCTTCCC GTGGCCCGGC AGGCCAGGGC	480
	GGCTGTGGA ACGCGAGGAG GATTTCCTTG AAGCTGCCCA ACGCCATGCG CAGGCAACTA	540
	CTATGTGTAC AAAAATTGCC GTGNTCTGCG AAAACCTTTG GTCTGTACAG AACCCANCC	600
20	ATGGCCCATG GAACGGNNTG GNTTTTGGC CCAAATTAAAN CCTGGANAA NITGGNAATT	660
	TTTGGCCATN TTTTCCNAIT AAAAANGNG GGTINNAAGT GGNAGGNGC CCATNNGGG	720
	GGGNAANTC CGCGCCTTTT TTTTTTNCAT AANGNCCNC NITGANNNCC GGGCCNNNC	780
25	CCAC	785

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1302UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

	GATCAACAAC ATACTTCTAA AGACATCAAT ATACGCGCGC ATGTCTCCGG ATGAAAACA	60
	TGAATTGGTT GAGAGGTTC AGTCCATGG ATACCAGGTT GGCTTCTGCG GCGATGGTGC	120
45	GAATGACTGT GGTGCCCTTA AAGCGGCGA CATTGGTATA TCTCTATCCG AAGCGGAGGC	180
	ATCTGTGCT GCGCCATTTA CATCCCGCTT GTTTGAAATC AGCTGTGTTT TGGACGTAAT	240
	GAAAGAAGGC CGTGCGCGT TGGTCAGTC CTTCGCCGT TTCCAATACA TGAGCTTATA	300
50	TTCTGCCACA CAGTTTGTTA CAATATTGAT CTGTACAGC CGTGGATCTA ACTTAGGGGA	360
	CTTCCAGTTT TTGTACATCG ACCTCTCTT GATCGTGCCG CTAGCGGTGT TCATGTCTG	420
	GTGGAAGCC TATGAAGTAT TGGCCAAAA GCGGCCAAG CCAATTTGGT TTCTCGAAG	480
55	ATATTGATTC CTTTGCTCGT GCACATGCTG ATTTGTTCGT GTTTCAGCTT GTCCCGTGGC	540

TCGCAGTCCA GCATATGAAG TGSTACCGGC AGCCAGTGGT CGCGACGACG AACATGTTGC 600  
 TTOCCANGAN NACNCAACCC TTTCCTINGTC TCCACTTCCA TAAACCCCTGG TCCCAATCMT 660  
 5 GCTTCCGGTN GTCCNCCCN NCNCNAAAC NAANITCGAA AATTTTGGTT TATGGCANIT 720  
 CCCCCCTCCC TGNCCCTCCC GGTGGANNAT TTCCCCCCCC CGAAACAACCT TGGCNCCTTT 780  
 10 CACTCCCGAA GTTNCCTCCAT NTC 803

## (2) INFORMATION FOR SEQ ID NO:406:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1303RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

GATCAGGTGG CCTTTATGGC CATACTGTGT GGACTCATAG TATATCTGGG CGACTGCACT 60  
 ATTACTGGAC TGCTTGTCAG GATCTTGGGC ACCCATCAGG CCGACTATAC TACATGTCTC 120  
 GTTGGGCTTT GCGTCGTAA CCGGCAGAAA AGATACTTTT ATACTTTATA ATACCAGTGA 180  
 30 GCGGGCCATA CCACGTAATC CATCTTTGTT GOCAAATAAT TACAATATTC CTTTTAGCTA 240  
 CTGGAATTGG GCTTATCCTT ACAGTGTGAC ATCAATTTTC TATCGTAATT CGCTATCTCC 300  
 GCTCGCAATC ACTGCACTGC AAACCATATAT CGTCTGATA GATAAAGATT ATAGGGTAGC 360  
 35 GATCAATAGT ACCGGTAAAG GCGTGACAA TATCTGTCTG GCGGTGTTTA GATGGCCGAG 420  
 ACGCTAGAAT GTGGGAGCAT GCTGGTTTAC CGATATGGGA AGCCTTCACT AGAACCCCTGC 480  
 CACTAGTAGA GCACAGAACG TTGAGACTTA CAGCTGTTGG AAGTATAAGT TGTAAATTTT 540  
 40 CAAGGGTGGC AAGTAATATC AATTGATTCT AAATGACTTA CCCTACGTT GAACTGCTTA 600  
 CTTTAANITG GTTGGGGCCC ATCAAGCCCT GACACTCTTG ACTTTCCTCC ATGAAAAAAC 660  
 TCCCGGGTGG GTTCNANCCC CATTCNCCAA ATACANTCCA TANGTCCTGG CCCTTAACCA 720  
 45 CTGNTCCGG AGGATTTTTT TNCANAAG ANNNNACTTT TNAATTTNGC CAC 773

## (2) INFORMATION FOR SEQ ID NO:407:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1303UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

5  GATCTAAGTC CTCTCCCCCA AGCGGTGACG CAAGTGGACT GTCTGTGCT CCGTTAATAA      60
   AGTTATCGAG ATGGTCCACA AGCTCATCCA CCTCGGATAT ATGTGGCTG TGAGTAGGCG      120
   CAGAGTCACG TCGGTGTGCG AACGTGACAT CAGACTTTGCG GGAAGGGCTT CCTAGCTCAG      180
10  GGTCCAAATC AATGGACACC TTTTCCAGCT CTGCCAGCGA GCGCAAGAAC TTTTGTCTA      240
   ATATATAGTC GTTAGTTTGG ACCACGCAAG AAACCGGTGCG TTCGTGGCCT CCTGACGCTC      300
   TCCCGTGTAC CTGGCTGCG CTGATGACTT TGCCAGTGGG TGGGTACAGG CTCTTGAGA      360
15  TGACTTGATC GGGGACTGC CACTTTGCCA ATCAGGATC GTCTACAGTT GTAAACGGGC      420
   GCACCTTCTT TCTGTAGGT GCTGGGCTG CTGGTACTGG ACTCCTCTG GACTGTCTGG      480
   GCCTTACTGG ACCTGTCTGT GCTGCTGTTA CTGGAACCGA AAAAGAAAAA TGACTTCCC      540
20  TCTTTTCATA TGACATTCOC NGTGTGANA CNTACTATTG GCGCCNAGAA AATAANTTAG      600
   GCGAAATAC ACTCNCATG TTTGCTATA TTTCCNTAC CATATACAGC CTGCTGATTC      660
   CCAGTTTAN AANTTTAAGT GCGTACCTT ATATGTGAA NCCGTTATA TGAAGAATAA      720
25  CCCCCAANT TTGCAANGAA CCGGAGGC ATTGCTCT TCANCANNAT TAAGNACATT      780
   TTGTCCTTTC AAGNACTTTA TAAGNCC      807

```

(2) INFORMATION FOR SEQ ID NO:408:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 778 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1304RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

```

   GATCAATGAG CGTGGCTACT ACTGATGCTT ACTGCAGTGC TGIGTCAATA TTACATATCG      60
45  GTGGATAGCT AGATAAAAAT GCTATACATA TATCTGTGCG CATTGTGCGA ATCTATATCT      120
   ATTTGTGCGG ACGTTGCGGA CCAGTAGGAG GTTGTGTGCC GCGGGTGGG CAAATTCCGC      180
   TGAGATCAAG CCATTGCTG TGCTCTTGCC CTCCCTAGA TGGTAGGTGC CACTGTGAAT      240
50  AAAACCGACG AGATCTTGTA CCGCGGCAG AGGCTGATCG GCGTCATGG TCCGTTTGCC      300
   CGCAGCATTG TATTTCCTGG AAGGACTGC CTGCCAATGG GCGAGATGCT TGACAGGCAC      360
   TGCATACAAG CCGGCATTGT CCTGAAATG GCGCGTTG AGGGCTGTAC AGACAACGGC      420
55  GATCACGGGA AGTTGGGTGG TCACAACAGC CAGTTGGACG GGCAAGCCTG TGTCATAGG      480

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AGGTTTGTGGA AAAAGAGACA ACTGGCTTAT TGTNAAGGTC CCGGGGANTC NCNAAAANAA 540  
TCTTGGTGGC AATACCAACN CCTAAGGATT TCANCGNGTT CCCCAACTTN ATTININITTN 600  
5 TNGCNCOCGT TTCAAATTCA TATNGGTGGG TTGNGGCGN GAATNTTCTT TTCNATTTCA 660  
AACCAACGNG GGGNGCCNT TTGAGATTTG GANACNCCC TCNAAANANA NTGTCCOCT 720  
TTCNCCNNA AAAAAATTN NGGAGGAAGA GGTTTTANCC CNNTATATNC CCCCNCN 778

## (2) INFORMATION FOR SEQ ID NO:409:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1305RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

25 GATCAATGTA TCCATTATAC CCAGCTTTG CAGGACATA ATATATTGAC TTGATTTTAA 60  
AGCGGTAGAA CTTTACGGGG CTAGGGCCGC TAGGTATCCA AGGTTTAGCA TCAGGATGCA 120  
CGTCTGCAA GCACTTCTGC AAGGCTGGAA TGGGCTGGAG TACTTCGAGC TCACCCGCGA 180  
30 AGTTTGCAAG AGGTGCTTTC ATGGGGTCTT CAATGATAT AGAGCAACT GAGAAAGACA 240  
CGTTGTTATT GTTTTACGG TTTACTTGTT GTAGTGTGTT GTGACCATC AAAAAAATGG 300  
GCTGGCCGTC ATGCTCTACT CCTCACATC TGTCGGGAGA AATATAGTAC ATTCTAATAC 360  
35 CATATGGAGT ACCGTTTGA TTGATTGTG TCAACTGGAA AGAACTTTCG TCTTTAATTA 420  
ATTTCCTGAG TTGCACTGCT GCTTGTGTT CCTCCTGCGA CGCTTGCGG AAAGCCGAAG 480  
TAACTAGTGC CAAAAACAT GTAACATG AAAAAATCGA CTTCAATGTT GCTATTGAGT 540  
40 GCCAATAGGC GAGACTCATC CATATGTAAT GAAAGCGTTT ATANATCMT GTTNIGGCTT 600  
GAAAGAATTA TTATACTTTT CNGGCGGTT ACATTATCTT CCAACCAAAT TGTTCCTTT 660  
TNGANAGGNA ATCCCCAAA TTTTINAAT TAATNGTCN NOGCANCGT TTTTCCCCG 720  
45 GNGGGGAAA NAAAGCNGN NACCCGCCAA ANCCGAATAA AGGATTTCCA TNAAAACCCA 780  
ATTNCCNAA AC 792

## (2) INFORMATION FOR SEQ ID NO:410:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1305UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GATCCCAAG AAGAACATCA AGATCCACGG GTTCTAGGCG CTATGTACTT TGTGTAACTC 60  
AATACATATC CTCTCTCTCC TCCACCACCA CCACCTCTCT CTCCACGTCC CTCTGCGCCT 120  
COGCATAGTA CCTCACACAG TACGGGAACA GCTCTCTGCT GAACAGCCTG GGCAGCTCGT 180  
CGCGTTTGGC AAACCTCTCG CCGGGCGCCT CGCTGTGCA CGGAACAC GCAAAGAAG 240  
TCCCGTCTGA GCGCTTGGC CACTCCATCT CCACCGCGC GCTCCGCACT TCCCGTCT 300  
CCCCACCGT GAACTGCTTC CTCACGCTCT GCGCCCGCAG CTTGCCCTCC AACTCCCGA 360  
ACTCCACCGT GATCGCAAAG TCCACGCCC CGGCCCGC CCACTCCACC TCCACCGCC 420  
GGATCGCTC CACGTACCGC CAGTCCGCG CCGCACGTA GTTCGCGAAA ATCCCGTGC 480  
TGCGTCAGCA CGAATCCCC AGAACCCCGC GATCCCTCG ATCGCTTGC TCGCGCGCG 540  
GTATACCGC CCCAGCGCG CTGCGCTCC AACTCCAGC CCGGTCTC CCGTCCCGC 600  
NCCGCTNGA NCCGGAAGN GCTCCACNG CGGCGCTGCN CCGTATGTC CCGTCCCGC 660  
CATTTAGNG GGGNNGGCG TTNNTGTTT NNNGAAGNA GNGTCCGNT TCCNGGCGG 720  
GNNNGTTT TGGNNGGAG NACGNGTTT TTGGANCC CANTCNGGA NTCCTGNGC 780  
GAANGNGT TNCNCCNN TTGAGCCCC CT 812

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 778 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1306RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GATCTGATAT TGGGTAATG CAACCTTTC ACCGCTTGA AAAGTACTTT AGGAAGTGGT 60  
ATTTGCAATA TAGTTCATCA TTGTAGTGA AGCAGAGGA TACCTTACAC TTGGTACCGC 120  
AAACCGTGA GCAGAAGTGT TCCTGTCAT ATAGCTTACC AAATGTATTG TAATACCGC 180  
CGCTCAGTGG CTTATTGCAC ACATAACACA ATAGCTTGT CCGGTGAAA TAATCTGCT 240  
GGCATAGCAG TACCACTTCA GACGTATCC GGAGCTATA AGGAAGAAC TTGGGGGAC 300  
ACAAAGCTCC ACAATCGTGA CAAACCAGAC AGTTTTCATG GTAGTAATCA CCAAGCGCT 360

TCAGGGAGTT CTGGGTGATA ACCCCCTTGC ATTGTTTACA GATTTTGGCC GTTTTTTGAG 420  
 ATGAGGTGGC GGTITATGCT CCGCAGAGCT TCGCATTACT TGCTCGAGC CACTGTGTCT 480  
 5 ATGGTTGATA TGGTCACTAT ACGTCCAGCA ATAGCTGTGC TTCTGTATAT TAGTCATGAA 540  
 AAACAGTAGC ACTCCCTATC TTACCCCTGC NGATCGTATT GGTACCGCCA AATNGTTAAC 600  
 CCATTTTCCA AGAACATTCT ACCNCTTCOG TTTTTCGCCA AAGAGAGGTN TGCTATATTT 660  
 10 GCCAACAAAA GCGCAACTGA AATTNAANAA ACCCTTTTTT CCCCCTTTTN TTTCTCCCGA 720  
 GGAACCTTTT CCGCAANTTT CNOCTAAAT TGTNIGGGGG NTGANANCCN AGAAAANC 778

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 806 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1306UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GATCATTTC A GTGGATGGCG ACATTTCATAT GGATATCAGT TOGACTTTTG TTCCAGTCT 60  
 TATTCAGCTG ATTTTCAGGT TACAAGAAAT GGAAGGGGT CTCCATTTTG TAGGGACGAA 120  
 30 CAATGTGTAAG ATGTCTCAGG AATTCAAGAC TCAGGTGTA ACGAAACTA TTATCTTATC 180  
 CCTTCTGTGA GGGGAGGATA CCTACAGAT GATTATCCAA CCCATCTCTT ACGAACTGTC 240  
 ACTACATACA GTTTTCACTG ATTTTATTTT CATATCTAAG GTACAAAGCT CGGAACTAG 300  
 35 GGATATCGCA ATTATTCGGG AAATTAATAAT TGGATATCAA ACAGCCAAAT TTCAAGTGAA 360  
 ATCGTACAAC TTGAAATTGT CGGAGAGGCT GCTAACATCA AAGCTACGGG GGAGTTGTTC 420  
 TCGAGCGGTT GAACTTTATT GTTCTGATAG TGACATCAAG TTGCTTTTTC ACGAATGTCC 480  
 40 CCCCCCGGA AATGAATACC CGCNATNINC ATTCTTNAAC CGAATTCCCA AAACCCNTTN 540  
 TNAANTAATC CCTTTAAAAA TTNATTTTTC CCNAGNITT ACNCCCGCNA ATTTTTTTC 600  
 CAAATGGGCC CCTTANATGA AAAAAACTN CACCCCCCN NCGAAAANAA ATTTCTCTTT 660  
 45 GGAAANNNN AAACGAATTA TTCNCCCT TTNCCCCC CCGGAAANAC ANNTTTCTCT 720  
 CCCCCCTTT AGGAAAANTG TTTTCCCNNA TTINANANIN TCNCCCNCC CCNNAACNA 780  
 50 AAATNTAAA NCACCCCNIN TTINING 806

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1307RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GATCCCTTTA TCTCATATTA TAGTCCATAG TACCCOGTGG ATGCOCTACCA CACAGAGGTC	60
CCTCTTCTGG AOCCTGAGACC TAGATATCTT GCGATATCAT TGAAAATATC GTTCAATTGC	120
TCTCOGTGA GCGCTTAAC TTCCGCTCG ATATCAGCAT CGGGTGTTTC CGAGATGTGG	180
AAGTTCCTAA CTTTGCCCTC CAAAACTCC TCAAATCTCT CTGTCTCTCT CAGTGTGGT	240
GGCAACAACCT CATAAAATTT CGCAAGCTTA TACAGCTTCA CATTGTCTAG ACTTTGGAAG	300
TGCCCCAAGC TGAGAGGGAA TAGCCGTCC TTCAGTCCG GAATCTCACC GTCCCGGTTT	360
GGCAATGGAG CCAAGAAGTC CTCTCTCTCC GACTTCGTGG AATTCATAA GCGCCGACC	420
GACCGCTCTT CCATGTGTG AAGCTGGCCC TGAAGCTCCC CCACTAGCTG CACTAAGTCC	480
TCATTGTGG CGAAATCCGT TGTATCAAAC TTGCCGGGCG CCCCCTTAGG AAGGAATTT	540
TOGTCTAAGT TTGCCATGTC ATGCTTTTGC TTGCTGACCT GTAGCTCCAG CACCGACTGT	600
CCTGTCTTGG TGATTAGGAC GCTCTGCCGT TTAAGTAGCG CCTGTAGCTC CTCAACTGTT	660
TCTTCAATGC CTGTCTGAC ATAAGCACT TCAAATTTAG TAGAAGCTT CTGAATATTC	720
CTACACCAAA CGCCGCAGAG AGAATGGTAA AGA	753

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 811 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1307UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GATCCACCAA AGGGTATTTT ACTATATGGG CCTCCGGGGA CAGGTAAGAC ACTTTGTGCC	60
CGTGGCGTGG CCAACAGGAC CGATGCTACA TTTATCAGAG TCATTGGCTC CGAATTAGTA	120
CAGAAGTACG TGGGTGAAGG TGCTAGAATG GTTAGAGAGT TGTTTGAAAT GGCAGAACA	180
AAAAAGGCAT GTATTATTTT CTTCGACGAA GTGGACGCAA TTGGCGGTGC TCGTTTGTAC	240
GATGGAGCGG GTGGTGACAA TGAGGTCCAA AGAACTATGT TGAAGTCAT TACGCAACTA	300
GACGGATTGG ATCCACGTGG TAATATCAAG GTGATGTTTG CTACCAATAG GCGGAACACC	360

EP 0 866 129 A2

TTAGACCCAG CATGTGTGAG ACCCGGTAGA ATAGACCGTA AGGTTAGAAT TCTCTCTTCC 420  
 GGATTITGGAA GCGGTGCCA ATATTTTCCC GCATTCACAC AAAGTOCATG AGTGTGAGC 480  
 GTGGTATTAG ATGGAATTGA TTCCCAATTG GTGTCCAAC CCACCGGCGC TGACTIONATC 540  
 TNGTTTGGCC CGAGGCTGGC ATTTTGTCAA TCCAATTCCC GACCCAGGTT ACCTACAGAA 600  
 ANGACTTCCT TAAACCNIGT GATAGGTCCT CCACGGCTAT AAAAATTCAC NCCCCTTCCC 660  
 CGTTTINIGC AAACCCNAAN CNNTNCCCC CCTTNGGCG TTTTTTAAA GNTTATTTA 720  
 TCCAAANNG TMTCTTTT ACNATACTAN TGTTCCAATT TCTATNAAAT NTINTCCCC 780  
 CCGTGAAANC CTNCCCCGTT NGCACCCCTA T 811

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAGL308RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GATCTGTCTG CTGTACACC GATGAAAGAA ATAATTGTGA CCGTCAOGGA CTTCGAGAAT 60  
 GCACTTCGGA AGATAAGCC TTCCGTCAGC GATAAGATA GAATGAAATA CAATAAGCTA 120  
 AACAAAAAAA TGGGCTGGAA TGAOGAAGCA GGGTGCAAG TGAAGAAGA AGCATAGACC 180  
 AGCAAGTTAA ATAGGCACAG CTATGTACAA ATAACCAATT TCAACTTGTT CAAAGTGTG 240  
 CCGTCTTAC AGATTTTACA CATGGAGACG GCGGAATTTA CTGTATTATA TGCCCTCTCC 300  
 TCGAAAGTT TTTTGAATC TTCCAGACAT ATTCOGTATT TCTTCTTTT CGAGAAAGAA 360  
 ACATATGGTA TTTCTTATT CCTGTAACTT GAGCTTAGCA ATTTCTGTGG ATATAGTTCC 420  
 GCAAAGAGGT AGATCCGTGG CACCTCTGAC AAGAAGGAG TTATTCTTCA GAGAATGAAC 480  
 ACGCCCGGAT ACATGCCAG AATGTATATG TTCATAAACT TGCGCTCCAA CATCAATGGA 540  
 ATGGATAAGA GCCAGGTAA CAAGTCCCAT ACTAGTATAG TCCAGCGGAA TGCTTCAACA 600  
 TTGGAATACC CGCATGTG ATATCCGGAG CTCTTTGATT GATATAACAA CCCCCNCCCT 660  
 MTNIGCCNC AAAATTCCCC CTGATGGTAC CCTAANGGT TCTTGCAAAA GCGAACCCT 720  
 ATCCCCTGGG AGCCNAAACC CTTTACGAGN AACNNATTAT GCGCCGGTNT TTNAOGTCCC 780  
 TNNCTGTCTN N 791

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1308UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GATCAAGTGG GCGTAAAGTC GCAGAGAAAC TTGCAACTGA ACTGCCACTG GGGCTCATGC	60
ACCACCAAGA CGGTTAAGCG CGACCATATC ACCTCCACCC TGGGTGTGCA TGTTCCTCTG	120
AAACCCCTTCA GCTGCTCCAC ATGCAGCGGT AAGTTTAAAC GCGCGCAAGA CTTGAAGAAA	180
CACCTGAAAG TGCACATGGA GGACACCATG AAAGAGCGTT CCGGTGGGGC GCGGGGCTCG	240
CGTGGTGTTC GCAAGACAGG CGTTAACAAG GGCTCTGGCC TACAAGAGAA GGCGGCAAG	300
TTACCCCAACC TGACTGTGGA GAGCTTTGTC AGCCAGGAGA TGCAAAATTA CTACCCCTAC	360
TACAAAAGCA GACAGCACTT AGACGAAACA CTGTGCACA TTATTTCTCC GCGGCCAGC	420
CGCTCTAGGT TGGTACTTTG GGTTCGGAAC CGCCAAGCTA CACAAGGAAA GCAGTGTCTT	480
CTTCACGACG CTGTGCAGG ACATGTCTCG TGCTTGCTT TCTCTGCTC CTTGCAACAG	540
CCCCCGGCTT GCGGTTAAGA TGGTAATGCT TCCCCCGCC CAGAACAGCA ATATGCACGC	600
CGTGCCCTAG ATATCCACAG GATGCCCGGA CTCCCTCCCT TTGGTGACTC TCCNGGACCG	660
AATCCCANCC TTTGCCCGAG ANACACTTCC GACCCNCTCC ATATCCCTGC TCTANCTGCC	720
CNCCTACCG CTTTCTCATA AAATGGCATT GTTGGCCGAN CCTATCTCA TCAAGCCCCC	780
TGATANACCC TGNAAGAGAC TGANTCCCC CCAAACC	817

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1309RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GATCAATTAT TAGAGGCAAT ATCAAAGAAG TOCCATATTA CTGAGGAGAA CAGGGAACAG	60
CCTGGAGAAA GAATGCCGCA GACGTACAGA TACACGCTGG AAAATCAGCT TGCCAGTGA	120
GTGCTCGAAC AGCGATAAG AGTATTGACA GTGGTAGCGT GCAAGAGTCA ACGACAAAAT	180

GAACAGAACA TCATACTTCG GCGCGAGAT GTTGAAGCTC GACTTGGTCC GCGCGTGGAC 240  
 CTTTTTTGAA GAAGTTGCGC CAGGATCCCA CGCGGGCCTT GCGCGACGCA GCAGGGACTG 300  
 GTCTCCAGCG CGCCAGCAGC AGGGAGCTTG TCACCACGCT CACAGAGCTC ATCGCCATAC 360  
 CCGCGGCGGC AGCCATGGGC GGCAATTGTA TGCCCCACGG AATGAGGACG CCCATGCTGA 420  
 CTTGGGAGCC ATGAGAGAAT TGTACAGGAC TGCCAGAAA ATGTTTCACT TGACGCGGTT 480  
 AACGTGGCGC GCGCGAGATT CGATGGCATA CAGAATGCGG TTTAGCGGCG GCGCGCGAGG 540  
 AATGTCCCAA ACCACGATTG CCGCGCGTTC CGCAGAGAT CACTGTTGOC GGACAGCGAA 600  
 ATACCGAGTT CACTTTTACA ATTGCCACAA TTTCTTTGAN GCGTCTTCC GATAAGGCAC 660  
 ATATNGTIN TTTTGGCGC ACTGCGCAA NGTCCACTT GCGCGCTGG TACTTTCCCT 720  
 GAACATTTTG ACGGATNCCC AANCGTGCAA ACTCTCCNC CCGTGTINN CCATACCAT 780  
 CCATTTTTTG GCNC 795

## (2) INFORMATION FOR SEQ ID NO:418:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1309UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GATCAGGACC GCGGTNCCTG ATTGATTTGG CCATGAGTTT AAGTATGACC CAGAGGCGCG 60  
 CCCTGGTGTG TCTAATCTGA TTAACATCGT AGCTGGCATC CAGAAGAAGA CTATCGGGC 120  
 GGTGGAGGCA GATATTTGCTG GATTTAAGGA CCACGCAACT TTTAAAACT ATGTTACAGA 180  
 CATCTAGTA GCTGAGCTGA GGGGGCCAG AGAGGAGTTT GCGCGTATA TGAATGATAA 240  
 ATCATACATA TACGAGGTTG AGCGCAATGG GCGTGAGCGA GCAGGTGCGA TAGCTGCTAA 300  
 AACCTTGGCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTCAGATT CCAACTTTGT 360  
 CTATAGACTA GCAATAATTA TAAAGATACA TCAAGAAGAC CAAGAGCAGA TCGTAACTG 420  
 GTTGTCATC TTTGGACCTG CCGGATATCA GCACATGCAA CCAATATCTG CTTTACAGT 480  
 CCTCCGCTT CTCGTTAGCT ATTGTGCCAC CTTGTATCTT CCATCGTTA TACAGCCAGC 540  
 TEAGCACATC ATCCATCTAT TTTGAGCCCA TTCTGCTAGG CTGATGCAAT AGACTTCCAT 600  
 ATTTGGTAAT CATTGTCCN TTATTTTTTA GGTACCACC ATCTNTTTC CNATGAAAN 660  
 CGTGACAATC CACGTTTTC TCAACCTCC CTCCATNAAA TTTCTTTCAT CGTGGGTTTC 720  
 GGATCAANCC CTNNGTNCN TCCCTNCGC CTCATCCNG GNATTTACAC CTTTNTTTT 780

CTCCCCCTC ATNAANC

797

## (2) INFORMATION FOR SEQ ID NO:419:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1310UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GATCCAAAAA AATTTTAATA CTGAAAAAGA AATGCCACAA CTAAGCTCAG CTACCTTAAA	60
GAATCGGGAC CAAAGCTGTA AGGCAACAGC TCTTCCAATG TTCGCTGCAG AACCTTGGAC	120
CCGTGGGGT TCATCATAAT CACCGTGAGC TTCTTOGGAT CAACGAATC GGGCAGGACC	180
TGCCGGCAA TCCACACGG GGTACGAGC TOGGACAGT CCCCCTCAA TGCGATGCAG	240
ACCCAATTG TATGCCCGG GTTACCGCC TTACGACCG CTGTGGTTC CGCGCAAATA	300
CCGGCTGGT AACTGGCATT CTGACGTTA GGGCGACAA TATACTGCC TGACGCTGTC	360
AAGATGCAGC AGCCACCGG GAACCTGGAG TTATGGGCTG TACGAGAGCT CCTTCGGGC	420
TAGTGCTCGA GCAACCGGC CCTGATATGG CTCTCCCTGT GTGCTTGGCA TTGGCTTCGG	480
TGGCGTCGC TCCTAGGTAT TGGGGTTC CTAAGTACTG GCTGCGAACC CTTATGTTTT	540
TTGCAGGGGA ACGAATTGG CCGAACCGG GTGAATCCG GGAACATNCA ANTACCCNCT	600
TTTGGVNNC GGGVAAAGG NNANNITCN NNCTINGCN CGGNGGAAN AAANAATGTT	660
AACCATGTGG ANTAAACCTT TAANATGANN CCTATGGCCN GTTTAACTTT ATCCCCCNC	720
CCCCCTTTT AAANGTNNNA NCCCCGCCVT TTTAOCCTTA NNCCNGGGG GGNGCANNAC	780
CCACAAATNN TMTGTGNGC GCNNGCGTN NCTAATATGG AGCTINGGN	830

## (2) INFORMATION FOR SEQ ID NO:420:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1311RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GATCTTATCG TTCAGGTAC CGTGTCAAG AATCTGAGAC ATAACTTGC GCTGCGACGA	60
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GTTCTTGGTA AATTCTTGGT AGTACTGIGC GTTGTCCGCT TCCAAGCCTT CCTTCCCCCG 120  
 CTTGTACAGC AGCTCCACCT TTTCGGTGGG GAGCGGCTCT TGCTGGGAG AAGCCTOOGC 180  
 5 GTCTAGCGGC ACCTCGTGCC AGGGCATGTC CGCAGGCACC AGAAGGTTGC CGCTGGGAAC 240  
 CGAGCGCAGG TCATCGACCA TGCCGCGGCG AGGTTCTCTC CCGGGGACT CGGCATOGAA 300  
 CCCCAGATCG GACTGGCCCG CCTCTCCGCG GACTCGGCG GCATCGCTGT CCTCTCGGC 360  
 10 TTGCTCTTGG GCTTGTCTCT CGGCTTGCTC CTGGGCTTGC TCTCTGCTT GCTCTCGGC 420  
 TTGCTCTCTC AGCGAATCTT CCGGCTCGCT GCTCTCTGCT GCTGCGGCTG CCGCTGCTGC 480  
 CGCCGGCAGC CCATGTTGCG AGCAGCCCCG TGACGTCGTT CTGCAGCCCC GCATCGCGGT 540  
 15 CTCTTCTGTC GCGGCTGAAT GCTGTGTCG TGAGCTGTC TGCGTCTGCT CAGCCCTTCC 600  
 ACAGCGCCAA GTTGTCTTCT CTNAACCCCC CANNGCCAAT NGTTCTCGGG CTTCTATCCC 660  
 CTTTCTTCTC CTGGTTTCCC CTTTGGTNGN CCCCNGNAN ACTTTTCTCC TGGCTTNCNN 720  
 20 CAATTCCTTT TTCATTTGGT TTTCCCCCCA AATTCTTAN ANNGGTTAN CTNNTCANN 780  
 NGCNGNNA GAGAACT 799

## (2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 790 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1311UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GATCTTCTGA TGCATATTTC CGCTCTCACC TTGCGGTTA AGTTTTTCCA TGTAATAGC 60  
 40 TCAAAGTCAT CATCCCGTC ATCTTTTTC GGTATAGAT TCTGTGATAC TTCTCTTCT 120  
 TCTCTTCTCT CTCTCTCTC TTCTCTCTG TCTATATGAT CTTCGCTGT CAGTTCATG 180  
 TCTATTCCAT AATTGGGTTT AACTTTGGG TTGGGCTCTT TTGCTGGCT ATGATCTTCC 240  
 45 TGGATAAGTT TCTGTCCATC TGCCAATCC GTTTTCTCAT CAGTAGCTTG CGAACCGGGC 300  
 ACAGTATGGA TTGTGTTTGA GCTAATTGCA TTAATACGT CAGATCTTC AAGAGGCTCT 360  
 TTGCGAGCAT GACTTTCCGA AGATTTCGAG CGTTTACCTG CAGGCGCACT CTTACCCCGT 420  
 50 TTATCTGCAG GAATGTAGTC CTCATCGTCT TCATCTTCTT GTATCGTCTG TATGCTCTC 480  
 CTCAGATGC CGCCCTTACG CTGTCCCTAC ACTCTTCTAT ATCTCTCTCC TCATATCTAC 540  
 CTCTTTTCCA GTCTTCTCCA CTCATACTAT CTCTACCACA TATCAGGATA ACGTATAATG 600  
 55 GTGTGACTTT TTGGATAGC ATCCTGCGC CTAGGAAGC TNGGTTTCGG AATATAATTT 660

AACATCTTCC CAATCACAAA TTNCTCAGTA ACNGTGGTAA ATTNAAACGN AANITTTTAA 720  
 CTTTCATAC GGTITANGNC CCATGGCTCT TGAAANCGGA AAAATCCGGG GCCCCCCTTN 780  
 GAACTTGTTT 790

## (2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 788 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1312RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GATCATTCTC ACCAGTACAA ATGTATATTT ATATGTAATT GTCTCTCTCT GCTTTTGGCA 60  
 TATTTTTTTA TTTTTTGGG TGACAGGTG CACTGACGT GACGCGCAAG CCGCAGGCGC 120  
 GATTCTTCGC AACTTTTGGT CAACGCGCGA CAGACAGTCA GAAAGTAATA GGAAACAATT 180  
 AAATACGTTG TTATGTTATA TGAAGTTATA CATAAGTGGC TGCCATCAGG TTATATATTG 240  
 CTTTAAATAA CCCATTGCTC TGGAAACCTC CTCTGTGAAT GCTCGCTCA AACCGGGATG 300  
 GTTCTGTTTC ATCTCGGGCA AATATTACTG ATAATTGATC TACAGCGTCT TTTGTCTCTT 360  
 GAGTCGGTGC TCTATCAGG ACGGTCGTA ACTGTAGCGG ATAACATGTT TAAAGAAGTT 420  
 TAGTTCCCTC TGTGAAGGAG CAGCAGCTTT GAGTGCCITT TCATCATTAAT ATTGTTCAG 480  
 GTAAGAGAGG AGGTAATGTT TGTCTCTGGG TTCTTTGAAG GCGTGGATAA TAATGACTTG 540  
 ATTGTGACTC CTGGTGATG TACATTTAAC ATGCCAATCC CAGTTCCCAA GTTAGATTCT 600  
 TACCGGTTTT GTTATACCTT GTTTNATAAG GGTACTTTG CCCCCNACT TGCCAAGAAA 660  
 TCATCTTATC CCTTTGANAG GTCACCTGTC CCTTAATTGT AAACCTACNC CCTTTACAAT 720  
 CTATGCTTAT ACCNGCCAT TGTCCCTGAA GGATTTTINT ATTAACCTG CNCACATCCC 780  
 TTGGCTGG 788

## (2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 769 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1312UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

5 GATCAGGCAA AGGATTTCTA CTCGTATGTT GGCAAGAACC TGTCACAGAA ATCCGACAGC 60  
 AAGTTGCTTC CTCGGAGGAT TCAATTGAA CTTCAGAGGT TTGACTATTT TCACTCTCTA 120  
 CTCCAGTATG TTGTAGGATG TAACGCTCGT GATTTTGCTG TGTCACTTGC GAGGTTTCAA 180  
 TCTTCGATCG ACCCTAATAA TAAAAATACA AACATGCACC TCGTGAAGAA GTATCGTTCC 240  
 10 CATTTCCTAC CATTTAACAA GATAAAGAGC CAACAGCGCA TAAGGCTTTC TAAAGTGTOC 300  
 AACTATTTCTG ACTTGAATGA CTTCTACCAA CTTCATCAG CTACCTCAGA ACCAAATAAG 360  
 CCCCCTCAAAG AAGGACTCTT ATGGTCTTAC AGGAATAATG GATGGCATAA ACAGTGGGTG 420  
 15 GTACTACAAG GATCAGAGCT CTCAGAATAT TCGATTGGA AGACGAAAGC TAAGGTGCTC 480  
 AGCCGACCGG CCATTAATTT GACGTTTGIG TGTGTTAAAC GTTCGGAGAA AAAGCCTAAC 540  
 GGATTTGATA TCATAACTAC CGACGGGAG GCTCGTTCTT TCCAAGCAGA GTCAGAGGAT 600  
 20 GAAATGAAGC AGTGGCTGTA TGGGCTTAC TCTGCTGTG GGATAATAGC CATTGAGGAG 660  
 ACAGATGAGA ACAAAGATCC ATGTCTATT GTCCGTAATG CGGATCCGTC AAATAGTGCA 720  
 25 TGCTGTGACT GTCCGAGCGA TAAGCAAGTG AATGGATATC TCTGAATAT 769

## (2) INFORMATION FOR SEQ ID NO:424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1313RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

40 GATCGTGTCT TGCTGACTTG CATGTCTAGC TCAGTTCTTT ATTACCCGCC TCATGTTGAA 60  
 ATTTTCCAGG AACCATCGCA CCAAATGTAC CGATGATATA GATTACATCT ACCCTTCCGC 120  
 AAGCCTGGAA GGAAGCTAGA CCTCTAATCT AGTAGCTTGC CATGTACATC CCGCATCCG 180  
 45 ACCCGCGAAG ACCAGCCAAG GTGACGGCCG GCCAGCTCTG CGAGCTGTGC CACGCGCGCA 240  
 AGGCGCTGGT AAAGGCCCC AAGAACTTGC AGAAAGTCTG TAAACTGTGC TTCTTCCATG 300  
 50 TATTGGAAC CGAAATOCAC AATACCATTA TGGAGAACAA GCTATTCCAG CGCGGGGAGC 360  
 GGGTGGCAGT TGGCGCTCC GGTGGGAAAG ACTCCAGGT GCTTGGTAC ATATTGAAGC 420  
 TGCTCAACGA AAGACAGAC TATGGTCTCG AGATTGTGCT TCTGAGCAT CGACGAAGGG 480  
 55 CATTGTGGCT ACCGAGACGA TTCCGCTAGC TACTGTGAAG CGCAACCCAG AGCAATACGG 540

TTTGCCCCG AGATTGTGTT CCTACAGGAC CTCTACGAAC TGGACGAATG ACGAATAGTG 600  
 CCTGCGCCCN GGAATGCNCA ACACTGCNCC TTACTGCGGG TTTTTCGAC CCAGCGCCTG 660  
 5 ATTCCGGGGG GGNAAATGCTT GAATCCACCN NTTTGTAAAN GGCCATACCC GAAAAAATGC 720  
 CNAAAGNGCC CANAAATCCT GCGCGGGAAA TTTGGCNAAT CNAAATAACN CTTTTCCCCA 780  
 AANAGGTCCC GNTAANNIT 799

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1313UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GATCAAAAAA GATACGGATG TTATGCTTGT TAAAATATTA TATGCTATAG TACAACGTAT 60  
 CGCGTCAAAC ATAAAGCATG AGGACTATAT TTTTAATTCA CTAAGTGG CGAAGCATCT 120  
 CCGGAAGAAA TAGCCTCCTG TATGGGGCTA AGTCCATAGG CGTCGGTTGG GCTCATCTCT 180  
 30 GGAGACTTTA AAGAAITTAAG TCCGAAGGCT AGGCTCCCAT ACCCCAAAGG CGAGTGGGCA 240  
 CTTTGTTCGA GAGATCCTTC TGACATAGCC TTCTTAGTG ACAGTGGGG AACATGGGG 300  
 CGGGAAGGAA TACTTTGTCC GTGCAATGAA CCTCGGATA AAGGCTACT TAGCCGTTT 360  
 35 TTGAAAAATG TGACAGTCTT GTCTTGATA TCTAGCTTGT ACCTGGTTGG AGTGGGTTC 420  
 TTTGCAAGAC CAGTGGGTTT TTCGGAAAAG CTTGGGTCT TCCCGGAATG AATTCTGAGT 480  
 CCTGGTAGGG AACATCCGAG ACTTCCCAA AACNNITCN CTNCCATTT TCNAAAAAT 540  
 40 GGAAATCNC CCGGCATTA TNGATCTCTT CCCAAATTAC NNCNCCNCCC TCACITTING 600  
 ACTTGGGNAT ANAGANCCCC NTCNNACCCC TCCAAANAAA AAAAATCTC NINGTGCCCC 660  
 NINATCCCC CCGGGGCCN NNITTTAATT CNGGGGAATT AAATTTTGT TCCNNGCNGG 720  
 45 TNGAAGCANG TTATNGCCCC CCTTGACCC ATNPTTINACT TMTAATTTT TCCCNNGG 780  
 GNTGGAAACT TTGCNAAAG GCANGCTTTT TGAACCACT 819

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1314RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

5 GATCCATAAA CTATCTTCTC ACTCGCCGGA TGCAAAGTAT CAAGGAATAG GCGACAATOG 60  
 10 GTAATGATTG GCTCGAGCTC ACGCAGATAT TGGCGCACTT CTGATATCCG TGGGTGTGTT 120  
 GATGCATGAT GCACATGAAT AAAAGGAAGA AGCTTCGAAA GAGGTACAG GCGCGGGTAG 180  
 CGTGTGATGA GAGCTGTTAG TTGGCTTCA ACATCAGCAA GTTCTCTAT AGGGGAOGCA 240  
 15 GGGTCGTCAA CATCATTTAT TAGACACTCC AGCAGTTTGT CTGAAAAAA GGTGTGCATG 300  
 GACAAGTGCA CCTCATCTT TGAGATGCG CGGATAACGT CCTCAGOGA CGCCAGTCTC 360  
 ATCGTGCAAC TGCGTCAGAA AACTCTTGAT TGATAGGTA ATGCAGTCAG AAGAAGTGT 420  
 20 TAAAGCACT TTCGATGCCC CAGTGAAAC TAATCCTCGT CCGATATAAA ATCGAACGTG 480  
 TTAGCAACAA TCTTCCATAT CCGGAAAGTG TTTTACAAGC TTCTTACGAT TTTCCACTCC 540  
 TCGATTGAAT ACTCGGCGCN AATTCTTTTA CCATATACAC CCGNINCGG GCTTTTGAC 600  
 25 GAATCTNTA TTTGTGTAAG AACTGGACAC TTTGAACTT TGACATTGC NGANTCCGAA 660  
 ACNCTTTTCN CNGCGAATA ATNINAACCC CAATCCTGAC CCAATACACT CCCCCCATA 720  
 CATGACCCCG CACANGATTN TTTTTCOCN AGAATTNTT NAACINTTTG CCCCCINANA 780  
 30 CATNTAAAT C 791

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1314UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

45 GATCTTGCTG CAGACAGATG CCGCGGAGCT ACCCTTTGGA ATCTTTATAT AAACCTTTT 60  
 CCGAGTGTAC CGCAGTAAAC TCCCTTGCT TCAGGAGCTC CAGGCTGCA CGCACACTOG 120  
 AGGCTACAC GGTGACTGC ATTGGCTTCT GTGGGCACAC GGAAGTCTTA AACGAACCTC 180  
 50 AATCCCATCC AACCAGTTCT GCTAACGTAG CTACTTCTGG CCAATGCTC AGCCCCATAC 240  
 CGTCAGGCA ATCTTTCCAA GCCACATAA CGAAACCTAC ACAGTTACTG CGCAAGGCAA 300  
 GTGCCAAAAG AACACAGGTT CCGCAGTACC AGAGCAAAA GCTTACCTGT CAACACTTOG 360  
 55 AACATTCCG TGGCCTTAAC CATATGCCAC ATGAAGCAAT AGACCCCTAA AATAGAAAGC 420

GATTGGCCCG GAACAGACAT TCCTGGTGT GTACTTGGAA CTCACATAGG GGCTGCACAC 480  
 TGCTTAAGT CCTCGCTTGC AGCTGAGGCC ATGTGCCCCCT CATTAGTGAC CCACGTTGAT 540  
 5 CTCGAGCCCCG CAAATGATCG TCAGCGTGCA TCCGACTGG CATTGCAAGG GATGTTGATC 600  
 CCTGANGGG AGGCTTGCAA CAGCGCCNCC CTTGTTTCNC ATCCATAGGC TGTGAGGCC 660  
 GGAATGATCC NCTCTCCAGG GGAACNCCCT CCCCACGCC CCATAGGCC CNCCCTGGGN 720  
 10 TTTTGGCCCG ANACTCCDA NCNNGGTTA AANNTTTTTT TAAANONCC CAGTGGTNTC 780  
 AAGGCCCCCN NGCCTTTTTC CANCCCGCAN TTTCTNAATT TTTGNCNGCG GNA 833

## (2) INFORMATION FOR SEQ ID NO:428:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1315RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GCGGCGCTC NNCCAACTAG TGGATCTCA TTTGTGCCC GCGGACAGG TTACCACCOC 60  
 TTTTCTCTCC CGTCAGCATC TCACTAGCT GCTGTAGCTG GTACTCCCTG TCGCCGCGGA 120  
 30 ACAGTTGCA CTTGTCTATT GCTGTGATG AAGATCGTG CAGCTGAAT ACATTACCGT 180  
 AAGTGATCAG CCCAACAGC GCGTTGGGG GCACCAACGA CAGAGAGGTG ATGATCGAAT 240  
 CCTTCAGCGC CTGGAGGTTT TCCTCTCCG CGGTACGTC CACGACGTAG AAGAAGATCG 300  
 35 GCGCCACCTG CACCGGCCGA TTTGTGATG ACTCAACCGT CGTGAGGTC AGTTCCGCGG 360  
 GCATCGCCTC CTGAGACATG TTCGCATAGT GCTGCGGAAG ATGTTCCGC GTCCCCGCAC 420  
 AGAGGGCAGC CCCACACGTT CGACCGCAGC TCGATCTGCG AGTACGGCTT CAGCACCOCG 480  
 40 CTTACAGTGT TGGCCCCACC CACACACCAC CCGGTTTGT ACGAAAACCA CCGCCCAGCT 540  
 CCTCCATC TCCTTCCACC GCGTTGTTAC AGCATCCCN CCGCCNCCAC GTTCCTTGT 600  
 45 CCGTTCCCG TCCGGGAAGC CCGGGAAC ATTCACCA GAACCGCAAC CCNTTTAGTT 660  
 CTTCTTCCT NTTTCGAAC CACCTTGAA CGGAGNCCA CTTTANNCC CTTTACCCC 720  
 CTTTGATCCC CCGGAACCC CCAAAATGA ACCAANNAGC CCAACNND TGCAAAAC 780  
 50 GANTTGCCCN TTTCAAGGTC CCATCCTTG CCCCCGNGA ANAAANTNC NCCGCCNA 839

## (2) INFORMATION FOR SEQ ID NO:429:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1315UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GATCTTGGCG AATATCGGCT CCCAATCCGT ACCCATCCAC TTGACACTA CCGACTGCAC	60
CGCCAGCGTG TTCATCGGCA CAAGCTGCTC TCCTAGGCTC AGCAOOGGOG GCACCACAAA	120
GTAGAACCGC CGGTGGTCT CCAGCTGCTC CCGCTGGTTG CGGAAGACA CGTAGTAGCA	180
ATAAGAGCCC GGTACGTACA CATCCACATC CAAGCAGCTG TCCTCCAAGA AACCTGGCT	240
CAGCAGATGC TTGTAAACT TGTTCGGCTG GAACCTCGTA TTCTTTCCG GCGGCAGTT	300
GGTCCACACT AGCCCGTCCC GTGTACAGG CGATCGGCG GCTACCACCA ACCGCACCCG	360
CAGCCCGCTG TCCTCCCCAG CGTCTGGCC AACAGGTAAA CATGGCAAAG TGAGCACACC	420
CTTTCCAACC TCTCTCTCA CCGCTCCCC GTGTGGTCT AATCTCAACA GCACGGTTTT	480
CATGGCTGTT TGCGCCCTTT GCTGGATCT AAAGGAAGCT TCGCTTGTC TGCAGTGTCT	540
AGCCTTGGGA ACTGCCATAG TCCTTTGACC TTGACCGGT GTTAAATAGT GCATTTCACT	600
ATACACAATT TGAATTACG NCTCCNCNG TGCTAACTGA GGGANATTAC CCNAAACCCG	660
GANGOGANNA TAACNGTNA NAATTNCCC GGTGACACNC NTGCCNTATG NTTCNTTTT	720
TGGAAANAAA CCTTNGGNN GGTNGGTGN NAAAAATTGA AAACCCNGN TNAATCTNC	780
NTTNACTTN TCGGAAAACA AAANINGGC CCCCCCN	818

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1316RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GATCAATAT ATGCGATGGT CTGAAGGTT GTCCAAGTGA GTAGCTTAGC GAATACTTTG	60
CCAAGGCTC TGCGACATCA AGAAGAGTCT CAAGATAATA ATAGTCTTT TTGGGCAGTA	120
AGCGAAGATT GTTCTCGCC TTGTCAATT CTGCGGGT CCTGGACCCA TTTGGTGGC	180
TGTTGAAAAA GCGCCAAAAG TACTTCAAAA TGACCGATTT TTGACCTGG AAACCTGOCT	240

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GGAGAGAGAA GTCTGTCAGC AACGTAAATT CACTGAGAGA CAGCAGTGTT TCGATAATTG 300  
 CAGATTCTTG ATTCTCTTC GTTAATTTTG GGTACAATTT AGATGAGCTT AATAAAAATT 360  
 5 GTAGTGCTG GACAGATGCC GATTGAGCCA ATAAATAATG GCTGATGGAT TAAATGATGC 420  
 CAGCTGCGCC AACTCATCTG CATTCGCTAA GGAAAGCATT GATTTCAGAC TATAGTTATT 480  
 GGCAGCATCC ATGTACTTTG TTGTACTCGA TCAGGTCTT CACTGAGACA CCGTCAGAAA 540  
 10 GCGTCACCGT CTCTGCAATG AGTTAGAGCC ATCCATAGAT TTCCCGAGG CAGTTCCCGC 600  
 CATGAATTTT CACCCACTTC CCCCCCGTC CATACCGCAA TTGAACATT CCGGTCAAT 660  
 ACCTTCTTCC TCCCCCGNT NTTCNCAAN AGGGAAGTTA NATTCCTGNC CTTTTTTTIN 720  
 15 AAAACCCAAT TCNCACTTT TCNGGGAANT TTTCGGGTT GAGNAAAANT CCNACNCCG 780  
 GINGCCGGTT TAATTNCC 798

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 820 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1316UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GATCAACACT CGTACAAAG AATATAGTCA CATGACCAGA TAATCGTGT GACTGGCAAC 60  
 35 CATACATCGG CACCATGCA CCCACATGAT GGTTTTCTTG GGGGTGGGC CGTGCTGGC 120  
 GGGCTCCCG GTCTACGCTG GGGGTGTAG GGGCCGGCT GGGCGGOCAG GGGAGCAAT 180  
 GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGCAGC TGGAGGTCC GGCATGTGTG 240  
 40 GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCTGT 300  
 AGGTTTGAAC ATACTATACA AGCTCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA 360  
 GATTGTCAAA GGGCAAGAAG GTTTGAAGA AGAAGGTGT TGACCCATTC ACCAGAAAG 420  
 45 AATGTTACGA CATTAAAGCC CATCCACTT CGAGAACAGA AACGTGGTA AGACCTTGT 480  
 AACAGTCCAC CGTTTGAAGA ACGCAGCTNA CTCTTGGAA GGCNNTTT TCACAGGTT 540  
 NGCNITGGCC AACCANCNG TTONTAGGAT TNNCNTTCC NAAAGGTTC AATTANAATT 600  
 50 TACAGGTCC NGGCAAAAC CTTTNGACA CTTTCCCGG TTTGGGATTC CCCCCCNA 660  
 CATTTTAATT CAAAGNCCA AAATTTGGCN ACCTTAATTA NNGNATNTCC TMTNAAACC 720  
 NNNAAAANN TMTNATNT TTTNCCCTG CNINCCCAA AAAATTNCC CATTNAAAA 780  
 55 ACNTTTTNCC CNCCCCCN NTNAAACNCC NAAGTTTTN 820



## (2) INFORMATION FOR SEQ ID NO:432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1317RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GATCTTTATC TTTCGATGAT ATCTTTCTCTG AAGAATCGAC AAACACCTGG TCCAGCAAAT 60  
 TGGAAGCTAA GTCTCTCCAA TOGGATGCAA AATAGTTGAC ATACCGGCGA TTAACTTCA 120  
 CTAACGGGGC GGCACCAATA TCTCCAGAA CTGTATTAT TTOGCTACGC TGAACGATT 180  
 GTTCAATCAG CGTAATATTC GTCAATACAA AGAACCCAAT TCTCTGCATC TGAGGTATCC 240  
 TTTTATGTGG AGCTCCGACT TCGGGCTCTA AGTTTGGATT TAGAATCTTT TGGGCTTGC 300  
 GCTCTAGAGA TATGGTTAAG TAATCTATAG CATCGCTGAA GAAGCAAGAG AGCAATTGCT 360  
 GTGCATTCTT CGGTGTCATA GATATCGTCC AAACATTTTT TGATTCAATG GGCAGCCATG 420  
 ATTCGGGAGT CATCGATTGT ATAGTAGCAA GGCAACCAGA CTTGTATTCA CTAACTTGC 480  
 GTAGTCTGGA CATAACATCA ACTGTGGCCT CCAGTTACAC CATTATCAGT GGTAAGTGA 540  
 CCCAGAGAAG CGGTTTTTGA CGATGTACT TGTNTCNATC TTTTGAACA NGGACNCGGA 600  
 AATTTCAATT CANGTCNGGC TNCNCTOC CAAAACNGTT CCNIGSTTCT NGTAAAGGTT 660  
 TNNCCCTAAA AATNGGGVIT CCNNGTINAG NITCCCCCCC AATTNNAACN NAANACCCNA 720  
 TTTTNTAAT TCCCCNCCA AAATTCAAAT ATACCCCCCN TTTTNGGTAT TNDAAATTIN 780  
 GGGGNNNN NITCCAAAAA GGGGNG 807

## (2) INFORMATION FOR SEQ ID NO:433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1317UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GATGTTCTT ATATTTGTTA AAGAAGAGTT TTCTCAAGC ACTTTGAGCT GAATAATCTT 60  
 GTCAAACATA TTGTCAGGGC TCCGCTGGTC GTTAACCGCG CGAAACCTCT TGAGGAACCC 120

ATCTAAGATC ATAATTGCGT TTCTGGCTC CGATAAAGCT TTAATAGATT GATGGTTGTC 180  
 GCGTCTTTCT GCAACGCGG ATTTAGTTAT TTCTCTAAG GATTCACAT CCTGTAAAGT 240  
 5 CAAAAATGAT AAACACACGA CTTTGACTGC ACTGTTGTAC GGAATATAAT TCTCCTTCAT 300  
 CTTTTCOAAC CATTGCAAAA GTTGTTCGG CTCGAACGGC ATATGATTGT TTCTGTCCAC 360  
 AATTACAGCT CTGAAGTAT CCTTTTGTAG AAACCTAGC GGTACCGCA TCAATTTGCT 420  
 10 CTTATCCTTA GTAACAATAT TATCATCTG TATGTGGCC CAGGACTCTC CAAAAATATT 480  
 CTTCAATGCC AGCGGACTG TCGTCTTTC ACAACCAACC GTGGCCACAG GGAATGAAAA 540  
 TGAACCTGGT ATCTCGTCT ACCTTATCGA GCTCCAGATG CATACTGGTC CCCCCNAGCT 600  
 15 CCTTTATATC CTCGAATTT CCATAATATC CAATCCAAA ATCCCCAAAT CNITCCTAGG 660  
 AANATTTTCC NNNACTINGAA ATCCCTTAC CTGTINTATA CCCCCTGNAA ATTTNGGATN 720  
 TTGATTCNG CCAGGGANTA CNATTCCNA TTTTINTTIG TGANNAACAA NGCTTTTGAA 780  
 20 TTTTGTGCC CCCCCCTGT GNATACCN CCTCCTCCC CCCCINTTIN TTACN 835

## (2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1318RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GATCGCCTCG TCGTTGCGCC GGCTGTCAG GCTCTGGCA AGGAACTGCC CGAACCGACC 60  
 AACCAAATCT GGCATGTCCT TCGGTAGAT GAAACCTGC TGCTTGCTGT CCACCGCATC 120  
 40 CCACAGTTG TTCAGAATAC CCTCTGCTC CGTCATGACT CTTGAGCGT GAGTGCAGTT 180  
 CCCAAGGCTT TTGTTGTGCT TGGCAGTTGA AACGACGCTC GCAGCGGCAA AACACACCG 240  
 GCCCCGCGC AATTGCTCAC GTGCTCTC GCGCACATA AGCAAGCACA CCTGACCGC 300  
 45 ACACGCACCC TGCAAGTAG GTCAATACCA AAGGGGCACC CCGCTGACC GTTGCTGCG 360  
 TCGAGCAGC GCGCGCCAG CGCAACGGC CACGAGCATG CCGTTCTCC GTAGCGCGC 420  
 GCGCGTTGG CCATGCGGA AATACTCG GTTTGGCCA CTGATGCGT CTGCGTCCG 480  
 50 CCGCGCGCC CCGCGGCA GGCACCGTG CTTGGTCAGG GCGCGCGC GCGCGGGTC 540  
 GGTACGTTG GCGTTACCC GCGGTGCTT TAGATGGAAG GTTCTAGGTC TGTGCGTGC 600  
 TGCCCCCTGT TGTGCTACG CCAACAGTGG GCGCGGCTA CCGGCAGGC ACCAAGTGG 660  
 55 AGTGGCTATC ACGTGAAAAG AGGCGGGTA ACGGTGGTC GCGCTGAGA CACATGCAA 720

CTATTTACAG GGCACCTTAGG NGITGACC

748

## (2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 758 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1318UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GCAAAAAATG AGGTCGGCCA TGCGGCGCGG CTGGCGCCCG TCGGCGACCA AGCTCGCGCG 60  
 CCGCTCGCGG CCCCACAGGC ACCAGCTGCG GCGTGGCGGG TAGCTGGCGC CCATGGCGCA 120  
 GTGCGGCACC GCGCCCGCGC GCGGCAACGT CCACATGTGG CGCACCACTT TCTGTGTGAG 180  
 CACACCGGCC CGCACGTGG CCGGCGCTGG CGCGCCCGC GGCACCTGGC GCTGTGTGCGC 240  
 AGCCAACTGG CCTGTTCATGA ACAACGCTGT AGGAATGCCC ATCTTTGCCC TTTCGGCTGG 300  
 CTGCGGCTGT GTGTGTGCTA TACGCTGCCT TATATACCTG CCAGGAGAAA TGTCTGCTAC 360  
 TATCCCCGCG AAAATATCCA TCGATGCGA ACGGCGGAAC TCGCGGAAA CCTGGAGCCC 420  
 CGCCTCTGTC GATGTTATGG AGAAACAGCT AAAATCGCTC AGCTACTCAT CTCTGGGCT 480  
 GTGGTTCAAG GTGCGCGCAA TGCGGCGCAT GCGCAAGTCC GTTTTCTCTC TGTGGCGGGG 540  
 CCAGGGAGAG CGGGCGCGAG ACGGCCAGAT TTTGTGCAAG GCAGACCGGG TTGGCTGTGG 600  
 TAACGGGTAT GAAATACGGG GAAGCGGCGA TTACCACTGG GTTTGCTGTG CAGGGGTGCC 660  
 TGGGCGCGCG GAACCGGGTT ATGGTCTATA TTACAGAATG TGTACAAAGG AGTCACTGG 720  
 GGGGGTGGC GGGCNGGACA GCTGCTCTG TTTCTTCC 758

## (2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1319RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GATCTTCCTG CCTTTTGACC TCTTCATTAA TCTTCTCCTT TAACTTCTTT TCGTGTCAA 60

GAATGTCTGT TAGCAGTTC TCTTCCTGTT TCGGTTTCTT CCTGTTCCTC CTGCAAGAT 120  
 GCAGCATCGA GTTTTGCTGG ATGGGCAAGA AATTAGAATT GATATGCGCG ATCOCTACGA 180  
 5 AGAAATCGTA CGGCACAACC TTAATGAGAT TCTCGCACCA GTTCCAGACA TCACCTCTAT 240  
 CGTCAATGAC TACGACCATC GACTGGTCCA TCGGGAACAG ACGCTOGAGT GATTTTGTGG 300  
 TCAGCGAACC GTTTTCATCG CGTGACAAA TTCTATOGCC AAAGAGCTTC CCATCOGGGT 360  
 10 CAATTATCTT GGCAATCTCT AGCGCATAGG CTGAGTAGC CATGGTGTAT ATATGCAGCT 420  
 CGAAATGCGG CGGATCTTC GCAAAGAATT CCTTCAGGCC TGGCOGTAAT TTCACGTTAG 480  
 TACCAACACT TGGCGCGTTG GTTGGCTTTT GGGCCCCATA TAGAACGGG GCAGCACAGC 540  
 15 TCTCCATCC GANAGANAAA AACTGCNCAT CCTTAGCGCC CGGTATTGGG GTTTGTGTTG 600  
 GTTCCCTTTG ACCACTCCCC CATGGTGGGT TCACACCGGC NATNGATTGN CGTCTGGTT 660  
 CAATTTTACC CCCAGCATNG CTGCGCNCN TCCNNCAAC TTGACTGCN CCNCTGACCA 720  
 20 AAATCCAAT TGCNITGGAC CGGATTTGTT TTTTNTTTG AAACGNANT TCTNGTGN CNCTGACCA 780  
 CTGGGNOCC CNCTTCCCN A 801

## (2) INFORMATION FOR SEQ ID NO:437:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 834 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1319UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GATCATGGC ATGCTGGAGA ACCCAATTTT CCAGTCTCAG ATGAACGAAA TGCTCAACAA 60  
 CCCGCAGATG ATGACTTCT TGATACAGCA GCACCCGCAC CTGCAGGCAA TGGGCCGGC 120  
 40 GGGGCGGAA ATGCTOCAGA GCCCCTTTTT CGCCAGATG CTCACCAACC CGACATCAT 180  
 TGGCAGATG TCTGGCTGC AGATGGGCAT GGGCGGTGCG GCGCGGAGC AGGGCAOGA 240  
 CTTTCCAGCC CCGGCTCG CGGCACACC CGAGCGCGCC GCGCTGCGC CGAACCGTT 300  
 45 GGCTGCCATC CTAGGCTTGC AGCCCGGCGC TGCTAACCG CTGGGCGCTG CGCCCGCAGA 360  
 CCGCGGCTT GCAATGCCCC CTCTAGACCC GGTATGCTC TCTTCCCTCT TCGGCGCTG 420  
 GCGCTGCCAG CCTTGGCGCC GCGAATAAC AGGCTNCCC AAGNANGNEN TANCAACAA 480  
 50 ANATTCGCC ANGCTNAATN AATNGGGCN TCTCAACTT GAANAANAT TTCCGGGCTT 540  
 NAAGCGCNG AAGATGTTCT NTCNNGGGCG CCTTNTIAT CTTTNTTAA GGNAAANTIN 600  
 55 TAGGTGNGA NTNTCTGCT NCNNGGGCG NGTTCGCGT TTTNTTAT TCCCNNTIN 660

TTGINTTCTC CNINCTGNIT TGCNACCCCA CNCAATTTTT TTINGGTGGG GGCINCCNIN 720  
 TTTTCATNNN TTNCNANNAC GNOGNTAATT ATANTTGINT ATCAOGTCTT NTTINTTTTT 780  
 5 NNCCNACNGN TTGGGTGGCC CCTTINANNT GAGGNTGGTG TAGGGAAAGA AAAT 834

## (2) INFORMATION FOR SEQ ID NO:438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1320RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GATCTTTTCA AGAAGTTTAA CAATGACTTT AAAGCTAGCA TTGATAAAGT ACTCAAGAAA 60  
 OCTAACAGAG CGGAGATGTA TGATGCTCTT TTGTCAATTA ACGTCCATTC TAACAATATC 120  
 25 ACCTCGGGAT TGAATAGAGC TATCTOACT GTTAATTGGT CGTTAAAGAG ATTTAAGATG 180  
 GAACGTGCTG GTGTACCCA TGTCCTGAGT AGGCTTCTTT ATATTTCTGC TCTGGGTATG 240  
 ATGACAAGAA TTCTTCGCA GTTCGAAAAA TCTAGAAAGG TTCTGGTCC TAGAGCTTTG 300  
 30 CAACCTCGC AGTTCGGTAT GTTGTGTACA TCCGATACC CGGAAGGTGA GGCCTGTGGT 360  
 TGGTTAAGAA CTTAGCATTG ATGACACATA TTACCAOGGA TGATGAAGAG GAGCCCAATA 420  
 AGAATCTTTG CTACTTACTG GCGTGGAG AACATTACAT TGGCTAAANA ANGGCNCCT 480  
 35 TCCTTTTAAA TNNNGGGGT TTTATTTGGA AAGGGTACTA CCCCCGGTNC ACAAATCCC 540  
 CCCCNGITTT TTGTCCCCC TTTTAACTN TANAAAAAC GNGTAAATTT CCNNATTTCT 600  
 TTTCCNNIN TCCCAANNIC CTCAAACTT NTTCTTTTGC AAGGAGGGGG GAAATTININ 660  
 40 ACCCTTTINT TTININGGAA GAGAATTTTT GTCCCGGNGG CCCCCAAAAA TTTTAAAGG 720  
 GAANTCNITA NATTCOCNAN NGGGGNINNT AATTTTIGGN TTTTANAAAA AAANCCCCC 780  
 CNCCGNAA A 791

## (2) INFORMATION FOR SEQ ID NO:439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1320UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

	GATCATGAGG GAATCCTTGG AAGAGGATGA CAAGAAGTCC GACGATGAAG GTGACCTGTC	60
5	TATTCCAGAT GCGCCTTCCT CTGAGGAGGA TTAGGCATAT AATGGGTGCT TTATATGTAC	120
	ATTAAATTAAC ATTCCGCTTT AGCTTTTTTA CTCCTATCCT TACGGTAGCT CACCCATATC	180
	TGTAGCCCTG CTCAGTTATC ACTAAAACGA GTGCCAGGCC CTAGTACTAT ATAATCCCGA	240
10	GTTCGAGCTG AGAAACAATG TCTGATTCCG CTGGTTTGCA TGGGAGTACC GCGATGCAAG	300
	ATCCAGATAG CACTTTAGTC GAGGAAAGGT TGGCGGCTAC GCCAAAAGTT ATCAACAAGG	360
	TCAGCAAGAA AGGTTCAAGC CCGCTTTCAG TGTTTAAGTT TAAAGAGGGG AGCCTATCCT	420
15	GCCNAAANTG CGCCAGGGTN CNIGAAATTN GGAGAAAAA NTGGTTTTTT TCCGGAAAAG	480
	CGCCCNVGA NNCCAAAATT TATTNGGGAC CCNCNACACC NCGAGAAATT TNNITNAAGN	540
	GCGCCCTTTA AAATNCCCAA TNICTTCNAA ANNATTGAG GNGGAAAGAC ANTTTNTTIN	600
20	AATTNCGGG GGGTNTTTTT TTGCGCCCC GNGNTCNIC CCNCTCCAC NANTTINAAA	660
	NATAGGAGGA ANGGNGGNG GCCANATTC CACCTTTCNN AGTINGANNG CCNGNAAANA	720
	GNTTGGATGN CCACCAATNC GGGTGNGA AAANANNCN NACTGCTTGT ACACAAATTT	780
25	TTTTGTGCCG CNGGTGACAG AAAAAAGAN GGATTTTTTN ACAACCNAA AAANAAAAA	840
	AAAA	844

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1321RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

	GATCAAGTCG TTCTGGACT TTCTATGTC GACGGTGCTG TTCTTCAGCC GGGAGGOGAT	60
45	ACGGCTGGCG ACGCTGGCA TCAAGACGGG CGGGGACGGC GGGCGGGGG GCGAGATGTC	120
	TGCGGAGCTG CAGACGGCGG TGAATTTTGC AAACATACCG ATGTGCATCG GGGCGCGCT	180
	GCGGGTGGTG CTGGGGTGT GGCAGTACTC GAACCTCAAC AGCTACTTCA CGCAGCTGCC	240
50	GTTCTTCTCG TGGTGCATCT ACCTTGIGCT GCTGTGATC CTGGCGGAGC TCGCGAGCGA	300
	GCGCTGTAC GTGGTGAACC AGTTCATGCT GAACTACCGC AAGCGGTGCG AGTTCGAGGG	360
	TGCGCGGGTA GCAGGTGCT GCTGGTGAA CTTCGCGGTG ATCTACTGGT ACGAGAACTG	420
55	GTTGAATGGG CGCGGCAGAC GTGCACGACA GCTACAGCCA GGAGGCATCG CGGTGCTTGC	480

TTTTNCCCCG GGAAGGTTG CCCCCNCAA AACTTTNCCT GGCCCGNTCT ACTTGAANAA 540  
 CTTGCGNCTC TGGGCCCCCA AAAACTTTTTT TCCTTTTNTT TNACAAGTTC CTTTTCGGN 600  
 5 NATTTTTTAC GGGNTTNTTC CCCCCNAAT TTNTTGCCCC TTCCNAAGGT TTTTTCOCCC 660  
 TMTTNTTTTA NCCNOCCTN NCAAGGGGGA AANNITTTTN CTTOCCCCNC CCGGGGAGAA 720  
 ANNGGGGANT TTCCTTTTTT TTAAANGEN NCCCCCCCN ANGNITTTNN CCCCCAGAA 780  
 10 NATTTTTT 788

## (2) INFORMATION FOR SEQ ID NO:441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1321UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GATCGAATTC GATTTCCTTT CGGTGCAAGG AAACAGAGCC TTGGTTAAAG TGGGATACGA 60  
 AGACCGTGCC CAATTTTCGT CGGCCCTTTC TACATACATC TCAAGGAGG AACTTATCGG 120  
 30 CGTGCCATTA GTGGTCCATA TATTGCAAGA ATGTACAAAG TTAGAGAGGA TGAAGGTTGG 180  
 GGAGGACGAT GAGCTATGGT TCAAAAGGAG TTTGGAGGAA NAAGTANCGG ATTCCAGTTG 240  
 TAATTAGCTA CAAAAGCGGA ACGGGTCACA CTAAAATTCC ATGCGCTAAC TTTTCCACTG 300  
 35 AAAGAAGCCA CATGAAGCTT TTATATCTTC TGGGGCTCCT CTGGGACGCT TACACGTCCA 360  
 GAACTGTTTC CCAAATTC TCGACGTTTT CGAGGTTTTA AGAACCGATC GGTCCTCGTG 420  
 CTTGCAGAGA GGTGCATTTG ATGGGGCGAA AAATGGTTTT TCAACCGCG AGGGTGGTTG 480  
 40 TTCAGGAGCT TTGTTAGTTC GAAGTTGGAG CGCCATTCCA TTGATTGCC CTGCTCTTC 540  
 CTCCTNGCA CTTGCCGCTT GCTGCTATGT TTAATTACTA NAAGCACCGA NCCACACTTA 600  
 TCTGGTTTTT TTTTCTATC CTGANACTOC CTTGAATTAT TGCTCTCTT TGAATTCCC 660  
 45 CCTGTCCAC GTTNGTTACA CTTTCTCTT GAATATCTT CTTTCCGAA GCACCATNT 720  
 TTATAATTAG TCCTATTGAC CCCCCCACC TGGTTTTTGT TTTCTTCCA ACANGTCTC 780  
 TTCTOACTN AGNTTGTAT ACNGAATGTC NACCC 815

## (2) INFORMATION FOR SEQ ID NO:442:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1322RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

```

10  GATCCAGGAA ATAGTACAAC GCCCTGGAT AATGCCAGG ATTCTGACT CCTAACGAAA      60
    AGCCTCTCCT CTTCTAATTT CTTATTAAAG TAGTTAGCTG CAAACTGTAA CAAATCCCCC      120
    GGCCGCTTTT GCTCCACTTC TTCTGGAAT GCGTCAGTA GGTCACGGTG TTCCTGTGAT      180
15  AAAACCATCG AGTAGTTTGT TGTGTGATG AGAAAACCTG CCTATAGCGG AACCAAAATG      240
    CTCTAGTAGT GTGACGSCAC CGTTTATCC AGTTTGCTAA GCAGCTGCC TAGGTTAGGG      300
    AGAGTAGAAA GTGTCAITGG ACCCGAATTT CCTTCTGCGC GCGCGAAGC ACGTTAAATG      360
20  TGATTACAGT GATCAGCTA CTGGGGCTAA CTACCAATG AGACAGGCTA GTTGTGAAG      420
    CCTGAGGAGG TCTCCGAAAA GCTTGATGTG AGGATACTCG TGTTCACTTA TCTTGTATGC      480
    CTGTATTGAT CTGTCCGTGA GACCTCGAGC TCTTCGTCCG TCAATGCCCC GCGCCTAGAG      540
25  AGCTAGGTG ACTCGAGIT CTACAAAATT TCNAAACNCC TTGAAAATTC NCAACATTGT      600
    TNIGGAOCAT CNANTTCCC NCCITGGAA NNAAGCCCTC CANCCTTTTT TNACGTTGCT      660
    NACTTNCN CTGAAAAAAC GTTCNATTTA CCTTNTNTA CNOGGCAGGA AACCCCCCAN      720
30  TTCTTTTCC ATNACCGGT ANCNAAAGA ATTTTNCNGC CATGNGGTTT ANG      773

```

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1322UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

```

45  GATCTTCACA ATCGACGCCA CGTCCATGCG GATGTTCCGC CGCACTGCGC TCACTGTGAG      60
    ATATTCTGAC GGAGAGAGCC GGTACGTGTT GATCATGAAG TTGCGCACAT CCTTGTACGC      120
    TTTGGCCGTC TTGAACGCCA CCGAGTCGTT GAAAAAGTCG GGCAACGGCG GACGCTOCAG      180
50  CTCATGGATC TGGTTGAAT GGAACCAAGA GGCAACGAC GGCAOGATCA CCGGGTGCGC      240
    CTGCTTCGCT AAGAAGCGCG CCGCCTTGTC CTCCAATTTT TCGCGCTCCT GCTCGTAATC      300
55  GATCTTGGGT TGTCTCTCT GCTGCTGCTG CTGTTGCAGA TGTGGCAGCA CAGGTACAGA      360

```



TGGATTCAAG CTGCCCCGTG TGCCCCGACG AAGCGTTCCA TCGCCAGCGT TGTCAATATT 420  
 GCCATCCTGG ACATCCATG GCTCGCTCAT CGTTATAAG AGTATGCCAC GCTACTTTCC 480  
 5 CGGTTTAATA GCTTTCAAAC GCGTCTTGGC TCTGCTACCC CGCTTAANTC CACACTGGTT 540  
 TWIGTTTTCC NCCATACCCA AANTTTTAAA ACCCATTTTT CCACATCAGC CCCATATCCT 600  
 CCGTTTGGTN GNGGAAATTT GAAACCCANC OCTCGCCTGG CGGAAAANNC TNCCTATGGA 660  
 10 CCCCCCTCCC NTCCTTCAAT CCGTCCCCCTT NACCAAGNNT TTAGCCCCCC GGNANANGAC 720  
 CAATTTGGTC CTTCGGTCNC TTTCCTTNT TAAATTGAAA AAGGTINCCC TTTGAAAATT 780  
 AACCNGCCC NCTCCCCC GANAATGGT TTTTTGT 817

## (2) INFORMATION FOR SEQ ID NO:444:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1323RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

30 GATCAGTTTG CAGGGACCAT GAGCAGGGCG GCGACGAA GCAGCTCTCC TTGTACACC 60  
 TCCGTGCAGG GGCTCAACAC GGCCTGCAG GCGACGAGC ACGAGGAAGA GGAAGATGCG 120  
 GCAACGTTTT ACATCCATCC AGATTTGAGG ACATCAGC TCTACTTTGA GAAGATGATC 180  
 35 GATGAAGAGC CCTCCCGGC GCGTGTAAAG CCGGTGTCT ACATTAATCC GTATGGAGAG 240  
 GAAATTTTCC CTGTGCGAA CTCTGGTCT ATCCACCAGC TGAAGCGATG CGATATGCTT 300  
 GTGTATCCA TCGGTCTCTT AATTACCACC TATTGCCATG GTGATCCTCC GGTACTTGCG 360  
 40 AGGTGGTCTT CCAAGGGAAG ATGAAAAAAT GCTACTGGTC NCTCCAATCA ATNNCNAACC 420  
 TCCGATTAGG GGGGGGGGNT TTTTTTTTAA ATTTTAACCC CCGTTTGGGG TGACCCGNNC 480  
 NAAAAAAG GGGGCTTGN NNNTTTTTTT TNGNCCCCC CNGCTNTTC GNAGTTTTTT 540  
 45 TTTTCTGGNG GGGGGCCCC CCGNNCGAA AATNTTNNC AAAAGGAAGN ATTTNCCCCN 600  
 NANGGGGANT TTTTTTNTA NNAATNNAA AAAAAATTN TTCCATTCOC NNAATTNNN 660  
 NTTTTNNNN CTNTTNGGN TTGNAANTT NACCCCCNC NANAANTTN TTTTTTTCC 720  
 50 CCCCCCCCC CCGGGNNNN TNCNTTTTT TNNNGATN 759

## (2) INFORMATION FOR SEQ ID NO:445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1323UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

```

10 GATCCGTTTT TCCAATATTT CACCGTCTTG TAAATCAACA GTTGAAAAAC AATGGCGTGC      60
   TTAATCGACG AACGCAGCAC AACCAGCAAT AGGCTTCGAA GCGTTCCAG AGGTGATATC      120
   GCAAAGTTGC TCGAGCACTA GAAOGGACTG GGTCAATTATA TAGGTGGTAG TAAGAAGTGG      180
15 GTAGAAGGAA GGGGACTATG GTACAGGCGG GCGGTGGAGG CAGGGACGGC GCAGTGGGTG      240
   CCGCTCATGG GCATGGGCAT ATGCGGCAGT TGTAACAGTT GGTTTACAAC CGGGGGGGGG      300
   TGGGGACGTA GACGTTTACT GCGGACCTG CCGCGGCACG GGAOGCTTGA CCGAGCAAT      360
20 GTTGTGTGCA CGCTAGTGGG GCTGTACCAC TCGATTCCGG GCGACATCCC GCTGATTAAAG      420
   ACGCATTGNA TCGCCGTTGG GTGINTCTGA NCTAAGTTGG ACCGNGAAC CTGATTGTTT      480
   TGTGGCNAGA ACACATNCCC TTGTGGTGG ACCCACCGA NAATTAAACC GCCCCNOCOA      540
25 GACNAGCCGC CCTCCCCCN GNGCGTTTGG GTTNNNGCCA TTINGCCGA CNTCCAAGAA      600
   NITTACTNGC ACCGNGGNG GCACCGCGN CCGGCACTT NITTCAACNC CNTTCCCCC      660
   CNTGGGGGGG NCCCCCCCCT TGAAAAANNG TGGGGGGGAC CCGTTGGGT CCCNTTCCC      720
30 CCATTGNATT TTNTTTANA NANNACCAAC CCGCTCCCT TNNCCCCACN CAAANNNGT      780
   TNGTTAANCT NCCCCNTAT TCTNCCCCC CGNCCNTAT TCCNACCGN CNGT      834

```

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 785 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1324RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```

50 GATCCTACCG GGATGCACGA CGCATACAAG TATATCAGG ACCTTGCCGA GGAAATGGGA      60
   CATAAAATTG AAGGACCGA TCACAATTGG TCGTTCTTA TCATAGCCAA GATATATATA      120
   TATATCTGGG ATAATTACAG CGCTTGGTAT GTATACCTC TACATACAAA TACTTACATA      180
   CACATAAATA TAATACAGCT ACTTGTAAAG CGAGAAAGT TACTTCTGGA GAGCCATTAG      240
55 AGACGCAACG AATGTCAAAA TCAACCTGG GCGGACTTCA TTGATATCTT CAGGAACCAA      300

```

CCAGATTAAA GCACCAAGTT TTCTCGGAT AGAAATTGCC AATTTAGCGT TTGCATACTT 360  
 CTCCTCTCTT GTTACGGGCG GGAGTAACCA AGTCATAATC CACATATCCT GGAGCTAATC 420  
 CGTTCAATAC ATCCAATAGG AAATGGGCAT TGCTCAACGA AGCATCCCTG GAAAGACATA 480  
 TCCTGCTCGA TTGGCCACCC TTGGCACTTG CCTTGGGCCC ACTTTAGATC TGACATCTGA 540  
 ATNCTCTACC AAACAAACTN TGAGGANATN TGTTTGACAA GTTTTCTGCN CCTCACTGCC 600  
 AACTAAACT AAGGTCACAC CTNTTTGCTT CCCCAATTCT AACCCCTTNN GCCCCOCAA 660  
 AAAAATTINA ATTCCAAAT TCANNCCCTN TTTGGTTTCC CCCCCAATNA NCNINAATTT 720  
 CNNCCNTNN CTGGNCCCGG NNGAAACCCN TGAAATAACC CCCCGAATAC CTNCNTTGCC 780  
 CGAAC 785

## (2) INFORMATION FOR SEQ ID NO:447:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1324UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GATCTTAAAG AGGCTCAGTA TGCAGAGGCA GTTTCAGAA GAAGACAGGC TGGGCTTGA 60  
 AATCCCTCAG CTCCCGCGGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA 120  
 GCAAACGCGG CTGCGGGGCG CGGCTGCAT CCTGGGTGCC CCTTATGAAC CGAGCAGGGC 180  
 GTGTCCACT GGTGCAGGCC AAAAGCGGGA CTAAGACTAC TCGTGTTC AATGAGAGCAG 240  
 GCTCTCACT GAGAGCAAGA TAGAOCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAAG 300  
 CGTATTCCAC CGGACCGTC CCCAAGACA CAGCTACCGC CCGACTTGC AGCCGCTCTG 360  
 CTGGACAGC TGGACGAAG GAAGGGAGAG CCGGGCGCG CGCAGAGGC GCGTTGAGA 420  
 AGCCCCGTT TGGTGGGTCT AGCATCCCC GGANATNCNT CCCAGAAAA ANNTTTTGA 480  
 ACAAGCGGCC CGCCCGCCCC CCNCAGAACC TCCNTTAGC GAACNTTNA AGAAGAAATNT 540  
 TNCCANTTIG CCGCCCTNCT TGGANAATGG TGGCCNGCT TNACNAAAG CTAGGTGNC 600  
 GCGCCGAAAA NCACTTTGCT TNACCGCATN CTCCCCGAA AGANAGANAG NTCCCCNCAC 660  
 TTTTNGCAA TTTTNTCCCC CGGANAAG GTTCCCGTIN ANCGANGGG NGGCGCANNA 720  
 ANAAACCTAC NCANTTTNAA CATTCCCCC CNTTTTTTC AAAAAAGANA ATGNNTTTTT 780  
 CACNTGACA ANTGATNCT TTTNTGAAG GNGNVAGTAC CCCCCGCTG CCTNTCTOC 840  
 CCTAGANCT NCNATTTTGT TTTNT 866

## (2) INFORMATION FOR SEQ ID NO:448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1325RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

GATCAATGCG GGAGTGGCAA AAAGCGACTC AAGGTGAACG TGTTTCAGCA CTGTTTCATGA      60
TGGGGGGTGG TCATTTTGCC GCAGCCATCG TATCTCACCA ACGCATAGAT ATCAGTGGCA      120
ATGCCAAGAG GCATGGAGAA TCGTTACAGG AACAGGCGGT GCACTTTCTT GAGCACAAAA      180
CGTTTCACAG ATACACCACG AGGCGGAAAC AAGGAGGTTC ACAATCGGTT ATGGATAACG      240
CCAAGGGGAA AGCAAATTCC GCAGGCTCTA CGCTACGTAG ATACAATGAG GCGGCATTAC      300
GGAATGACGT TCAGGACCTG TTAAAGAAAT GGAGGCATA CTTGGAACGC TGCGAACACA      360
TATTTATTAG GGCCAAAAAT GTTGGCGACA GGAGGTATT CTTTACGGAA AATACCCCAT      420
TGACCAAGGT TAGACCCGAG GATTGGGACA TTCCCATTC AACCCTAG ACCTACCACA      480
AATGAGCTAA GGCGAGCATG GTGCGAGATA ACATACTTGA AGAAGACATT GAAGCCAGC      540
CATCACATCG GAGCGGCATA CTCTAAAGC GACAATGATC CACTGCCAAT AAGCGACGTT      600
GTACGCAACT TAACCCCGNG GNAAACCTTA NCAGGAACGG CTTCTTTCTT TGGATTGAG      660
GCCCCNNNT ATTCCCTNIT CNAAAANNT NNTTCCCCAA CCTCTTTTTA AACCCCGGA      720
AAAANNITIN AAACCCNCNC CCCCCCA      749

```

## (2) INFORMATION FOR SEQ ID NO:449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1325UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

GATCGTGCCA TGCTGATGT GGTATTTGGA TCGGGGCGCG GGTGGGAGTG CCAGCTGGAC      60
TACGAAATCA AGGACGAACG TGAATTTTCA GCGCCCTAG ATACTGTCAA GGTGCGCTA      120

```

GCGCCCGAAA AGAAGTGGCC CTGCCGCACG ACCGTGCAGC CTGGGCTTGG AGCAGGGGGG 180  
 AACCAACACGC CGACACGCGT ACCTCTGTCC AAGCTCTTTG TAGGTGOGAA AAACACCAAG 240  
 5 TTCAAGCCAG TGATGCGCTC TGCGGATGCC GCTATGCGGG CAGGCAGTGC CGCTTCGGGC 300  
 CGCCACTGTG CGCTATTGCA TAAGACACAG ATAGATGACC CACTGGTCAT GAACAAAGCC 360  
 GGTGACGACG AAGTGAAGT TGTAGTCGAT CCTATTTTGT CAAAAAGCT ACGCCAGCAT 420  
 10 CAGAGAACAG GTGTTGAATT CATGTATGAC TGGTCCGGG GGCTCCCAAG GTCCGAGAAG 480  
 GACGATGATA GAACAGTGAT GATCTTGAA TATGATAGTG ATGTCAAGGG TTGTCTGTTG 540  
 GCGGACGAGA TGGGATTAGG GAAACATGC ATGACGATTG CTCTGATCTG GACGCTACTG 600  
 15 AAGCAGCATC CCCAGGCCAT CGTCTGTTC DATGCTCCGC AATTGGGGGG TTGTTTTC 660  
 AGGGTTTTTT GCCANAAATT CTCNIGGTAT GCGGGGIGA CTCTGATTGG CGACTGGGAA 720  
 AANGATTTCN CCNATNGGN GCGANGAAT AAATTGGANC CTNGAANCN ATTGCNAANT 780  
 20 ACCCCCCAAA ANAAAAAATG N 801

## (2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 774 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1326RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

35 GATCGAATTA AGTCAGATTT GATTGOGATG GCTACTAAGC AAGTGCATT GTCAGACGGA 60  
 CCGAATCAGG TACACATTGA AACTCGTGAG TGGCTAGTGC AGACAATCAT AAATGAAAGT 120  
 TGTGGCTGGA GCAAGGGAAC TGCGATGCGT TAACTTTCTC AAAACACTCA TGGGTGGTCA 180  
 40 AAAATCAATC TATTCAGTAT ATAGTATATC AAAACATTAA ACCAAACTAG GCGCCAGAA 240  
 TATTGCCAAA ACATTGCACT GGAGTATTAG TATGCAGAGA AGTAGCAATG GCGGGCTAGC 300  
 TGGTTACGTG GCATTCAAGG ATGACTTATA GAAGCCCATT AATCATCTTT TAGTGACAGT 360  
 45 AAGATCAGAC ATTAAATAAC GTATCGAATT TTAGGGGAGA AGTCATCACA CTTGCATTAG 420  
 TATACCGCAA TAATTGCGG ACCACATCAG TTAATACTGG GCATGGTTTC TAAAAAGCGA 480  
 AACTGGGTTC ACATTCAAGT TGTPTTGCAA CATAGATGTC TCTCCTCATG CTGCTTCTCG 540  
 50 GTTGAATAAC CATGCTTCAG TAGGCACCGT TCCAGTATT TGGTAATTAG TTGCCAGACT 600  
 CCTTTATAAA GGATGACCCG AATATGANCT TCATTAACA TTGCCNGGAA AANANATTTG 660  
 GCANCCGTAN ATATTTTCTT GCCAATTGAN ACCGTTCTINT GAACCCCTINC TTGGGGNOCN 720  
 55

GCTTCCCAAA AACGAANTTC CCCGGTNGNT NTTTTATAGG TNCNAAGAAA AANA

774

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 779 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1326UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GATCAACAAG CGTTTCGGGC AGCTGCGCGA GAACCTGCGC CTCACCGGG TGACGCGGAG	60
CGGCAAGCGG CGGCTGTTTG TGTGCCACAC GTGCACGCGC GCGTTTGGC GGCAGGAGCA	120
CCTGATCGGC CACAAGCGGT CGCACACGAA CGAGAAGCGG TATATCTGG GGATCTGCGA	180
CCGGCGGTTC AGCGGGCGGG ACCTGCTGCT GCGGCAAGCG CACAAGCTGC ACCGGGGGAG	240
CTCGGGGAC GCGCTGCTGA AGAAGGGCTC GCGCGCGGG CAGCGGCTGA GCCGGGCGGT	300
GCGGGCGGCG AAGAGCGCGG AGGGGCTGCG GCGGGCGGGC AAGCCACGGC GCGGCTGTC	360
GTCTCTCTGG CAGTCCGGGG AGAGCTACGC GTGGTGCGG CCGGCGAGCG CCGGGGGGGG	420
CGAAGAAGGT GCAGTTCTCG ACCCGCAGC TGCTGCGCGT GGACCTGACG CAGGAGCGGT	480
CGACGTTTAC GCGCTGGAG GCGAAGCGTG GTTGACAGGAC GTGAACAGCC TGTCGCGGCT	540
GGACGGACGC CGGAGGAGGG GAGCTGCAGC CCGCGTGGC GCTGTGCTGG CAGGCCACGC	600
ACACGCGGTC GCTGTTTGCC CACCTTCCC NGTTGGCGGT CCTTACGGGA ACCTGCTTGN	660
CGCTTTTGCC CCGAATTGCA GGTTCGAAGG GCTTNCOCG CGNGGQNCN CCGCCCCCCC	720
CGCATCCCC CCGTNNCCC AAAATTTCAA GTTAACCCAA NAACATTCCC TTCTTGCT	779

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 763 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1327RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GATCCAAGCG TCTGGAGTAT GCTAAACGAG CGTCTCATGC CAGGAACAAC GTATTATCTC	60
GTGTAACGCT GTCTCGAGC CTCGAGCCAA ATCTGACCGT TTTTGTGCTA GAGCATACCC	120

AAAAAGAAAC ATCTTGATGC GCTAAACAAC ATGACAATGA TTAGOGOGAG GATGOCCTTTC 180  
 5 ATGTTCTAAA TTCATGCCTC GAGGTCCAG TCGGTGCGC ATGTAGTCCT GCGGCGGAT 240  
 TATATTGGG CGTAGCTGTG GTGAAACATC GCGCTAATT GACGGATAAG CAGCTGTGTA 300  
 CCTTATTTTC ACTATTTCTT TTCACATACC AACGACTAAG GTTGATTCCA AGAGGTACTG 360  
 10 ACTGACCCAG TGGACAGCGT AGTTATOGGA GTAACTGGGC AATGTGTAC GGGTTCCTCG 420  
 GGAGCGGAG AATGGGCTGC TCAAGGCGA CGACGCGGA GCTGACGAAG GAGCTCAACA 480  
 TCCCCAAGGA CGTGGCGAGC GGCATGAGGA AGTCCTGTG GTACGACTTC CTTAATGTGC 540  
 15 CTGGCGGGGA CGACGAGCG AGGCCATCG GACGCGAGC ACAGGACAG CTGAGGACGG 600  
 CCGGACGGA ACTGAAAAC CAAACGGCG AANGGCGCN AGGGGNGG ANCAANGNG 660  
 GAAAGGGGA ANTTTGGCGA NTACNCITGT TGGCCNCCC CCGCGTTCC GANTTTGGGT 720  
 20 TGNCAAATC CCTCTCTAC TTNCAACCT NCTGAGTNA AGT 763

## (2) INFORMATION FOR SEQ ID NO:453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1327UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

35 GATCGGAGC GTGCTGGAG CGTGTCTTG TTCTGTCTCT GCTTGGCTAC GCGGACTTG 60  
 GCAGCGCGG CGCTCTGAG CGTCTCATAC TTGCTGCTG CTACTTCAT GGTTCCTATC 120  
 GTCAAGGTG AGCAACTGG ACAACAGCAC CCAGCAACGG TTGCATTTAT ATAGTGTCTA 180  
 40 CCTGTACGAT AGGGGACTGA TCGCTCTGG ATGCGTATCT ATCTCATTC GGAAGTTCT 240  
 CGAAACGAA AGCGCCAGTC GCTGTGAGC GACAATAGCG AACCAATG ACACAATAGT 300  
 GCGGTGGC GACCGATCC CTGCATGAAG ACCGAATGCT CGAGCAGATT CTTGTGCGG 360  
 45 CGTCAGCGG TAGCGCGCT CGTGTGTGG CGGAGCGCG ATATGCGATG GCACCGGATG 420  
 GCGATGTGCT CGGCGCTGG GATTAATCTA GCTCTTGGG GATATGCTTC TGTAGGAGGA 480  
 AGAGGGGTA GGGAGAAGC CTGGACGCG GCTTGGGAG CTCTGCAACG TTGCGGGGC 540  
 50 GTGCGCGGT AGGCGCGGC ACACCGGNA AATNCGNGN GANCTNGTN CCTCCNTTC 600  
 CCCCCCAA ACTTGGGGC NTNCCNCC CGAATNNCA GNGNCC NAAATCTNA 660  
 ACCCCCGNA GGAAAGNITT GCGCTNTGA NCAANNACN CGGTINAAA NTCCCGGGG 720  
 55 TTTGNGGCC CCGAAAANG GATAAACCN GGNACNACC TTTTGAAATC CGTTTCNTT 780

TTNCCCCCAN ACNT

794

## (2) INFORMATION FOR SEQ ID NO:454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1328RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GATCTCTTCT	GCAAGTTTCT	TTATCGGAAG	CCCAGGCTCT	GGATTTCCTT	TCTCAACACC	60
AATGGTATTG	TCTTCGATAT	CAGAGAAGGA	GCGCTTCGAA	TTTTGCGCAC	CACCATATGG	120
ACTCTCTTCA	TTATTTTTCG	TATTTTCTCC	ATCATTTCGG	CTTGCCAAAG	AAGAATCCAT	180
CGCACCCATT	ACATOGAATT	CTTCATTATC	AGCTTCTCCA	CCTGTTGTAG	TATTTGTTTC	240
ACCATTTATTA	TCCTGTTCGT	TATGTATTGC	ATCACGGGCC	ACACGGCTCA	TTTGTATCAT	300
GCTAGATGTA	TATGGGACAT	AATCCACCTT	TTCCAACAGA	GGACCGAATC	GCTCAACCAA	360
GTATTGATTT	AAAACCAGGA	AGTTCTTTGT	ACTGACCTCG	GCATATTTCCT	GATCTTGCCC	420
GAAACGTGCC	GAAATTACCT	TAAATAAGTC	GAGCAAGCAT	GAGTTGGCCA	TGTTATCAAA	480
GTAAAGATTT	TCTGTAGCA	GCTGACAAAT	TGGATCAAAA	AGATCTTAGA	TATGAGATAG	540
TTTGATATAA	ATTTCATCATT	TACAGCCAAG	ATACCCCTGA	TACCCGAACT	GCAGCCAGCC	600
TTAACTGTAT	AATATGGATG	GTTCGATTAG	TTTCCAATAG	TCAATAGATG	CCATTTTCCA	660
ATATNAACCC	CCCTTGACAG	CATAATATCA	GTCCNIGTT	NINATAATCC	CCCCATTTTA	720
CCAAACCCNC	NCNGTTGATT	NCCCNCTC	CACCCCT			757

## (2) INFORMATION FOR SEQ ID NO:455:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1328UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GATCGGAGGT	ACATAAGTGC	TCTACCGACC	AACCCCGCTC	TCCATGCATC	AACCAATGGA	60
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GTTGAAACAG TTGACTGGCG AGCAGGCGGC CGCACTAGAT GCGGAAGTCA TGGGCCCAGA 120  
 CGTTGGCTAC TCGCTGCATC AATTGATGGA GCTAGCAGGT CTTGCGGTGG CCGAAGTGGT 180  
 5 CGTGCGGCAT TGGGGGCGCG CACAGGCGAA GAAAAAGGTG CTTGTGCTAT GTGGGCGCTGG 240  
 CAATAACGGC GCGGATGGCT TGGTTGCTGC ACGGCACTTG CGGCTCTTGG GCTATGACCC 300  
 TGTTGGTCTAC TTGCGCGGGC TGTOGGCCAA ACAGCCCTTC TAGGCACAGC TTGCCAAGCA 360  
 10 GCTACACTTC GTGGGTGTCC CAGTGCTCTC CGAGGGCGAT GACTGGGTGG CGCATCTTGA 420  
 GGCACGTGAC ACGCTCTGGG TTGTGGATGC GCTCTTTGGC TTTTCTTTTC GTCCGGCGCT 480  
 GCGCGAGCCC TTGCTAGCA TTGTGCGAGA GCTCAAACGC CATGAGGATG ACATCCCAAT 540  
 15 TGTCGTGTC GACATTCCCA GTGGTTGGGA CGTTTGACGC AGGACGCTCA CCGCTTCAGA 600  
 CTTATGCAAG TTGTCTGATN TCTCNIGAAC GCGCGCCAAA AGCTGCTCCC NNCACATTG 660  
 AACTGCGTTT TTTACCNCCC ATTANTTTGG GNGNGTTTC ATCCCNAAAC CCGNGCCCGN 720  
 20 CCTCCNTGTT TTTANTCCTT CCGGATATCC TGNCCCATC CANANTGGGT TTTTGANITG 780  
 CCATGCTNIN ATCT 794

(2) INFORMATION FOR SEQ ID NO:456:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 176 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: DNA (genomic)  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1329RP  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:  
 GATCCGGTAC GCGGTGCTGC ACTTCGGGTT CTTGCGCTG GCGTCTCGT TCGGTTGGT 60  
 GCGGTGTAC GTGCAGTTCA AGAAGGCGCG CTTGTGAGTT AAGTAGAATA TAGTCTAATG 120  
 40 CTATGCAGGG CCGCGGGCGG CGCGCGCGGC GCGCGCGCGG TCACTGACG CCGATC 176

(2) INFORMATION FOR SEQ ID NO:457:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 176 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 50 (ii) MOLECULE TYPE: DNA (genomic)  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1329UP  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GATCCCCGTC ACGTGCCCGC GCGCGCGCGC GCGCGCGCGC CCGCGGCCCT GCATAGCATT 60  
 5 AGACTATATT CTACTTAACT CACAAGCCGG CCTTCTTGAA CTGCACTAC ACCGCCACGA 120  
 ACGGCAACGA GAAGCCCAGC GCGAAGAACC CGAAGTGCAG CACCGGTAC GGGATC 176

## (2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 767 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1330RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GATCTTGAT TTGACATTGT CAATGGTGT AGAGGACTCG ACCTCAAGCG TAATAGTTT 60  
 25 CCTGTCAAA GTCTTCACAA AAATCTGCAT ACCTCCCTC AAGCGCAACA CCAAGTGCAA 120  
 CGTAGACTCC TTCTGGATAT TATAGTGGGA CAAGTGCGG CCATCCTCTA GTTGCTTACC 180  
 CGCAAAGATC AAGCGTGTCT GGTCTGGGG AATGCCCTCC TTGTCTGGA TCTTGAITTT 240  
 30 GACGTTGTCA ATGGTGTGAG AGGACTGAC CTCAAGGTG ATAGTTTTC CTGTCAAAGT 300  
 CTTCACAAAA ATCTGCATAC CTCCTCTCAA GCGCAACACC AAGTGCAACG TAGACTCCTT 360  
 CTGGATATTA TAGTGGACA ACGTGCGGC ATCCTCTAGT TGCTTACCTG CAAAAATCAA 420  
 35 GCGCTGCTGG TCTGGGGGAA TGCCCTCCTT GTCTGGATC TTGGACTTGA CGTTGTGAT 480  
 GGTGTGAGAG GACTGACTT CGAGTGTGAT TGTCTTTCC GTCAAGGTCT TGACGAAAT 540  
 CTGCATACCA CCTCTCAAAC GCAACACCAA GTGTAAAGTA GACTCCTTCT GGATATTATA 600  
 40 GTGGACACG TTGGGGCCAT CCTCNNTTG CTTACCTGC AAAAATCAAA CGTCTCTGT 660  
 CCTGGGGGAA TGCCCTCCTT GTCCCTGATT CTTCNANTTT GACATTGTCT ATGGGTNCCN 720  
 AAGANTCCNC TCAATTNTG ANTTCTTCC CGNCAGGTN TTGAANN 767

## (2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 794 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1330UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

5 GATCAGATGT TTTGTGCTAG TACGTGCGGA TAGTACTAAA ATTACCATAT GGCATCAGC 60  
 ATTATACTAA CTAGTGTGTG TTTGCAGTAA GGGTAAACC ACCCATTACG CCTGTTGTAT 120  
 CACCAGAATC CAAATGCGTT TTTGAAAAGA GGTTAATTGA GCAGTATATC GATGAGCATG 180  
 GGGTAGACCC AATCTCCAAG ACAAGCTTGA CTAAGGATGC GCTAATTGTC ATTGCCCAGA 240  
 10 CACCCCAGCA GTACGGGCTC GCAAAGCAG TTAAGTGGC TACGCTCAAC GCGAATTACA 300  
 GCATCCCCAA CCTTCTGTCA ACACTACAAA ACGAATGGGA TGGCGTGATG CTGGAGACAT 360  
 TTGAGCTGCG GAGTCAGCTG GATATGTGCA AAAAGGAGCT ATGCTCAGCG CTGTACAAGT 420  
 15 GCGAGCGGCG TATCCGGCTC GGGGCACGGG CGAAACAGGA GAATGATGAA CTCAGACACA 480  
 CGTTGACGGA GCCTGACGGA GGCAGTGGC GGGCAGGCTG CCGATGCCCC GCGGCTTCCA 540  
 GCGGAATTGA TTACCGCGAT GGCAGAAACG CACAAGAATA TGTGCAGCAA ACGAAAGAAA 600  
 20 GAAGGAAATG AAAGCCAGGT AGTGACGGCA TTTGCTCTCG GAACAGCGCG TCCAAACGGG 660  
 NTGCGAGGTC AACCGGTTTT TTGGTTACCC GTTNNVTGG TTCCGGAAAA ANAATTANCT 720  
 NNCTTTTAA CCAAAGGCA GGGCCNNTT GCTGAACAAA AAGGGTTTTT GCTNCTNNAA 780  
 25 AATNGCCNC TNAC 794

## (2) INFORMATION FOR SEQ ID NO:460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1331RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

40 GGATCATTTCT CAGGTATFAG AGATTGCTGA TGGCCACCGG CTTTTTCTTC AAGGAATTGG 60  
 ATCGGAGGCG CCTCTAGAGT TGAAACGAGT TTATTATACT CAGCCATTGC TACAAGCATA 120  
 45 TAATCAATAG CCGCAGCGCA ACTCTGAAGA TGATCTAAAG AAGGAGCATC TGCTTTTCT 180  
 CGTAGAACAT TGAGAGCGGT TGCTCTATA ACTTCATGCT TATAAGTGA AGCACTCGAA 240  
 ATAACATGIG ATAAAGGTGG AGAGTTGGCC AATGIGTICA AAGCTTCTAA TTCTGAAACG 300  
 50 GAAATTAGTG CATACCCAGC AGCTGCAGCT TTATTCTTCA AATGATCGAG AGAAGGTGAT 360  
 TCGGCTACTG TTCTCAAATC CAGAAGAAGC TTGGAATCAA GGATTTCOA GTTCTTTTCA 420  
 GATGCATGTT TCTTGAGGAA GCCTTCATCT GGGCTCTCCG TATATCTGCT TCAACTCATC 480  
 55 CATAGTAATC AGCAGAAATG ACAATCCATA TATGGTCTT GGCTTTGGTT TGTAGTTAGT 540

CGATGGCTGG ATTTTCCCAT GGTAGAAAGA AGAATATCGT GCTCTTTCTT TTCAAACAAC 600  
 AAATATCATA TGCCCTTGGC TTCTCCTGC CAAAATTOCA AAATTAGANA TTTCINATOC 660  
 CCTTTAATAN TTCCACATGT TOCCAATTOC TOCCATNANA TNACTGTCTA ACTGTTTGTT 720  
 GCNNACCCAA AAANAATTOCT TOCTNTCCCT TTTOCCCANa TGCTOCTTIN CCAGTC 776

## (2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 808 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1331UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GATGTGCGC CTGCTCCAG AGCGCTGCC CAAGGCCAG CGCTGGAGC TGGCTGCAT 60  
 CAAGAGCTAC GTCTACGGC AGCGCTGGA CGAAACCCC TGGTGGGCT CCATGCAGC 120  
 CCCCCCGAC TGCCCCGGC AGTCGAGGA AGCCAGGGC AGTGGGGC CGGGGACGA 180  
 CGAGCTGGC ATCTTCAGC TCTGCAGCT GCTGGAGAC CAGTCCGGT CCGAAGATGT 240  
 CATCCCGAT AGCATGGATG CGGGCGAGC GGTGAGCTG GGCTCCCCG AGCCCCAGGC 300  
 AGGCTCTCG CAGCACAGCT TCTGCCAGA TTCCAGCAC GGTGCCCCC TTGGGCCCCG 360  
 CCGTTAACC CCTTTGAGC GCGGCCCCC CTCCTACTC CCGTCCGGC TGTACACCGC 420  
 GCGCGCTCC CCGCTTGA CTATTTCCGA CAGCAAGGA TGAACCCCTA CGTCTOCAG 480  
 GCGCCAGCC AGGCGCCAG CCGGCTCC CTGNTTGAAG GTNNGAANG CACCTNCCA 540  
 AAANITTAGG GGTNGGCG CNGGGCGCT CAACGNITG GGTCCGNAA AANCCNITG 600  
 CGGGTNNCC CCNCTTTAA GCGGCGNCG AACNCGNNT NITTOGGGNA GGGTTTOCAN 660  
 ACNCAAACNG TNNNNCCCC CCTTTTCT TCAANAAG GCTNITTTGT GTCNITTCOG 720  
 CCNGGNGGN AATTTNITT TGIGGGCTG NNCCCTNAGA AAACNCCNC NGGNGNNG 780  
 GGGAAAAAA AANTTTTTTT CCNNGGT 808

## (2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 762 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1332RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

5 GATCTTTTAT GTTCCTTTAG AGCAAGGTCA ATTTTCACAC CACTTCTATC ATCTTATATC 60  
 CAGAATAATT TGAACAAGAA GGTACCGTCT AGTGAACGAC GTGATTTTCAT GCCGGCGTCC 120  
 AAGGTTCATG AGTCATTACT GAAAATGAAG CAGCACTATA TCGAAAATAG GTTGCTCGAA 180  
 10 CTACAAAAC TTCATCAGTT ATTCTGTAAA GATAACGTGA ATTTTTCCAA AAAAATGATA 240  
 AATGTGAAG AAAGAAGAAT CGTAAATCTT CTAAATGACC TAGATGATGA TGCTAACTTT 300  
 ACTTTTGAGA CTGTCCATAC TAATTTTGIG AATAATGAAC TATTCATGGA ACTACATGAT 360  
 15 CACAAGTCAG TGATATCGCG CGTTTGACA TTAGATACTG CGGAGGATTG CAATCGCATG 420  
 AAGAAAAGGT TACGACCATA TACACTCAGC TCCTCGACTA TTTCAGGCTC AAGTTGTCCA 480  
 ATATTGATGT AGATCCAACC GCCACTATGA ATTTNAGTTC CGAAACTCCN TTGANCAGTG 540  
 20 TTACCTCCTT ATTGIGTTTG TTACNCAAT TGATCCCTCC ANTTTCOGAT TCTGGAAAAT 600  
 GNGGAAAAC CNNGAAANT GCNGAAAAC CTAAAANAAG GAANACCGTT AACNGGGTTN 660  
 GGAATGTCTA TTGGGGGGGG GCCNNANCTT TTAAAGNNNC TTTGNGGGG AANANNCCNN 720  
 25 NCTCCCNINA AANTTTTTTC CCCNGGGNAA AAANTTNTCT GG 762

## (2) INFORMATION FOR SEQ ID NO:463:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 798 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1332UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

40 GATCTTTTTC AGACGCAGTG TACTATCGAT GAAGCATATG ATTATTATAC AAAACTTCTG 60  
 TCCGATACTA TTGCATTAAA CCGCTTAAT AGAAACGAAT TTTTGGAAAG TTGCGACACA 120  
 45 TTAGAGATGT ATGGAGTGC TTCTATTGAA AATGGCAAGC ATGGCAAAAA GCCAAACAA 180  
 TTGGTAAAC TGATCAAGAG TACAGTTGAT GAAAAGCAGT TCCATGATGA AATATGTAAG 240  
 ATGGACTTGC TTAAGAAATT GATAATATAA AAGGCTACGA GCTTCAATAT TATAATACGC 300  
 50 ATTGCATAAT TTATTACATT AAATTGATAT AGGTATATTT TTCTTCGAAG AATTAATTCT 360  
 AATCATTTCC ATGTGAAGAT ATCGCCCTCT GTGTTACCTG CGGATATTTT GACTCTTAGT 420  
 ATATCTACAT ATTTTGGGGA GCCATTATTT AAACGCGCA GCTTGACTCT GGACCCAAGA 480  
 55 GCCGTAAATGG CAGCAGCTCT TCCTGAGCGC AATTTCTTCC AGCAATTGAG GCACCATGTG 540

EP 0 866 129 A2

CCGTCCTTTA ATTCCAGCAC ATATAACAGA CCGTCCCGTC CAATAACCCCT AACACAATTA 600  
 TTCCCTTTCT TTCCCATCAT GTTTCOGATA CTGGACATTC CCTGAAATGC AANTTTAACA 660  
 AGCCTTATAC CAGTGAAATC NTGCGTTTTG AAANATGCOO TGCCAATTTC AACCCGTGAG 720  
 GTGCGTAACC TGAACTTTTT TTGAAATTTT AACCCCCCOCA ATNANINTTC NTTTTTGNA 780  
 CCCCATGCCT TGTTCNCT 798

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1333RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GATCACCGGG TGAATATGCT GCTTGGCATA GTTGATATAC ATTGTGAGAA AGTGACCGG 60  
 AAGGATGTCC GACTCGGACA CATGGGCGGG CTTGTCTCT AGGTAGAGGC TGGTCAGGTG 120  
 CTTGGCTAAT TCTCGATC 138

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1333UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GATCGAGAAT AGCCAAGCAC CTGACCAGCC TCTACCTAGA GGACAAGCCC GCCCATGTGT 60  
 CCGAGTCGGA CATCCTTCOG GTGCACTTTC TCACAATGTA TATCAACTAT GCCAAGCAGC 120  
 ATATTCAACC GGIGATC 137

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 766 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1334RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

```

10  GATCATAATC CAGTCGCTGT CGAGATACTC GACAGGAATG GACGTCAGCG ATTTGCTCGA      60
    AGAGCGCGCG AAAACCTTGT CCGTTGGCTC CGGCGTTGCG GTGAGCGTCC CGGCGGCGT      120
    GCCACGCTC GACTGCAGCC GGCACGCTT CCGCATTATC TGGTTCATGG AGAATAGCGA      180
15  CGATACTGGA CGCTTCATGA TGCATTAA GGCACAACC TGGGCGTAT CATGCTGGC      240
    CCGCCGGCAC CCGGCCACCC GTGCCCCCG CAGGACAGTC CCGAAACGGC CTCGTCTTAA      300
    CCGACCTCC AGCATATACT GGTTCACCTG CACGCTTCC CCGCCCGCTA TCAGCGGTGT      360
20  CGTCTTTTGC AGCAGAAOCA TCTCCACAG CTGTGTATAC TCCTCAAATA ACGCTGGTA      420
    TGTACTGCG TCCCGCGCG AACCGCTCT CCCAACACC GTGTGCTCA AACGAGAGCT      480
    GCTACGCTG GAGATGCTG GCAGCAAGAG AGAGTGCTC CCTTCATTGA ATTGCACGAT      540
25  AGTAGGTAC GAACTCATG NCCTATGCC CTACACCATG NANTGGTTT CTATTGTNN      600
    TNGGCCCC NATNCTGTT CCAACINTIN TTANCTGGC CACNTTTTTT TNGGTGGC      660
    CCGGAACCT CCTTCCCTTA ACCAATCTG GGCNCTTTC NCAACAGGAA ACCTTINIGAA      720
30  CACTTCCCC NAAANGTNG GAANAAAAAN TTTTNTINAT TNCCT      766

```

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 796 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1334UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

```

45  GATCTGCGC GGCTCGGCG AGCCGACAG CGCGCGCTG GCATTCTGG AAAGCGCGTC      60
    CGCCGCGCG CGCGCGGTG GCGGCTAGT CCGGCTGTA CAAGTCGCC CGAACAAAC      120
    GCTTTTGAC ATCACTCTCA ACGGCTGCC CGGCGCTGCG CAGTACTAG CCTGATCCG      180
50  CGGTCGTGT GATGTGTCC CGCGCGCGC GTCCACGCG CCGCGTGGC ACGTGTGGA      240
    AGACGCGTC GGTGCGAGC GCGCCAGCC GCTCGGCGT GACCTCTGG CCGGCTCCG      300
    CCGTGTGTC GCGCGCTCG CCGTCAGGC GCTGATGGC CGCGCTTCC TCGTGGGCG      360
55  CGACCGCGC CACGCGCTG CGCGCGCGC CGCGTGGC GTGCTGGCG GTAGCGCGG      420

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CGCGTGGCAG AACGACAAGG TCGTCTGCGC GTGCTCCGGC GACACGCTGT GGCAGGAGCG 480  
 CGGCTCCGCG CGCTCCGCGA ACATCGCATG AACTGTATAC TACATACCTG CTACGTTGTG 540  
 5 CTGCGGCCCC CGGCCAAGCG CTNCTCCAN CGGGGGGGGC CCGGGGGGOC TTCCAACCTCA 600  
 CGGCGGGGGG GCGCGGCTG GCGGAAAAC CCGCTTCGCG AACGNCCAAN AANNCCANN 660  
 CCNTACNACN CCCANTTANC CAACACNITC NTCACGGGT TNVINGCCCC CCCCCGNINC 720  
 10 TTCTCCGGNG TTTTTTTTTT CCGGANNATT NCTGNTCCCN CGGNTCCCN CCTTATTTTG 780  
 NNINGCCCCC CCCCC 796

## (2) INFORMATION FOR SEQ ID NO:468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1335RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GAGGCAACGG AGGTGGCGGT GGTATCAAAG GTCTGGTAGT CGCTATGTCC TTTCGGAGCT 60  
 30 TTGTGGGTTT TGTGGTCTTG CTTTGTGTGG AGCTAAGGT TGGGGGGGC GAAATCACAT 120  
 GCAGTGGGCG CGATTCCAGG TCCGCCAAGT TAATGGGANA CACCGGCGCG CTCAGCATAG 180  
 TGCTGTGGGT CCTCCTATGT GATTGCGACC CAAACGTATG GTCCGCCCTT GGGTGTGCAT 240  
 35 TTCTGAGCT TGTATATCCC TCCGGGCCAC TAAACTGCG CCTACTCTGA TTCTCTGTCA 300  
 GTAACGAGA GTAAGACACA CGTTGCTTC GTGTAGCGA TAGTGTGCGA CATAAATTAC 360  
 TATGCGGGGA NCCNINCCAA NTTTAACTIN TGNAANAAA ANACCCAAAC TTTTCAAAA 420  
 40 CCCAAANTTC NATTTNGGN NCGAAAATN CCGNTGGGN AACCCCCCGT NNINGGGGTTT 480  
 AAATGGGGTT TCCAAAAAAA ACCCNCCANT TTTCCCCCC CCCCNAAT TTTTAAAAAN 540  
 NCTTTTAAA AANNINNTT NTGTGGNENC CCCCCCCCC CCGNAAAAA AATCCCCCN 600  
 45 AAAAAANCNG GINTTTTCCC CNINGGGGGG AAACCCCCC NAAAANNNN ACNINCNNN 660  
 NNGGGNCC CNCCCCCN ANCNNTTG TNCCTCTT TNANAAAANG GNCCCCAAN 720  
 CNTTTTTTN NNNNNNNAA AACNCCCTT TNCNCCCC CCGNAAAAA AATTTTNNN 780  
 50 NNNNTTTIN G 791

## (2) INFORMATION FOR SEQ ID NO:469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs  
 (B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1335UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

```

GATCAGATAA GAATTGAAGC TCAGCGGCTG ATGAGCGCAC TGCTTCGAT ACGTGGTGC      60
TGTACCAGGC TGATAAAATG TGACACTATC ACCATAATGG GGTGTAGCT GGATACGATG      120
TCCGGATGCG GATGGACTGT TCTGAACAAG ACGTCCAAOG TGGAGGGGCC ATAGTGGGAA      180
ATCTAATTAA CGTATTTTACA TATCAGTGGC GATGTGTCTA GGTGCCGGCC AACTCGAATT      240
CCTGTCACTG GACAGCGCGG TCATATAAAC ATTATGTGTT AGGGTTTAAA GTTGCTTTGT      300
GCGGTGGAAA ACAACGTCAC AACTAACTA AATCTAACTC GAGCCAGCAA GCAACTATGT      360
TAAATAAGCC GAACAGTTTA CGATTCCAAG GGCAAGGTGG AACCCCCCAA GGCCCCGCTC      420
CNANTCNFTC CCTTACAAAA AGGGAGGGGG GOCCTACCAC TACCGAAACC ATACNGGTTN      480
NAAACAACCC NAANCCCGTT TTTCCCCCCC CCAAAATTAA ANANTGGGCG CCCCCTGNNC      540
NCNATTTGTT NNININANGG GGANAGGACC CCCCCCGGG GNNNGGNTCC CCCCNNTCNA      600
AAACCANNAC CCCCACCCCN ANAAAAANGG GGGGGGGGNN GGAACNCCC GATTTCATAA      660
AAATTTAAAA ATTNNNGGAA ACCGNAAAAC GNGTGNNCN TNCCNNING AAAAANGTTT      720
TTGTNGNNA CANCCCCAA CNNTTNINAG MNCCCGNNC CCCCAAACNN AAAANTTTNC      780
TNGNANGGGG AACCAATCCC CCCCNT      807

```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1336RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

```

GATCATGTTT AACCCAGATA CGAAAACCTGA GAAGCTAGAG TGGATAGAAA AGCTGCGAAA      60
AGTAATAGAG CTGAACAGGT TTCACCAACC ATGGGTAAA AAGTTCTTGA ATAGCAGTGA      120
GAATATCTC TGAAGAAAAG CATGACCACA GGATTACATA GAGTAACTTT TGTGCAAAGT      180
TTATCTGTAT GTACAATTC ACGTTATAAA TTTTAAAAGT ACTCGGCAA AATGGCACT      240

```

TGGTAGCGAT AACGCACACT CGAGTGAAGT CCATCCAGTA CATAAACATT ATGTCAACTA 300  
 CTTACCATT A TTGCCATTGC CAGATGAAGT ACCCATGTTC TGGTGATTGC CTGACCCATT 360  
 5 GTTACCACCTT GCAGCGCCCA GGTTTGGGGG AATCATGCCA GGAAAGGGAA AGGGCGGGAA 420  
 ACCCCGAACA TGGGTGGCAT ACCCATGGGA AACGCCAGGC GGCTGCGGCA GAGAACCGTT 480  
 GTTTTTGTTC CGCCAAATTG AAGTTCCTTG GTTTCNNNN CCCCCCGCA AAAANCTTAA 540  
 10 CCGGTGCCCC CNGCCCCCN TCCCCAANC TTTCNNNIG NNGTTGGAGC CCCCCAACC 600  
 CCCCATTATNT TNNCTGGGCC GGGGTTTININ CCCCCGGGA GACCCCCCCC CGCNTTGTGN 660  
 NTNTTACCCC CACCCNCCCC CCCCCCGGAA ANCCNGTINTT AAAAAATNCN AANAANNINT 720  
 15 GGGCCCCGNG CTCCCCGGGG CTCCNTATA CCCCCGGNN GTAAATNNC NAAGNGGNC 780  
 CN 782

## (2) INFORMATION FOR SEQ ID NO:471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1336UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

ATCGGCATTT TAGGGATGAT CCGATCACC ACAGCTCGA GGCCTTGTA GAAAGCCAGC 60  
 AAGCCCTGCC CGCTGTAGAT GTTGGCCCC GTGCGCAAAA ACCCAGGGG CTTCGTGCCC 120  
 35 TCGTTGCGC GCTGTAGAT CTGCATGCGC ACCTTGATCG TGTCCAATGG GTGGCAGCAG 180  
 AGCGGCTCAA ACAGGCCCC GGTCCCCGC GCAACTAGGT TCACGGCCGG GTTGGTAGAT 240  
 TTCTTAGACG ACATGTGGTT ATCAGGGTAT GGCTGCTGGC AACTTGCGCT GCACGGATCC 300  
 40 GCTACGCTTC TCGTGGCGC ACCTATATAT ACAACGGGCA CGACGGGGG GCGGCCGCA 360  
 CCTGTCTCC GACGCAGGC CAATAGGAGC TCGGCATAC CCCCCGGGA ACGGGGTGAG 420  
 TCAACCCGGC CGAAGCGCG GGCCAATGGA ACGTCACTG GAAAAGCAA GACTTAAAGT 480  
 45 ACTATGTAGC TACACACTTA GGCTCGGCC ATCTGGGCA GTCTGGGAT CGTGGAGGCG 540  
 ACGTCGGGC GGCAGCCGTG GAGACGTGTT ACGCACCACC GGCCACAGTC NTCCTTTGCA 600  
 CNAACTTGCA NTCCCAAAN NCCGNAGCG CCGCGCTCN CGCCTTCTT TGCCGCAAAA 660  
 50 AGAACATCCT TACCAACTTC TTGTGGCCT NCCACTTCTT NAACCTGTTT CCNACAGAA 720  
 NAANOCTACC CCCCCCNVT TTNCGNNAA TCGNAOCTIN TNCNINCTTT TACCATTNT 780  
 55 NTNAAAGGG TGN 793

## (2) INFORMATION FOR SEQ ID NO:472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1337RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GATCTTAATT TAAATTTTAA ATTAAGTATT TATAATTTAG AAATATATAA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTGG TGGCATCTTA 180  
 ATTTTATTAA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300  
 AAATATACCA TTTTATTATA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
 TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TCCCTTTAAT 480  
 TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT 540  
 AATAATTAT TATCTAAAGG TATATAAATT AATTAAATCC TTTTATTATA TTATTTAAAT 600  
 TATTATTAAT AGTAAATTAT ATTATTTAAT TTATTCACCA TAATTTTTTT GATNATAATA 660  
 TATCCTTTNN TAAATGGGGA ATTTATNAAT AATTANCITC NANGAATTTT AATGAANAAC 720  
 CCCNTTANN ATAAAATTAG TTAANNNTGN NCTCAAAANN CCNATCA 767

## (2) INFORMATION FOR SEQ ID NO:473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1337UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA 60  
 CTACCTGATT TTATTGAATC AAATAATAAT TTCTTAATGA ATACTACTAA ATCATCATCT 120  
 ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCAATTCAT TTAATACTOC TCTAATTCAA 180

TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAAATG 240  
 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT 300  
 5 ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360  
 GGTGTGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACATAA AAAAATAATT 420  
 AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480  
 10 GTTATATTTA AATAGATCAA AATTTCACAA ATTTTCATTT CATTAGTAC TACATCACC 540  
 TGACCAATGT TACATCATTT AGTTTAATAG GGTTTACTAA TAACCTTTAN CCTTTTACCA 600  
 AANNANNGGT ANTANINGGA AAAATTATNC CCTTAATAAT AACCTTNATN AANNATINT 660  
 15 ATATACCAAA ANNTTINIGAN ATTTNAAAAA ATATNGGCOG AANNNCNTA TTTTNGTAN 720  
 CCCCCNCNTA CNGCNGAAAA AANGNTTACC CGTGTTCGCC CNTATNNTGN NINCCCNAAA 780  
 ATAAAAAATG NGCCCCCAC 799

## (2) INFORMATION FOR SEQ ID NO:474:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1338RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

35 GATCAACCGC AACCGTCAC TCANGTCAG ACCGTTATAG AGACGGTCGT CGATGGCACT 60  
 ACAAGGCGCG CAAATGCTTT GCTTATGAAT AGCAGCGTTG AGGTGATAAC CGTTAAGGAA 120  
 ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG 180  
 40 AACGCTTTCT GTCTTTTGT CCAAACCTAC CTGAACACCT AAACCTAGTT ATTACAACAT 240  
 GAGTTTATTT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT 300  
 GCCTTGATAA AAGATATTCA TCCCTATTCA GCGACCCCTC TAATAAGCAT TCTCTAGAAA 360  
 45 GTTCTTGGC TTTCATTTTA ATCTCTGIG CACCTCGTCC GTAACAGTGT CTATAGTATC 420  
 ATTCOGTATC ATTTCTGAAT GAAGTAGATT CCATATCAAC ACTTGCTTTG GTGGAAAGCT 480  
 CATPATCTG AGCAGTAATG GCTTCACCTC TATCTGTTT CAACATACTT TTTTATAGCTG 540  
 50 CCGGATTAA CCTCCCTGAA TTCCCTTACG ATGCAGTGA GACCATGCC GATTATCAA 600  
 ATTTATCTGT CCTTTAANA ATTTTAAACC TTTGACNCCC CTATTATTAT TTTTATAGCT 660  
 ATCGTAATGC TGCCNGANCC CCCNAANGAN ATGGGGTTTT CCTLATTANC CTTTGGTTCC 720  
 55 CCAANTTAAA ACCCNCCCCG GNCNCCCCC CCCCCACCN GGTGGGANAA T 771

## (2) INFORMATION FOR SEQ ID NO:475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1338UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GATCAGGTTT TCOGGTACGT GAGAACGTAT CTAAGGCACA AAGGGCTTTG GGCGACTGTG 60  
 CGGACGCTTG AGTTGCNAGA TACAGGACAA AGCTGTTACG GCGGCAACTG GTGCANCAOG 120  
 AGCAGCCGAG GAGCGATTCT GCGCGAAGCG ACGGTGAATT CGAGCCAGCT GGTAGCAGGA 180  
 GTGCCGGATC GTCTATTTAG TTGCGACGGG CGTCGGAACA GGATGCAOGT AAACGTTGCG 240  
 GTAACACGGG ACGCTGACGC GACGGCTGCT ACGCCGATAG CACGGGAGCG CAAACGACGG 300  
 CAGCCGCTGT CGCCAGAGAT GTCTTCACCA CTGCGCGGTA GCAAGCTGCA GCGGCGGAAG 360  
 CAGACACTTG AGGCCGGTCC GGGTCGGGCC AGTGGGACAC ACACGGTGGA CGAGCTGGCC 420  
 GCGCAGCTGG AGCGCGGCTG CGAGCAGGGG TCGGAGGGGA AGCCGCGGTA CTGCTATGCG 480  
 GTGCTGATCG GCGTTGCGAT CCTACAGTGG CAGGAGGGCA GCTGACGCTG TTGCNAAAA 540  
 TACCGNTGNA TTTCNCNCNT CTCGCCCTAN TAACCGGTGT TTTTAACCCG GGGTTGGAAA 600  
 ANANCTTCGG GACNACNINT TNCTTAAACA ANGGINTTGT TTTAAGGGGN GGNINCCCC 660  
 TCAAAGGANG GGCTTTTGG AAAATTAAGG GGGCCNITNA NGGGGGCTC NCTTNNOCOA 720  
 AAAGGGGGAA TNATTTTNG GGGCCANATT TNNCAAAAAT TVINCANTAG GGGGNTTNG 780  
 NNAANTTTNT TCNCTT 796

## (2) INFORMATION FOR SEQ ID NO:476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1339RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GATCATGGCC TTTAGGCCCA TGTCACCTT GCCCGCACCG ATCAACTCCG TCAGTGGGA 60

OGGGTGTGTG GGCTCGAGCA GCGCAATGTC CACACCCCTOC TGCTGAAAGT AGCCCTTGGA 120  
 CTGGGCTAGA AAAATCGCAA TGTGGTATGG CGCAGGCTGC CAATTCAATA GGAATGAAAC 180  
 5 TTTGCTAGAC ATCTTGGTG CAGTCTCCGC AGCTACACC CATTCATOC AGGCTCATCA 240  
 GCGCTTTTAT ATACCGCTGG GCCAAAGATG ATTGAATACG GTTGCAGAC GGCTACTGGA 300  
 ATACCCGTCG CGCCACAAGC CGCCACTGG ATGCCATGG CCAATGCGGA AGCCTCCTAT 360  
 10 GTGACATGTA CTAACAGAGC AGCTTCTTTA TGCATTATC GAGCCAAAAC CAACATCTGC 420  
 GGAATCACAC TTGACGGAAT CCGGCCCCAT GCGCAGCTGC TGGAAACACA AATCCAGCAA 480  
 CTAATAGGOC TCAGTGGTAT AACGGCCCAT CGCTCTCTCA ACGCCAAGTC CCTCTCTGGG 540  
 15 GAAAACATGT GATCAGTGC TACATATTCA ACCCCCGTCT TACCTCATAG CTGCGCATGT 600  
 CCAGCCCTGA ACTGTTCCGA CCTTCCTCT TCCNGAAANC CTGATTGCGT TGCTTTAATT 660  
 CCCCCTCTCC NCCAACCATG TNCGCCCAT TTACTTCGGT TGCTTTTITA TTTCGTGCAT 720  
 20 TGTTTTNTA AAAGNNCTG TTAANTAAAT NCCNTCATIN TGGA 764

## (2) INFORMATION FOR SEQ ID NO:477:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1339UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GATCAGGCA TTGTGATA GTGGCTTTGA TTGAAAAAT CGATCATTA CCATGCTGAC 60  
 TATACTCTA CTGACCAAG CCTTTGCAA CAAGACTGG GGCTTAAC TAATGTGTC 120  
 40 TCGCCAAATG TATACTGA TATTTGGGT GATTGATGA GACCACCAA CTGTCTCTC 180  
 TAAGCAACAG TCATCACTG CCGTAGCAAT AGCTACCTA ATATACAAC ACTCAGTGT 240  
 GGTAGTAAA GAGAACAAC ATGACATCT AGCAATTGTT GCAGAGGTT TAAACAACA 300  
 45 ATACGGCTCC TCTTCTTTA TCTTGGGAA CGAGGAGGC GCATACAGAC TCTTGTGTC 360  
 TTACGGAAAC TTAAGTACTG TGAAGGCAC CTTCGCAG TTTGCTCCTT CTATCTCATG 420  
 GATAAGGAAG CTGAAGAGC AGTATGGCA CATATGAAA TTCCAGGATA TTTTAAATGA 480  
 50 TATTTAAAGA AAGGTGTAC TATATATCT ATTCTTTGA TCGCTGTCCC GAGGCTTCC 540  
 CGGAAAAATG GTGAAACTT CGCTCTTTGA CACACAGCT TTGCGCTTCA ACAGGATAGT 600  
 TTGAAGGAC ATGTCTGTT GACAANNCT GAACCAGGT ACTGGTGNAA AATTINAANA 660  
 55 TCTTTCTCC NCCGAAANC ANTTCTNCG AANTTAACG GAAAAAANC CCCCTCINN 720

CTTINTTTAN TAACCCCCC CAGGNTINTG ACCTTGATTT TTACAAAACC TTTTINTT

778

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 766 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1340RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GATGCGCTGA TATCGACAGG CACTTTTGTA TATTAGCAGT ATTCTTGACG AGATAATGCA	60
GTCAACTCCT ATATAGAAAC CGGATACAGT GGTA AAAACG CAAATGTAGG CAATTATATA	120
TTACTCTTCT CGACACCACT AACTTCTCGA TAGGGGCATA TCTTGTAAT TTGCATACAC	180
CTTTTCCCAA CTTTCAGTGG TCTOGTTGGC GTACTTTACA TGCATCTTGG CCCATTCTTG	240
GAAGACATGT GTGATACAAA ATTGAGTCTC CTGAAAATT ACAAATTCCT CTAAAATGCA	300
CTTTCTAATT AGCCAGGACC TGTTTAGITG CTCAGCAATT GTCGGTTTGT CCGTTGAAT	360
TGTCGTCTGT AGTTTATCAT ATTCTGCACC TTAAAGTCC GGATTACTCT CCATAGATTG	420
AAGTTTGTC ATATTTATTT CCACTCTCT CTGCAAAATG GCTATGTTAT TCCCCGCCAT	480
AATTTTATAC CTATCAAAGA CCCCTTCAGT GCTATAATAA TATCTATGAA GGTCTTAAAC	540
TTACCGGATA GGTGTCTCT CACTTCTGA CGCTCTTTC TTAGAGGTAT CGGCCAGCT	600
ATTGAGATGT TTTTGATATN NTGGAAATAT GANATTTAAA TATCTGTAAT AGTGCTCTT	660
CCTATGGGT ANAANTGTTN CNGAATTATC AANCAATTC TCCATCACNC NGCCAAGCAC	720
CCNCGTCTCT TCNAANACCT GCNCTNGCC CCGTNGGTT NNNNNA	766

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 790 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1340UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GATCTGCTGT AACTGAATGG ACTTTGTCTC CTGAAGTAGA AATGTAATGG CCCCTTCGGG	60
AATACATAAC AAACATAGCG GAGACAAAAA CAAAAGCGTT ATACAGGCAT CTGCGGTAC	120

ATCACOGTCA GCTCCTTGCA GACCAATAAG CCTTCAAGTT AAATATAGGC TAGCTATAAC 180  
 ATATTATGTC GCTAAGAAGG GCCAAATCGT TGCCATCGCT TAAGAATATC GCTGAGGTGG 240  
 5 CCAAGCCCAT CACCAAGGOC CCCCOCCTCC CCGTCTTGC GTTTGAGGGC OCTGGGCTGT 300  
 CCACATGTGG CTGGTATCCC ACCACCGTGC GCACAGTGCA CAATACCCCC AGTAAGGOGC 360  
 AGACGACGCT GCTCTOGACA GCGAAGAAGG AGAGTGGGTT TTCCGCAATG AACCTGAAGG 420  
 10 CCTTGGCGAA CGAGTGGCGC TCCCGAGGCT CAGGGTCTCC GGGCGGAAGT CGGATTGAT 480  
 CGAGCGCATT GTGACTTTCG AGCTGAAGGG ACCGCTGGGC AGGCGGGGA CACGGCGGGC 540  
 GTTCACAGC CCGGGCACGA GCAGCGCCAG CGTATGCGC CGTGGACAA GTTCACCATG 600  
 15 CCGGACATCG CGCTTGACAG AACGAACCCC GTGCCACACC CTGAGAAAAA CTACATACTC 660  
 CGGANCCNT CNTTGINCCN CCAAGGGGGT TTCCCTCCCC GTTACCNATT CCNAAAAGAT 720  
 TTTTGCCNCG GAACCCANGA AGAAACCACC CGAACTCCCA GAAGGGGGNT TTNNNNANCG 780  
 20 AACCGAANCT 790

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1341RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GATCACATCC GATGCGAAAC TGCTATATTG TTTTCCACA ATGATGAAGG TGAGTGIGGG 60  
 GCAGCAATTG TCOGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACTG ACCAGAAATT 120  
 40 TGCAATGTGA TTCATGATGC AAATGGAAAC CCCATCCAAG TTTCACAGTC GCAAAAGAAC 180  
 AGTTGGATCC TGACAAGGTT CTTCTGTTAG GCAGCTCTAT AGACACTCCG GTTGCTGTTC 240  
 CTGCGGATGC AACGAAAGTG TCCGCCCATG CTTTACTCCA GGCCCTTTTT AACTCTAAGC 300  
 45 AAAGTGAAGT AACTCCTGGA TGTATTACCT TTCAGCAAGT CAGAAACCTG ACCAGGTTCC 360  
 ACTAGTTTTT TATTGAAGTC CGTGCTGTCT CAGTATTGTA AGCAGTTAGT CCCACGAATG 420  
 AGAACTTAA AGAATAATAG AATGGGGAAG ACTCAAAATT TACGGCTACC ATAAGACTCA 480  
 50 CAGACTTACT CGACTCGAAC GTTTTGTGCC GCACTTTGTC CTGCGAGTCA TATACAGAGC 540  
 CCTGTATGCG GTAAACACC GGATGCGCTA CAGCAAGGTA CTGGCTACA AGACAACACC 600  
 CTACGTAGC CGTTTCACAG TATGCAAATA ATNGAAGGCA TTCTCTCCNG ACTTTTTAGC 660  
 55 NAAAGGNTT ATNCGAAGTG ANCCCTGTCC ATACTTTATT CCCCNNANCC CNGTTTTTCA 720



AAAANCAGNG AACCATACNA TCGGTTTAAT AATGAACNTT CACNT

765

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 810 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1341UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GATCAGAGTA GATTTAGTAA AGAGGTAAOC ACCACTGTTC CAAGAAGTCC AGGGCCTTGG	60
CTTGACCAGC ATTGGTAAGT GCTGTGGCTG GAAATTTGCA CTTAAACGGT CTGAGCTCAT	120
CTGGTTGGCC AAAGACCTAT GAAGTTTCAA AACACCAACT TTGCTGCOCA TTCTATATTG	180
AAATGTATGA CAGATGGCAG GTGCCTTACC GTACACTGTT TTATTGGTAA CTGGGTCTAC	240
ACCTTTCACG TTCACCTTTG CCACATGGAT CAACATAGAA ATTAAAAGAG AGCCAACCTT	300
AGCCTTGATA TTGTGGCGCC AAAGAACFTT AGACTCCTCA ATTGTGTAT TTCTAAACGT	360
GGTTTTTGCC CTTTGGACCA GCTTCTTGAA TTGGTTACTA TTGGCCCTAA CTTCCTTAAA	420
AATOGATTTT TCACTCTTCA ATAGTGCTTC CGATCTGTAT TCCATCTCGA CAGCCTTACC	480
TATAGCCAGA ACGCTCCTG GTTGTCTTCA TACCTTCACT GACGCTCCA GTTAGAATTC	540
CAAGCCTTTA CCNATTCOCC AAATGTGTTA TGAANACACA TTTNCTING ANINACCCCA	600
AATTGAAATT ANGGGGNCTT TTCCANNCCN TGAAANAAAA TGINGAACGG NGTTTCAGTT	660
AAGCCCATNT ATCACTINGN ANCATTCNNN AAAAANGCTT CCCCCCTCCC TTTTAAAAAC	720
GGGATCTTNC CAAAAAACCN CCCCCTNAAT GAACCATTTT NCGAAANCOG GAAGCCCNNG	780
CCCTCNCCGN CTANATTCN GCAANNCAIN	810

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 759 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1342RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GATCCTGATT TTGATTTCGC CATTGCTGAT GTTAATGCAC TCAGTGCTGA TGTCCTATAT 60  
 ATCCAGCATG AATTATCCTG GTGGATATGC GCTATCTGCA TTCAACAAAT ATGTGCTGGA 120  
 5 CAATAATATC TCGAATGCGA CCGTCCACCT AGATGTCCTC ACTTGTATGA CCGGTGCAAC 180  
 GCTGTTTGGA CAGCTGCCGG ACTCCTACGG GATCATATAT GACAAGACTG AAGGTGATGA 240  
 ATTATTGGAC GCATGGTCAT CGTTCGATTA TGTCATTACA ACTGATCCCA ACAGCTCACT 300  
 10 GCTCCTGTGT ACAGGCTACA AATGGGAGCG CATCCAAACT ACTGAGGCGT TTGACCGCTT 360  
 CGACCTTAAA ACTATACCGG AAATAATCAA CTCAGAAGTT GCTAAGGGAT TCCCTATCTT 420  
 AAAAGATGCA ATACTCTCTG CAGACCTGCA ACCTGTGAAG GCTGCGTICA CAGATGTGAT 480  
 15 CAGGTGCAGG GATTGAGTGT ATACATATAA AAGAGTTGAG AATTAAATAGA ACCAGCGCTC 540  
 CGCTTACGGA CAGTTTCCAT ATAAATATTT ATTATTTAAA CTAAAAAGTT CTGCGAGTTG 600  
 AGGAGGAATT TGACTGCTGG AGATTCCGAC ATACTGAAAA CATAAAGTGC ACATTTACAG 660  
 20 GATTGGCAG TTAATTGATT CCCCNTCCIN NNCTTAAAT GCTGATCNA ACTTNAACA 720  
 TCCTATTGAA CCCCCTTTGG TGNITCAANC AANINITAA 759

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 802 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1342UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GATCGGGCAG GCGCGGAGC AGCAGTCGCG CGCTTCAAG GAGGCGCAG ACTTCGGGCG 60  
 40 CATCATCCTG ACCAAGATGG ACGGCACGC CAAGGGCGGC GGTGCCATCT CCGCGGTGGC 120  
 CGCCACGAAA ACACCCGTGA TCTTCATCGG CACAGGCGAG CACGTACAG ACTTCGAGAA 180  
 GTTCTCGCG AAGTCGTTG TGTCGAAGCT GCTCGGCATC GCGACATCG AGTCGCTGCT 240  
 45 GGAGCAGTTC CAGACCGTCT CCAACAAGGA GGACACCAAG GCCACCATGG AGAACATCCA 300  
 GCAGGGCGCG TTCACGCTGC TGGACTTTCA GAAGCAGATG CAGACCATCA TGAAGATGGG 360  
 CCGCTGTCC AACCTCGCCA GCATGATCCC CGGCATGAGC GGCATGATGA GCGGCATCTC 420  
 50 CGAGGACGAG ACCAGCCGCA AGATGAAGAA GATGGTCTAC GTGCTGACT CCATGTCCCG 480  
 CGAGGAGCTC GAGTGGGACG GCGCTCTTCA TCGACGAGCC CGCCGCGATG CTGCGCGTGG 540  
 CCCCAGGNC CCGGCACCTT CCGTCTTTCC GAAGTNTGAA AATATCCTCC NTTCGCTCAG 600  
 55 CCANATGATT GCCCCGNTT GCGCCANGGC GGCNANAACA TTGGCGGCTC CCGTGGGNTG 660

CCCCOCNGOC CCGGNATGT CCCCOCCTCT CNOCTOCAA NGATNTNACC NGCCCNANCN 720  
 TCNNTTINCT CAACCCNCCC NTGANNCCCN CATAATGGCT NNNCCGNGG GGNCCNGGGC 780  
 5 CCCCATGCCC OCATTAGGCN AT 802

## (2) INFORMATION FOR SEQ ID NO:484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1343RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GATCAACCAA TGTTTAAGG AAATTTTAA CGTTTTCOGG GGATTGGOC ATCTTTCCT 60  
 CTAATTGGTA GGAACATAG TCTGTAGCAC CCATGATATT AGCAAGTTTC CGCCGAGCT 120  
 GAAGCAAACCT CTTAAGCCTC TTCACTTGTT TTTCGGAACA ACTAAACATT GCGTCCATA 180  
 OCTGCTCCG AATAGCCTCT GAAGGACAAG CATTCAATAG TGTATACGGA GCATACCCAC 240  
 TAGTTGGTAT CTTATAGTTA TTACCCATGG TGTCCTTGGT GAGCTGACGA AGAACAAGAT 300  
 GGCTAGTGCC ACTCGATTCC AAATCTTTGC ACGGAATCTT TATGTAGCTG GAAGATAATG 360  
 ATTCTGTGTT GTTGATGAAG TCTTGGCCAA TAATGCTGAT GTTTTGGGAT AACTGTATAA 420  
 ACTGCTTTCT GACTTCGGGC GACGCATATG OGCTGCTTT TTCAAATCC TCTAGCAATA 480  
 TATGGCCTAC CGTATCTCC TGCTGCTCA GTTFACTGCT TATATCTCG TCCGATAGCA 540  
 CTGTTTTAA TCTTTTGCAA AGCACAACAT CTGTATTCAA GATATCATAA TCTCAAACAT 600  
 CTGTTCATGA CATTCCCTGA GCTGCGGCAA CAAATGTTC ATCCGGATGT TGCAACCCGT 660  
 TAAACTCCNC ACAATNCAAT CCCCCGGCAT AAAATCCTGA TTTGATCTAT CNAATGATNT 720  
 NNNCCCAACC TCTGTGACA ACCCTCNCAG TCCTTACAAC CCTACCCGTT ATGATTTTNG 780  
 NAATTCCTAC CCTCNGCAT TTAGTGTTC NNNATACCTT TNGNCCCGG GNGGACTTA 840  
 45 TCAN 844

## (2) INFORMATION FOR SEQ ID NO:485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1343UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

5 GATCGATTAA AGGAAGCATC TGCTTCCCGT CATATCATAT AACATTGTAC CCGGGGCTGA 60  
 GCGGGACCAG TAGCGAATTT GATAGCAGTG TTCTCCACGT CCCCCTCCA CTGTGAGCTC 120  
 CTTAAAGTAT ACCGGCTTCA TACACCAGTG CCCACAATGA TGCGTACTTG ACTGTGAATC 180  
 10 GAGAGCAITG GGCTTATACT GTGATTACGA TGAATGTAGC CAAGAGAGAA AAGGTTCAIT 240  
 CACGATATAC AGTACTCACA TTCATGGCAT GCCATCCCCA AATTCCAATA CAGCCATTAG 300  
 CACCAATGTA GCGCTACTAA TCCGGCGAGC TTAATTGGCG TCAGTTCAGA GTGAATCTCG 360  
 15 AGCTTAAAG TCAGATTGAT TAAGTAAGAA AATGACGATC AACAGGGTGC TCAAAATAGT 420  
 TGATTACCAG ATTCGGGGGT GTGGTCTAGT GGTATGATTC TCGCTTTGGG TAAGCGAAGT 480  
 TGCGGTTTAC TGCGGCTTAA CTACTAAACA TGTGAGAGGC CCTGGGTTCA ATTCCCAGCT 540  
 20 CGCCCCAAT TTTTGTCTCT CGCTCCCGC GGGAAAGGTG AATATCAITTT TACAAGTAGT 600  
 TAACTCTCC CAGGTTACGT CCTTCTGCAG ACAAGTTGCA GCGGTTTACA ATGCTCAGGC 660  
 TATTTTGGCG CTTCAA 676

## (2) INFORMATION FOR SEQ ID NO:486:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1344RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

40 GATCCTTGGG TACTAAGAGT TAGACTTTAA TTAATAATAT TATTTGTAGA AGATAGAAAC 60  
 CATACTGACT CACGTCGTAT TTAACCCAAC TCACGTAACC TTTTAATTGA CGAACAGTCA 120  
 AACCCACTT AGCTGTTACA ACCAAGAGGA TAGGTTGAGT CGACATCGAG GTGGCAAACA 180  
 45 TAACITACAA TAGCTACTCT ATCGTTATAT TACCTGTTC AATTTTGTTA TCATAATAAC 240  
 ATTTAATTAT TATTTCAATA ATTCTCAITA TTGTTGAGAC TATTTCAITA TGTATTATTT 300  
 ATTAATTAAT ACATAATTGGG CTTTCGTGGA TATAATTATT GTTAATCCTA CTCATATATC 360  
 50 TAGTCGTTGA ACGTTCTTAT AACTTTATAA AAAGGATTGT TATAAGCTTC GCTGCAGATT 420  
 GTCCTTTATT ATTATAAAAT AATATTAGGA GTTCTTTGCA ATTAACCCAA TTTACTCAAT 480  
 ATATTTAAAT ATTGATAATT AAATTCACA ATTTAATGGG ACTATTAAAT AATCCCTAGC 540  
 55 GTAACITTTA TTCGTTTATC AAATACCATT ACAATATGTT ATATTTGTTC ATTATGCCAA 600

ACTTACGTGA TTGTTCTACT TGTAGTATTA CNATTATAGC ACAGTTAACC CATCATATTT 660  
 ATTTAATANA TACCCCAANT AGNTTTTTTT ANCATAAAAA GGANCTAATT TCCCTTTTTT 720  
 5 CNOCAANTCC NNCTCTCTCA ATATTIVTAA AAATTTTAAA CNNAANTAAG AAACCCCNVN 780  
 TNAACCNCAN CTTTTTTCAN GGCTTTTCNAN CCTIVITNAAT ANCCCN 827

## (2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 872 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1344UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GATCCTTATA AAATGGGCAA TAGACGTGTT ATAATATAAT ATACAAAATT ATAAATAAAT 60  
 25 ATTTAATAAA ATATAAAATT AATAATTAAA GTATTATAAT AATTAAATAA ATTATTTATT 120  
 AATAAGTATG GATTTTTAAC TGAAATTTGT TAAATGAAA TAAGAATTGC TAGTAATCTA 180  
 TTAATAAGAA AGTAATGGTG AATACICTAA CTGTTTGGCA CTAATCACTC ATCAGCGGTT 240  
 30 GAAACATATA ATTAAATAAA GAATATTAAAT TAATTTATTA ATTATTAATT ATTATTAATA 300  
 TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAAATGG AAGTTGAAAT 360  
 ACAGTTACTG TAGGGGAACC TGCAGTGGGC TTATAAATAT CTTTAAATAT CCATTTTTAT 420  
 35 ACAAATAAAT ATATTTTTTA ATATATTTTA TAATACTAT AATTAAATAG TTAAATTTTA 480  
 AATTATAATT TAATAATTTA ATAACCTATT AATTAGAGAG TTAGGTACA TCCCCCTAA 540  
 TGCTATGCAT TATGGTTGGT ACCACTCTAA TTAATAAACT ATAATAAATA AATACTAATA 600  
 40 TTTTATATCA ATTAAATTAT AATTATTTTT TATTAATATT TTAATATTAT TTAATGAAAT 660  
 ATATAAATAA AGTATTATAA TTTAATAATT AAATAAGAAA TGAAGANAAC GACTCTCANA 720  
 ATTAAATTGC ATTATAGTT TACCATTAAA CAACATTCCC TTATTCATAT TATTINATCN 780  
 45 ANTAATTAAT ATCTTATTAT TNATTAGAAG GANAGGNINC CNCCCTAAT GCTNNGCATC 840  
 TTGTGGTACC NNNAATTAAA AAGTTTACAT NA 872

## (2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 835 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1345RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

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GATCCCAACG TCTGATTATG TGTGTGAATG CTGTCTCTCT GCTCTCTCTG AGTCTCTCTA    60
GCCTTGGCCT TGTACACTTT GCGTATGTT CCTGCTGCAA TATAGCCGAT GATTTCGTAC    120
TTCTCCAGCA CTGACACCTT ACGGGGTCTT TTCGCTGCC GATATGGCCC TATOGAGAAC    180
ACATTGTTAT TCGCCATTAG CATCGGCGAT TTGGACGTGC TGGCGCTGCC TTTGGTATCG    240
AGAAGCTGCT GTTGCTGTTG CTGGACCAC AGGCTCCGGG TGGATGCCTG GTTGGATACG    300
TTGAAATACT TATTCTGTTG TGTTTGATGC TGATTATTCA TACTATOGGA GGACTGTAAA    360
CGTATCCCCA TAAAATAGAG AGCTCGAGCT ACCACCTGAC GACTTGTGTT ATTTGTAGTG    420
TTAAATGGAT ATCGGCTATG TTCTAAGCTC GTTTTAAAGT GTAAAACATT GCAAATCCAT    480
ATGCACACAG CTCATCCGGT TCTACCGACA ACCCTCTTGC GACCGGAGGG GTGGAGCTGG    540
GGTGGATAGT TCCCGAGCCC CTATGTAGTA TATACAGCGT GCCACGGCTG CGCTGCGGG    600
GCTGCAGGGC CTCAGCACGA NTGCCCTTC CNCCACTGCT TTATCTCTCT GAAAGCCGTA    660
CAACCNCCGG NNAAATACGG GGCACCCAAA GCNGCCCGAN GCGCCCGGAT AANAACNTGA    720
CCAGCCNTAG NGAGGCCCGG AAANAACANT GCGCTTTTTC AGCGGGCGGT CGCACAAAC    780
CCAAGGNGGN TCCCNITGG GNNTTTAAAT NGCCNNGGGG ANGCCCNIT NCTCT    835

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(2) INFORMATION FOR SEQ ID NO:489:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 863 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1345UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

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GATCCGGGCT CAGCGCAAGC CAGTCTACTG GGGGACGGAG ACGCGCACAG CATTGGCGGA    60
GGGAGAGCTG GAATATCGCG ATGACCACAT TTGGAAGGCA GCTTACGTTT ACTTTCCGCT    120
AACGGAGGGC GCGAGCGCCA CGTACGCGA GCGCTGGGC ACGTCCCTCC CAGAACAGCC    180
CATCGTGTGT CTCATCTGGA CGAGTACACC GTGGACTCTG CTGTCAAACA GAGCCATCTG    240
TTTCCACGAT GACCACGGT ACCTGCTTCT GCAATGGAAG GGTATGCTGG TGGTAGCCGA    300
GAGAACTGAA CTAGCTGACT TTAAATGGAG TGGTGACACG CCGGTGGTGG TCACCTCATT    360

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CCGGGTTTCT GACCTCCGGG GGCTCTATTG TACCAATCCA CTTCCTGGGG ACGCCGTTAG 420  
 TAGGCGCTG CTGCATGGAG ACCATGTCAC GCGCGACACA GGTACTGGTC TGGTACATAC 480  
 5 TCGCGCCAGG CACGGCCAGG AAGACTACCT AGTAGGTCAG GCGCAOGBCA TTGAAGTCTA 540  
 CTCGCCAGTC GACCATGAGG GGAGGTATAT TCTGGATGAT ATTCTCCAC AACTCCGTGA 600  
 TATGCTAAGA GAAGAGAGCG GTAAGCCGCT GAAGGTTACA GACCACAAAG ANTGCNGNT 660  
 10 CTTTCATCAGT TTGCTANAAA AACCCAAGAT GCTCTGCAAT TCCCTGAATA CCACNCTONT 720  
 NTCCCTNCAA TGGAGTCNAA NAACNTGTTT TCNAGANCTA CCCNCCGTIN GTTCNAACT 780  
 GATGGACTGA ACTTCCCCCN GGAAACCTGA AACTTTTATT TTTCCTNCC AGGGGAAAAA 840  
 15 NOGNTCAAGG TTCTCNAAAN CGA 863

## (2) INFORMATION FOR SEQ ID NO:490:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1347RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GATCATCATG CCAGCGCCCA TGCCGCGGC GGCACACCTT CACACCCACC CGTAACTGAC 60  
 AATACTOGAG CACCTTCGTG CGCTGCGCCG CTGCGCGCTG CCTGGCCCAT TATGCAACCA 120  
 35 CCCACAGTT TTAITCCACT TAAAAATTAC TTAAGCTGAC GTTACGCCCTG TTGAAAAATT 180  
 TTCCCTTCAC GGAATTTTTT TGGGTGAGAT ATAAAAGGGG CTAAGTTGCA CAGTGAAGAAG 240  
 GTGAAGTTTT TTGTGTTTAG ACTTCTTTTA TGACCTCATA GAAGGAATTT GGGAAATCTG 300  
 40 ACTTCTTAGC AGCCTCTCTC CAGTTGGAAG TGTTTACATA CTACTGCTAA ACGTCCGCTA 360  
 AGTTAAGATT TTCTTTTCTT TAGTTTTTAA CTCAGTACCT TAITCCATAA AGCGACACTA 420  
 CGATGCTTC TAGATCTCC CTGCTCTGA ACCTAACGAG ATCCTTGAGC TCTGTGGGGC 480  
 45 GGATGCAACA GATGCGGTTT GCATCGTGA AGTCGATGAC TGTGCGGGAT GGGTTGAACA 540  
 GTGCGATGGC CGAAGAGATG GACCGTGAT GAOGATGTGT TCATCATCGG AGAGAAGTTG 600  
 GCGCCAGTAC AACGGTGCCG TTACAAGTCA CCAAGGCTT GTTTGACCGT TCCGGAACG 660  
 50 CGGTINGING ANACCCATCA CCGAAANGTT TTTCGGTCTT TGCGTGGGTN CNCTGAAGG 720  
 CNTGACCTA TGTATTCAN TNGTTCACCT TCCAGCAGCA NGACANTTCT GAATCCGGC 780  
 CAAATACANN TTCGTGTGTG CNACNTCAN TGTTCCAGC NAAGNGCGNC NOGNNC 836

## (2) INFORMATION FOR SEQ ID NO:491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1347UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GATCCTACAG AACTCAACTC TTATATOCAG GACTCAGTCA CGGOGTCTGC AATCCGCAGC 60  
 AGCCACGGGT GCTCCAGGCT GGGTGGGCAT TGGATGGGIG GCAACGACCC GAGTGGGCAT 120  
 GTATTCTCTGA TAACTTAAT GTGTATGTTT ATGCTGGGCG AGCTGCAGGT ATTGGGCGC 180  
 CCGCAATCG GGAAGCTTTC TGCTGATGT CAACAGCTGC AGGGGCTCC TGGTAAATTT 240  
 GTGGCAGCA TTITGCAAGC AAGTCCGATT AGAGAGCTAA TTAACCTCTGA AGCCCCCAA 300  
 CATATTTTAA GAGGCTTTT CGTCAACIG CCACTAGAGA GTCTTGOGAT TCTGGTGAGC 360  
 GCGGTGTGTT TTGGCTTTTC GTTCATGTIG CTGGAACACC CGATTCTATT GCTGTGCGT 420  
 CTTATCTCTGA CATGGACCTG GTCACCTCTG GTAACCTATC TCTCTTTCCA TTGCTTTGCG 480  
 GAGCAATTGA CCGGTTTGCT CTTGCGATAC CTCTAGTGT TGGGTTTATA CTGGTACATA 540  
 TAATGATCTA AGTAAATCT GCAATATTAC ACACGAAAGT TAACTCGCC AGCTGGATAT 600  
 AGGCAAAGAT TGCAGATGCT GTGCTTTTCG CCTAATATGC GGAAAGATGA GCAGGCCAAA 660  
 CCAATGCAG AGTAGGTTTC TCATATAGTA ACCATCGGCG AGAATGACAA CTTCCGCCCCG 720  
 CTTTGAAGC ACTCCCCCTC GGAAGGAACA TCCNATGGGC GAATTTTGGC CACCTTANAA 780  
 TTNAANAAC TATCATCGCC ATAATACATC CGANACAATT ACCCCANAA TATCAAGTAT 840  
 CNGAAATTTT CNTANTTCN CCAATACGN 869

## (2) INFORMATION FOR SEQ ID NO:492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1348RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

GATCCTTCGG CAGGTTACCC TACGGAAACC TGTTCACGAC TTTTAGTTCC TCTAAATGAC 60  
 CAAGTTTGAC CAGATTTTCC GCTCTGAGGT GGAGTTGGCC CCTCTCTTAA GCAGATCTCG 120



5 AGGCCTCACT AAGCCATTC ATOGGTACTA GCGACGGGCG GTGTGTACAA AGGGCAGGGA 180  
 CGTAATCAAC GCAAGCTGAT GACTTGGGCT TACTAGGAAT TOCTCGTTGA AGAGCAATAA 240  
 TTGCAATGCT CTATCCCCAG CACGACGGAG TTTCACAAGA TTACCCAGAC CTCTGGGCA 300  
 AGGTTATACT CGCTGGCTCC GTCAGTGTAG CGCGGTGGG GCCCAGAACG TCTAAGGGCA 360  
 TCACAGACCT GTTATTGGCT CAAACTTCCA TGGGCTTGAA ACOGATAGTC CCTCTAAGAA 420  
 GTGCGCAACC AGCAAATGCT AGCAGCACTA TTTAGTAGGT TAAGGTCTCG TTGTTATCG 480  
 CAATTAAACA GACAAATCAC TCCACCAACT AAGAAOAGCC ATGCAACCAC ACCCACAATA 540  
 TCAAGAAAGA GCTCTCAATC TGTCAATCCT TATTGTGTTC TGGACCTGTG AGTTTCCCCC 600  
 GTGTTGAGTC CAATTAAACC GCAGCTCCAC TOCTGTGGTG CCTTCCGTC ATTCTTTAT 660  
 TTTCAGCCTT GCGAACATAC TCCCCCGAA CCCCAAAAT TGATTCTCCT AGGTGCCGAT 720  
 TGTTCATAA AAACACACCC ATCCCTATTC GCATATTAT GTTAAATACA AG 772

## (2) INFORMATION FOR SEQ ID NO:493:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1349RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

35 GATGGTTATA TATCAGTCTC TTGCTATAGA TTAATATAGA GCGACCACT AATGTACAAG 60  
 TTATAACTAC TGGTAACACG TTATATAACA GGTAGGAAAC GGGGCGGCG GGGATTTTTC 120  
 CCTATGGCTT GCGCAGGTAG CAACTGCTAT AAAGGGGAC GTTCTTCCG GAGCTTTTTC 180  
 40 ATCTTGGCA GTTCACTTG CTAGTTAGTT TAGGGCTAGG TCGACAAACA TATTCCACAT 240  
 CGTTTAAATG GCTGGGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCTGGTT 300  
 AGCTCCTTAC GGGGACATCC TCTCTGGAG ACGGTTCCTT GCGACAAGT GGAGGCACGA 360  
 45 TATOGAACAT GGGGTGCCC GCGGGCGCG CAGTCTAGTT GAGTTTGGC GCGACGATA 420  
 CAAGAGCTAC GGGCTGACG CGGACGCGA GAGCAAAAGC ATAAGTACA GGGAGTGGC 480  
 GCGCAATGCA ACCCGGGCT TTCTAGTCG CACTTCAAC GGGTGGATGA GACCTGCAC 540  
 50 GAGCTCCAGA ACAAGGACGA GTTCGGGTGT TCAAGGTGTG TTCGGACCTG GCGGACGGC 600  
 GAATTCATAA TCCGCTACT CACCTTTAA GTTGTGTTCN AACTTGCCAC CGGACCGA 660  
 TACCGGTTG CCACNITGAT TCAAAGGAC CACCCCAAC AGAANCCAA GATTTGGGC 720  
 55 NCCTTACAAG CGTCTGAC CCCCCCTT ACATTCCACA CAAAGCCCC NGACCAACTG 780

ATNOCCTNAAA NNACAGNCNC TTGCTCTCAC CGACCCCGTT TGT

823

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1349UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GATCGCGAAA ACTAACGCAC CAAACCCGAC GGAAGCCAGA GCTCTCTTGT AAAGTGGCAA	60
GATAGTGTAT GTCTGGCCGG ATGGCTCAGA GGATTTCCTG CGAGCATAGT GGCAGCGATT	120
GACATATGGA GTTATCATTG CAAAAGCAGT GGCAATAGCA AGACCGGTTT TGTTCGAACC	180
GCGTTTCTCT TCTTTCAATTA TTGGCCACAA GGGATTGTTC GAGTAGAAGG CCATCTTCAA	240
CACAACGCTC GCAACAAGGC CTAGAGACCA AGTAATGGCA AACTGCGCGA CACGCGCGTT	300
GTCTTCACA ATGCTCTTCA AGGTCACGTC AAAGTTCATC GTCTGAGAC CCGTGGCAAC	360
CGCAACGCTC ATCAACCTCC ACTCCGGTTT CTCAACTATG TAGCTCCGA TACCGATTAC	420
ATTAGCAAGT AAAGGGCCGT ACTGTGTAAT CAACGTTGGG AAAAATGGAA CATAAAGCAG	480
AACTGGGCTC AATACCGCCG CTATCACCCG CCTCATAGCC GGAGATACCC ATGTACCAGA	540
GCGGGAAAAA CCATATCATA CACAATAGGG CAGTCAAGTT CGTCCAGAAC ATAAACGAGT	600
CAAAGTACT GACAACAATG TAAAACAGAC TTGCTGTGTT GGTGATGGGC TGTCCGGCA	660
GGTAAACGAG TTCTGTGCT CCTGGTGAT AATCACCTCC TCCAGCATT TCCTCCATTG	720
CGCCGCGCC GAGTCCCTTG CCGGGCTAGA NAGCNGGTG CTTGTCTTTG ANTGCACAAC	780
CCCNCGAAG GCCTGTGCC TGGGTGCCN AACTTTNCCT NAGTCTCCC AGTTTGCNTT	840
ACTTACCTC CNAAAAATTC CAAATATCCN GGACNCCN	879

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1350RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

5 GATCTCTTGC AATTCCTGCT CGGTCTCTCT GTGATCTCTA TTGATCACTT TTTCGAGTTT 60  
 GGTCGCTTGA GAAAGCGTCG CAAAGTTGTT CATAAGTTTC TTATACCGTG CCAGTTTTCG 120  
 AGCCAGCACA TCGTCGCTGA TCGTGTGGAG CGCAATTGGA TCCCATCGG CGGCCATGTT 180  
 ATCCTTGACC GCGATATTGC GTGTGTATGA AGTCTGAACG GCTCTGTGGC CTGGAAGTAA 240  
 10 GGCGAAAAG TAAAATTATA TAGAACAGGC ATGAGATTGG CTGGAAGTTC AGGGAGCCAG 300  
 GCTCTGTGGC AAGCAGCTTA GAGAGCCATA GGAAGCCACA TCGCAGGAA CTAGAGATGA 360  
 GACCCACCCA AGGTGAACTC GCCACGGCA CAGGGGCAGT CTTAGCAACG TGGTAAACAT 420  
 15 TAAAAATAAT ACATACGTTA CAAGCAGCGC GCATAGCAAC TGCTGGAGT CATGTTTTAG 480  
 AGAAAAATAG AAAAATTATT ATAATATTCC TTGTGTATGA AATAAAGCTG CTTTGCAACA 540  
 CGCGGCAGAG ATTCAGACCT GCTGAAGCC GTAAAAGGAC GAAAAACCGA ACGAATAGAA 600  
 20 TTAAGATAGA AAAGCAGCAC TCGGCCAAGG CGAAGCGGGG CGGCAAGCC GCGCGGCTT 660  
 TCCCTCNCNC TCAGCTGCAA ATGCTCTCA GTGGATCTG CTCCCCCTGT CCGCTCTCA 720  
 CCTCTCCAC TCTCTGTCNT ATCCTTTTGA TGAAACNAGG CTGACGCGCG TGTTCACTCC 780  
 25 ATCTTCNCNC GCNCGCTCG ATAAATTGCT CAGNCIACC TCTTGGNG 829

## (2) INFORMATION FOR SEQ ID NO:496:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 875 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1350UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

40 GATCCGCATT AAGCGGACG ACGAAATCAA TACCAAGAAG CTCGACGAGG AGAAGGAGCG 60  
 GCGCTCAAC GCCATCATCA ACGGGGAGC TAGTCATATA AGGTGCATA TAGCGCAATT 120  
 45 AAAGGTTTAG CGTCATCGAT AGTTACATAA AGTTAGAATG CATGCTCCGC CACGCGCGCG 180  
 TTCGACTCG CGAGCCAGCG CGAAAGCGCG TCTGTGCGCG CGGGTAGGAA GAACCGCGCG 240  
 AAGAAGTGA GTTCTCCGC CCACCGGTC TAGAGGTCTT GGCTGAGTAC GTTGTACTTG 300  
 50 ATCGGGTGC CCTTGGAGAT GGCATTCATG AGCCACTGTG TCTCTGTCAA CGAATGCGTC 360  
 GCGCGCTGC TGTGCGACTT CATCATGAC AATTGCGGA ACGGCTGAA CCGCGTGATA 420  
 AGCGCAAGCA AGCAGAGCCC CGCAGGTAC AGTCCGTGC TGTGCGTGG CTGGCGCGCG 480  
 55 CCGATCAAGC CCGCGCGCA GTACTCAAGC GTCTGTGTA GCGGCTCGG CCGCGGTG 540

EP 0 866 129 A2

CACACTGCCG COGACGTGAA GTCCGCCAAG AATGCTCCTG CCCGCGCAG AGCACGTTG 600  
CGGTCTTGAT GTCCCGGTGC ACCACGCAGC TCTCGGAAG GAACTGGAGC GCCCCAACAA 660  
5 GGTCACGTGC GTACCGCCAC CACTGGCCCT TGTGCGGGC GCGCGCCGGT GGNCCGCTTC 720  
CANGTGGGT TCAACCGCTC TACACAACGC CGGACCCNC TOGCCACCGC GAANCGGGG 780  
GTATCCCNAC GTTTCGCGC GGNCCCCGN GGAANGGACC ACTTTCGGTC NOGANCNC 840  
10 CCGCCCGGT GCAAGNGGG AATTNTTAC CTTCT 875

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1351RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GATCATAATG ATTGTCCTA ATCTTTTCT TAATTATCA TTAAATAATT AATTAATATT 60  
TTATTAATAA AAAATATTGA GAGTATGTT CGTTTATGAT AAATTCTAAA ACTTTGCAGC 120  
30 ACGAACTGAA GACAATATG TAACGCTGT AATTAATTAT AAATTATTAT AATTAAATAT 180  
TCAAAAAATG GTAAGATTGA TCGAGGATTA TGAATTAAA TAACATGTTT CACTGCTTAA 240  
GTCTGTAACC GTCTATTGTT TTGATTTTGA TTATTGCTAA CGTAGTCATC AGCGGAATA 300  
35 CTTTAATTTT CATTAAATTT ATCTTTTAT TAATAAAAA TAAATAGGTA TTCATTGTTT 360  
ACTGCTAAA CTACTCGGGT ATCGAATCCG ATTGCTACT TTAGCCTTCG TTCTCAATG 420  
TCAATTAATA TATAATTTAA ATTTTCACTT TATAAGTCTT ATTCATATAA TTATTATTTT 480  
40 ATCTTTACTT GAATAATTCT TAAATTATTT TTATTAATTC TAATTATTAT TTAAATAAT 540  
CATCTACGAA CCTTTAAGC CATTACGAAT AACGCTAACC CCTTTGCTTT ACGCAGCTG 600  
CTGGCACAAT TTGGTTTGA NGANTTAAT TATATATCTC TTTTAAAAAT ANAATCTCCC 660  
45 TCATATTAAT AATTTTATAT TGAANTAAAT TATONTATT TAATAATTAT TGAATTTATT 720  
GTTACCCANA NTAANAANAN ATTATTATTT ACATCCCCNA GTACNGANCA CTTACATTG 780  
50 CCAATCCCN CGCGTTCCNA NAAATGATAT ATTCNANCAC GGATNTCTTC TT 832

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1351UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

10	GATCATTATA TTATAAAATA TAATAAGAA TATATTTAAA TAATAATAAT AATATGAAAT	60
	ATTATATTAA TTCTCCATTG GAGCAATTG AGATTAGAGA TTTATTAGGT TTAACATCAC	120
	CAATAATAGA TTTTAGTTTT ATTAATATTA CTAATTTTGG TTTATATCTT ATAATTCCTT	180
15	TATTAGTAAT TTTACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTTCTA	240
	ATTGATATTT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA	300
	TTGGTGGTAA AGTATGAGGT TATTATTTTC CATTAGTTTA TACATTTTTT ATTCTTATTT	360
20	TTACTATAAA TTAAATTAGT ATAATTCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT	420
	TTGTAGTATC AATAAGTATA ATTATTTGAT TAGGCTAAC TATTATTGGT TTTTATACTC	480
	ATGGTTTAAA ATTCTTTGGT TTATTTTAC CACTAGGTAC ACCATTAAIT TTAGTACCAT	540
25	TATTAGTATC AATTGAATTA TTATCATATT TTGCTAGACT TATTCATTA GGTTAAGAT	600
	TATCAGCTAA TATTATAGCT GGTCATTTAT TAACTTATT TAGGTTGTTT AATATTTAAT	660
	TTAATAGCTA TAAATATTTT AACATTTTAT TAGTTTCTTA CCCATGAATG CNAATTTAGT	720
30	ATGGTTGTTT ANAATTGGCC ACCCTANTAT CCACCTAANT TGAGGTTTTT TAAATCCNC	780
	ATTTTAAAAA TCCATTTAAT TACATNNATT AANAATAANA TATTTAATAA TATCCANNAT	840
	TNAANATTTT ATAANITTTAA AAN	863

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1352RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

50	GATCCTGCAT CGTTTCGTG GCTGCAGGT TGATTTTGT GCTCTCAATT TTATCCTTTA	60
	TCAAATTCAC AACCTGGCAA TCCACCTCAT GCCTTATCTT CAACGAATGC CTCATCGTAT	120
	TGCTAACCT GAGGACCATC TCCACCTTCC GTTTAACAAG CTGACGGTA TCTGTGTCA	180
	ACAGGTTTAT GGCTGGGTG TOGACCCCA ATTGGGCATC CCAGGCAGTT ACGTATCTA	240
55	TGTGTCTCTT GGTGTTCGGA GAGAAGGAT ATGTAACTGA CTGCATGTTA AGAAGGCGT	300

AGGGGAGATC CTGCTCCCGC AGGTCCCGGT CGAGCAACTC GCTGGTGTG ATGTTGATGG 360  
 CGTCTCACA CAAATCGCTC AACAGCGAAA GCTGCTTGAA GGGGAAGCGC ACGTGGTGGA 420  
 5 ACAGCGACCG TGCGTCTTG CCGAGCGGC TCGCGGGCG GAACGGGTG TGCTGTGTG 480  
 CGGACAAGTT CGGGCAGCTC AGGGACGGAT GGAGCATCAC GGGCGCTGC TTGCAGGGC 540  
 CCAGGTGCT AGGGTCCGGC TCGGCAACG CGAGACTTG TACTCCGCG CCGCGCCGG 600  
 10 CTGGCGAGC GCGCCNGTCA GTCTTCTACA CCGCTTGA CTCCCACTC CTCCGTNGAT 660  
 GACTGCGGC GCTCTNCATC CGGTGCTGC ACACNCACAT CTCGGAATGN TTCCACCAC 720  
 CACCCNGAC AACTTTCCAC ACCCGGAAAC TCNNVINGNT TINGGACCT GTCTTTACNC 780  
 15 TCCAATCCN TCTGCTGCAT TTTTGNAAAA CTCGCCCAA CCGACCCCTC N 831

## (2) INFORMATION FOR SEQ ID NO:500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1353RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

GATCTAACTA TTAATGTGTT CCTTGAAATT GTGCTGAAAT ATAACGAGCT CTTAAATGAT 60  
 GTCTATCTTG ATGACGATGT CGTCAAGTTG AGCCAATGGG TACTTCAAAC GTGTAATGAA 120  
 35 TAAAAATATA CAAGCGCAA GOCCAATAAC CTTACCTA TATATCTTGT AATATATTA 180  
 GTTAATTGAA CCATTACGT GGCATATCTT GCGCTGGCAT GGTATCCGTG ATTTTATAAT 240  
 ATATATTTCT CGCAGGGGAA GCAGAAACAC TCAAGATCGG CGATTGCCGA TAAAAGAATT 300  
 40 GCTCCCTGAT TGATTGTGTG TCGAAGGAGA TGCAGATGGA TTGTCCAGAA AAACCGGTTT 360  
 TAAGACTCGT TCATCAAAC TGTAAACCA TTGCCATCG GCTTGAGTA TATTGCCAA 420  
 GGTTCGCGG ATATTTCTTC TGTCTAATGA TAATGTCC ACAGGCTGGT CAGCGCTGA 480  
 45 TGCAGAGCG GAAGAGGGTC GGTCTATCAT AGGAGGAAAG CTTTCTTGAT CCGGGAGCC 540  
 GGTCCGGCTG TCGCTAAAA ATGGAGGTGC GTCTAATGAA GACATTAGCT GGACAGGTCT 600  
 AGGGGCTTCC ATATCAAATT CATCATCGT ATCTCTGT TCTTCTACG ACCCTGTCT 660  
 50 TATGTTTAGA TCTCCAGCAT ACCGCAGTAT ACCTCCAAT ATGATACGT GAGAACCCCA 720  
 CTACCACCA GTGCGNAAA AGAAGTTGAC CCGCTGTAC CTTNATGCA TCCACNACC 780  
 CACCCCCCA ATCNCTGT ATGGTATGAC CCTCAGANAN CCGCTCNGA TC 832

## (2) INFORMATION FOR SEQ ID NO:501:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 877 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1353UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

15  GATCGGCGCA CTCTGTGGTT CATGTCTGTC ACAAGTTGAC CACTGTATAC CAGTTTGACA      60
    TCAGAGGGCG AAATCATCAG TGTGTGGCOG TACACAGAGC AAATAAACTC CTTTACTTCC      120
    TGCACGGTGG TGTGACTGT CACITTCATA GTCTTCATCG CCAACACGGA GTCCGAAACG      180
20  AACTOGATAG TTACACCATC CCCGTCTGG COGTGGTTGG TACGGAACAT AATTAAAGCAA      240
    TCGAGAATG GGGTGGGCGC AAAGTCAAAG CCCAATACTT CCTGTAGGCT CAACCCGCG      300
    TGTTCGCGG CGTCTTCGGC GCCCAGGTAC ACAGGGGTAC GATCGCCCTG CAACTTGGA      360
25  TGCAAGCATG TCGTGGGCA CATGGTCTTT GTTGAACAC AGGTCTTTC AGCTGCTGCG      420
    CTGTTACTCG TTCCTATAT CACATGCCAT CGTCCGACG GCCAGCACAG ACGTCTTCAG      480
    AGGCACAAGT TGCTTATCA CGGCCACCAC TTTATCCATG GAAAGCGTGT TGACCTGGAA      540
30  CTTGAAGTTC ACATACGCAA ACTCACTGTC GGCATCGTAA GCCAGGTCTA CAGTGGCGCC      600
    TCGACCTGC TCGCACATC CAGCTCCAGA TGGACCAACC CCGCGCGCA GCCTGCAATC      660
    TCCTCGCACA ACATGGTCAG ATTGAGCGG ACGCTGTTGG TATTGAGACA GTATTGCTCA      720
35  GCGGCGCAAG CGCATGTTT TCCCTGATG CATGATAAC AATGCCNTAC TGCNATACT      780
    NGCNACTGAT AANTTGGGGG ANGCCCCGCC NTTCACGAAG AAGATCCANG CTCCNTTCA      840
    AATAGNAANN CNGANTGAAC TGGCGNATNC CNAATCT      877
  
```

(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 871 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1354UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

55  GATCGAACAC GCCTGTGCCA GGGAGCTTAG GGTCGTGTGC ATCCAATTGA GATOGAAGCA      60
  
```

AAAACCGAACC ATGCTTGTGTTG AACCGAAAGG CGGATGTAGC ATGGCCCTTTT CCCAACGGTT 120  
 GAGATCCTGG TTGCGCCCTC TTACCCCTGTG CTGAAATTTCT CGCAAAGTCA GCGTGGTCCG 180  
 5 TCGTCAGCAG CGCCTCAAGG GCATGGCCCA GCTGCGACAG AATGATCTCG CGGTCTGCAG 240  
 AAGAGTCTGA GCTCAAGCTG AAAATTGGGG GGGCCTGCGA CCGGCGCTGC AGCAGCATTG 300  
 ACGACGTCAT CTTGCAGCAC TTGCTCACTT GGGGCTCTTT CCGCAGCAGC GTCCGAGACA 360  
 10 GGTGCCGACC ATTCAGAGGC CGGAAGTTGG ATAGCAGATA ATGCAGGTGC GACAGCACAC 420  
 CAGACATGCG ACTGGTTGAC GATACATAAC GTGCTTGCC TTCTTTGGCG CGCTCCAGCA 480  
 GTCCGAGGTC CCGCAGGGC GGCACGAAGT CTGGATGGC CTCAAATCGA AGTCTGCAC 540  
 15 CTTGATCACC CGCTCGATGA AGGCTCGAA GTTGATACAC CCGACCGCC GGTCCCGGAG 600  
 CGGCACCACC GACAGCGGGC TGGAACAGGC AGGTTCCAG CCGTGGGCC AGCGCGGGG 660  
 GCAGCTCTGT TGCACTGCTC NINCCACCCC ATTGCTGAAC GCGCCNIGAT TACAAATTGT 720  
 20 TCNCTCCCG GCGCGCTTG CCGCGGTGC CCTCCCGC CGGGCACCC CGGNCNNNT 780  
 GGATGANNGT TCNCTGATTN NCCAAACCG TTCANNITGT CCGTTTINT CANGNCANT 840  
 25 NCCNNTCINT TGTNCCNNT NAATGCCNC N 871

## (2) INFORMATION FOR SEQ ID NO:503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1355RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

40 GATCATGGCC AAAAAATTGG GAATAGGAAA CTGTTCCAG TACTCATCAA GGTCACTAAA 60  
 AATGTTTGGC AGCAGTGAAG ATTGCATCCT TATCTTGCCA TTTCGGGATA GGACATTTGT 120  
 TTCGATATAC CTGTGGTGAG AGGAAAAGAG TGTTGCCAGT TGGTAAAGTT CTCGTAAAAA 180  
 45 CAAATAAACT TCTCTCTGG AAGTCTTACC GTACGCGATT CTATTCAAAA TCCTCTCCAA 240  
 GTCTGGCCA TCAAGCAACA TATTATTTAA CGACTCAATG AAGATATTAC CAACTTCGGT 300  
 TGAAATGCAC TGAAGTGGT CCAATCTCTG TTGTATCTGA TCAATATTTA TTAAAGGCTT 360  
 50 TGCAATCCAG TTCTTCAAGT TCCTTAACCC GTAGTTTGT CTAGTATGAT CTAATACCCA 420  
 TAACAGGGAG CCTTTACTGC TCCTATCTGT ACTGTTCTCA AAAATATCTA AGCTTTCAAT 480  
 AGGCTAAGA AGGAAGAATC ATGTGCGTCT TCGAGCAGAA TGGTTTAAAG TTTTCCTTGA 540  
 55 AGAAGAGTAA ACNNNCATTT TTGAAGTTTG TTAGGTAGCC ATGCACCAGC ATGAGCGCTG 600



TTTGACAGAG AACGTTGCCC TTAAAGGCTG GGTGGGGCTC ACTGAAGATT TCTTCATACA 660  
 ACCCGAGAG CTCGATCTTA TTAGAGTGA TATCGGAATC TGAAGTATGA AACACCTTTT 720  
 5 CGATTCTTGA GCCAAGGCCA TCTCCGACCA CAACTTCACT CGGGTTTGIG TATTTTATTC 780  
 GCGTCTCCAA AGCCTCCGTC AGAAAACGCT CCTCTTTGAA GTCATCGAAG ATAACTTCAC 840  
 CGCTGTGTAG ATTAACTA ACCAGGAAGT ATCGCGTGA TGAAGGTTGT CGCTTGACA 900  
 10 CAAGACCCCA CACAGAAGCG CTATCACCCA GGACCCGAG ATCTTTGGTT CGAACGTCTC 960  
 ATTGATGCCA TAGGTAGCCC TGTGAATAT ATTGGGTACT TCCCTCGAGA AAACAGAGCT 1020  
 TGAGGTCCCA CTGTTCTTTT TCACTGGGGA TGTCTCTGTC TGCTCCAAGA CCCCCACTTT 1080  
 15 CAGATTGTGG TGCATCAAGC GCTGCAAGTG GACTTCGAGA CGGGTGTCTG GGAATGGTGC 1140  
 AGTAACGCAA CTCTTTGTGC TTGIGA 1166

## (2) INFORMATION FOR SEQ ID NO:504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1355UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GATCATGCTA TCAAGTGAG AGAACACGGA TAGAGCCTAC TCTGCAGGTT CGGCTCGCT 60  
 GAGCGCGCG CAGAAGTGA AGAAGCGGCC AATACCGCC TTCCGGCAGC AGAGGCTGAA 120  
 35 GGCCTGGCAG CCCATCTGT CGCGCAGAG CATCTCCCA CTGCTAATAT TGCTGAGCGG 180  
 GCGTTTGGC CCAATCGGGA TTGGCTGAT CATCAGTGCA AACACGTGC AGAACCTGGT 240  
 GATCGACTAC AGCCAGTGG GCAAGCACGC CACGTCCGAA TACAAGCCA TCCCCGAGAA 300  
 40 CCTGGTGAGC TACCACTTCC GGACGTCCAT GTCCGAACAG CCTAAGTGGC GGCTGCATTC 360  
 CAAGAATGAG TGCGAGCTAG AATTGAGAT CCCCACGAC ATATCGAGCT CGGTGTACAT 420  
 45 ATACTACAAG CTGACGAAC TCTACCAGAA CCACCGCAAG TACGTGCAGT CCTTCGACCT 480  
 CGACCGACTT AAGGGCAAG CTGTTGCACC AGACAAGCTG TCCGACAGT GCCACCGCT 540  
 CTGACTAAG GACGGCAAG CTGTCTATCC CTGGGCGCTG ATCGCCAACT CAATGTTCAA 600  
 CGACACCTTC ACGCCGTTC TCCGGGTGT CCAACGGGT CCCCCGACTA CAACTCAGCC 660  
 50 AACAGGAAC ATCGCTTGC ACACGACCG CAACAGGTNN CAAGAGAAC AAGCTACAAC 720  
 CCGCAGANA TNGTGCGCC CCGGCGCTTG GCACGAACGT TTCCCCNAA TGGTANNAC 780  
 55 AANCCAACT GCTGACTNN CTACTTGGGA GAATTCCCG TMTGGANTG NNCCCTGCAG 840

NCTGCCNCCT NNTAAANCTN CNTNCAAAAA AAAAGCAACN CCCTCCC

887

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 823 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1356RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GATCTACATA TGCATCAAAA CATGTGCTT CATGGCCTC AGTAGTTATG TTTCGGCTGA	60
GAGGCGAGCC ATTTCAGCT TGTCTGCACA ACTCCATATC ATTTCATCA TCAACCTCAT	120
TATCGCTATC ACCATCCTTA GTCGAGTATG GAAAGGAGG TGACACAGCA AGGCCAGAGG	180
TATCAGTTGA AGACATATCT GTGCTCATGC GGTGGGCGC ATCATAGTCC GATGACTTGG	240
TGGAGGATTT AAAGTCATTC TCGGAGGAT TCTGTGGCTC TACTGACCTT GCAGATTCTG	300
TTTCACCTTC GTACAGAATG GATCATCTT CGAACTTGAG ATCTATCGT TTGTGATCAT	360
ACGGACTCT TTTTCAACC TTCTTTGTG TCATGGCAC GGAGTTTATC AAGCTAGAGC	420
CCAAGGAATG CTGCTTATCA AAGTCTTCT TAGCATGGG CATTTCTGAT CTATCATCTA	480
TCCCTTGGT CGAACCATAC TTCACCTGGT AGCCATCTT TGTATTATAA TAAGAGTTGC	540
GATAATGCTT CGTACCAGAA CTACCGGCAC TGCTAGACTC CAATATGGCT TGGATGAGGA	600
CTGGCAGCG GAAGTTTACT GGCATCCATA TCAATTTGGG CNTGGCTGCC ACATTGAAA	660
ANANTAAGAA GAAGTACGAC TAATCTCCA CTNGCTAACC CGTCCNTAGC AGCGAACCG	720
CTGCTGTCTN NCNATCCAC CCGGTGCTT GCTTAGCTCC TACNCCNIG TGGTTCCATA	780
ACCCACCCCG TGTACCCCA TCCCTGANC ATTNIGAGAG ANN	823

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 873 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1356UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GATCTGAACC ATATTACCA AACCACCAA AGAATTGGG CCAAGCGAC CGTCCGGGC	60
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GTAAAGCOCT ATAACCAGCT TACGGCTCTG TGGGCGCCAT AGAAATTTGC ATTTTCAACG 120  
 GAACCAACAC GTCAATCOCA AACTACACTT ATCATGCOCT AAAAGGGATT ATCTTTTCTA 180  
 5 ACGAGGAGGC CGGCTGCGC AGTAGGAAGC GGATCTTAGC GCGCTCOGGC CGGCACATTC 240  
 GCGCGTTGGA CTGCAATATC CTACTTCTGC AGCGGAAGAT AGCGCAOGAA AATCTGCGGC 300  
 GGAGCAAGCT CAGAATTATA TGTAGGACCA AACATTGTCA GCAACGCGTG CGCCGAGTTC 360  
 10 TGTATCGAG TAGGGGGATT TOCTGCGAAT GCGTTCTCTT TTTATCGTTT CTTTTTTGAG 420  
 GGGCATCTGC AGAAGCGATG AGSTCCAAAG CATCTTGTG CATCGATCAC CGAGCCACACA 480  
 GGGCAGGTAG AGTAAAGCCT AGTCACCATG GTGGTAGTTG ATAATAGCOG CGGAGGCGCA 540  
 15 TTCGCATACT ACGCGGTAA GCTGOGAAAC AAGGTAGCGA CGCGGCGGG GCTTTTAGGC 600  
 GACTACGACT ACAAGTACCT GTTCACGCG CAGATATTCA AGCGCCAGAG AAGCTTCAGC 660  
 CATTTTCTCG ATCNATGCAA AATCCCCGGT GGIGCTTGGG TGGCNTTTGG GGVINCACNC 720  
 20 CCGNNGCAAN NCTGGCGGNT TNNTTNCNCC NCCAATNNVG AATACCGNG GNGGGAANTT 780  
 TGAAAGNNAA NCCNACATNC TTATTGGGCT TNCNGNIGT NGACCGGGC TTCNNNNAAG 840  
 GNGNAATANN CCTTNGAA TOCTTAANAA AAT 873

## (2) INFORMATION FOR SEQ ID NO:507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1357RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GATCCACGG AGGACATCGA AGAGGGACTA CTGTACGCA TGGACAAGCT TCGCTGCCGA 60  
 TTGATGAGCG AAGACCGAGA TGAAATGACA GATGGCGGGA CGTCCGGAG CGTGATCTGG 120  
 AAGGAAATGT TTCTGCGGT CGGTATGGTG TCCAGGCTCA TGGTAGTACC TGCAATGATTC 180  
 45 TGCTTTTCCG TGATCGGCTT CATGGTGGGC GTTAGCGACT TATAATAGTC GGTGCGGGTT 240  
 GCTGGCGCAA GCAGCTGGCA TGCAGTGTG TCCGACAAAT AGGAGTACCG GTTGGTGTTC 300  
 TTATTCTGTG TGTTGTCAGA AATGTTTGCA AAGGAATAGA AACCATTTTC CATGGTGTTC 360  
 50 GAGGGGACTT GCGAGTTCTG TGCGGGTGTG TCGGCGACAT GACATTTCAT TTCTGTCTCT 420  
 GCGCCGCTT CGCAGGAAA ATGCGGCGC TGTTGCGCCA TGCTCTCTTC CTGCTGTGTG 480  
 CCGTCTGTG CCATCTCCCC TAGGGGCTTG CCTGAAGAG TTTCAAAGCT TTGGAACCTC 540  
 55 AAGGAGGGCG ACGCCGGGOC CACGAAACGA TATCGCTTTA CTCTCTCTCA GCTTCCCGAT 600

AGGCATCTCN ATGCCATTTT ATTAATATAT TTCCCCCGTC CGAACCCCAA ATGTATGTCT 660  
 CCGGGTTGGC AAGGGATTCC GACTTATATA TTATTTGATG TOCACCACAG GTTTCNNAAA 720  
 TATTATACAT CNATTGCCNA ACCTCCCCNT TATNCATCAT CCGACCCNC NCATTTGTGA 780  
 CNCACTAACN TGCACATNNC CCNATVINNT AACCCATCAA CNCACCTTNC CTGCCCATCT 840

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAGL357UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GATCCTCGCG TTCCCATGCA ATTGTGTGTC TTGGGTGAC CCGATATGAC CTCAAAACCG 60  
 GGTCOGAAGC CACCAGCAC TTGTGCTAT GTGACTTAGC CCGCTCAGAG AGAGCAGTGA 120  
 CACAGATAGT ACGCCGAAG GAGGGTGGT TCATCAACAA GTCATTGCTA GCGCTTGAA 180  
 CCGTCATAGC CAACTTAGC ATGTTGGGAA GCCAGGCCAA TGGCCTGCAG CCGTCTCCCG 240  
 CAGCCGCCA CATACGTAC CGTGACTCAA AGTTGACCG CATCTTCAG CCAGCATTGA 300  
 CAGGAGACAG TATCATTACG ACCATCTGCA CCATCGATTG GAAAGCCGAG TCCTCAACCG 360  
 AAACGACCAA TACCGTCGCG TTGCGGTCTC GCGCCAAGAA TATCGCCCTC AACGTGGCA 420  
 AGAATGAAAT GGACTGCGAC GCGAGAAAG ACAACATCAT CCAGAACTTG CGCAAGCAGC 480  
 TTGACGAGCA GCAAGAGACC ATTGTGATGC TCGGCGCAG TGCTGCAGCG CCTAGCGGCA 540  
 ACGGCTCGAC CAGCCCGCTG GACAGCCCTG GCGTCGGCG CAGCCAGCTT TGAGCGAGCG 600  
 CAGCCACAA CATTTGAAAA AAGGNTGCT AAAGGTINGAA AACAGCATCC TCCAAGAAGA 660  
 ANCTCCGAGC CATTTGCGAA AAGCNCTCG AANNAGGAAA TGATGTCTC CGAAGAACCG 720  
 CANTTTNCA NATCTTINAA ATCTCCCCCT TGGAAATCC CCGTCCCCC CAAAACCAGG 780  
 NINCAAGGGT TGATTTCCNC NGCCCATTA CGGNTTACT TTCAAANTA AATNCACNCC 840  
 CCCAGNCCN NGAAAATNCN TTCCCCCCN TMTGGNGTTC ACCGCCNA 888

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1359RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

10	GATCCATGTT TATTCACCCC GCTCACTGCG GTAAAGGATG CTTTACGTTG CTCACATGCG	60
	CGCCACCATT AACAGCGTAT CACATTTTAC GTTTCOGTGC AGCAAAAAGT CGGTCCGAAC	120
	ATAATGCTCC AATACCAAGA TAGGTCCGCG CAAGCGCCTA ACACGTGCGA TCCTGCTGCG	180
15	CTCCCCACGG GCGGCTGGCG CTGTGCTGGA TGAAACTGCC CTCCAGCGTA TGAGCGGACG	240
	GGCATTGCGC CTGCCATTAC TGCACGCCCC ACCGACAGGT TTCCCATGTC AGCATCGACG	300
	GCAAAACCGC AGAAATCGAT AAGTAGCAGG ACACGGGTCA GAAAGACCAG TGTGGTATCA	360
20	TGGCGCAGCA GGAGCTAGGC AACCTGCTTT TTCCGCAAC ATGCCCGGCC GCAGGTTCGA	420
	ACGCGGGAGC GCTTACCAA GCGGGGATTG CTAATGTGCC TTCCGGCCAA AGGCGGTCAC	480
	AGCTAAAAGA GAGGGGCCA CGAAGGCATA TAGCTGGCAG GAAACGATAC GATTCAGCGC	540
25	ACTGCGAGCG TAAGGAACAG GAGCATCACA TCGAACAGTC GCTGTGGIN TCCATCCCTG	600
	AAGGTGACA CTAACCTGAA AAGCGGCGT TGGCACTAAN TACAAACNTT ACCACAGTAG	660
	ATGCCNAATA CTGCTGACAA ACGAACTGGG ATTCTCTACC GGTGCTGNGG ANANAAATCT	720
30	NCCAAGAACN TTAACNCAA TTGGCCACTA CCCCTCTTGA TCCCTCTTNN ATCNCAAGGT	780
	TTGGGANCCG GNGNGCAAAG CCTGATGNN ATCCTGACN AANITGGACT NNT	833

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 871 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1359UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

45	GATCGGTGTA GTACACGGTT TCCGGCGCCG CTTCTGGCAG AGCAGCTCCG ATCACCGCGG	60
	TACCCAGAA CTGCCCGGGC GGTGCGCAAC ACTAGTGCTT GCTGCTGATG CCGGCTTCT	120
	AGTCGTGCCC TATTTTATTC CTGCGCGGCA TGTTGCGGCT GTCACGGGCT ATCTCGATGT	180
50	GCGCGAGCAG GAAGGCTATC TTCCGCAGAC CGTTCTGTG CATCTGGTGG CACCACCGCA	240
	ACCGCCGCAC GAGCTGGTGC ATGCGCTGGA CGCCTGCCG TGTGATTGCG TTCTGEGACT	300
55	ACCGGTGTA CAATCCGTCA TATACATCGG CATCCCGGAT GCGCCACCT TTGTTGGTCC	360

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AGAAGAACTG CAGCGCACTG CTGCCGTCAT CGCGCACAAAT CAAGGGGCOCA GTGGGCCCAA 420  
 CTACGAGTAT CTGAAGCTGC TCCACAGGCG GCTGCACTCA ATAGCCGAAA CGTTTGGGCG 480  
 5 CCGCTTGTGC GAGCTGGAGG ACCATTATCT GGACGAGCTG CTGGAAGCGG TCGACCGTCT 540  
 ACGGGGCCAG GCCTGTGCCG CGGTAGGTGC CTGATCTTCT GCTAAACCCA CGCCGAAACA 600  
 AAGATAGCAC CCGCGCTCC GGGTAGCGGC CGCCGTCGT GACCAGTGC TAGCGTTTAC 660  
 10 TTGCATACCC GTATCTGCTT TAACCGTTTG GAAGGTTTAN CATCAITAGT TNNTTGTGC 720  
 GCTTTGTGTC CCTGCGNTTG GCAAGGGGCG CCTATTTTAA NTTACGCGC GNTTAACGNC 780  
 NOCTGAACAA AAATGAATTC NITTINGANAN TCCCGNATTT TNAGGATATC CCNGTTTGA 840  
 15 ATTGANAATA CTGATTTGCC NTTTTTNT A 871

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1360RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GATCCTTCTC CTCGCAATC ACAGAATATA TCTCGCGGT CATATCCTTC GCGGTGAAA 60  
 TAATGAACG TGAGTCCCGC GACCATGTGA GCGATGTGAT GTGGGCGAAA TGCCCCGCGT 120  
 35 GGACCCGGTA GCGCACAAA GCGCAAACT GCGGCTCAGC ACTGACCCCT GGAGTCGCGC 180  
 AAATCTGAAG AAACCTCCCA CATGCCAGAG CAAAGAGCTT ACGTCTGTG GAAAACTCA 240  
 CGTGTGTTAC TTGTCTTCA AAGTTGAAAT GATGTATCAC ATTCTCTGTC TTTATATTCA 300  
 40 CAAGGATTGC CCGACCGTCC ACGTCAACG AAAGAAGCAG TGTACCTGG GCATTGACGT 360  
 CGATCCTCG CTATATTCT TCTATGCTCA TATTCAAAGG TAAACGACTT GTTACCAATC 420  
 AGGTCAAACA CCGATACCT GTTGCCAACG GCGAGAATA GCAGCGTTC ATCCTCGAA 480  
 45 AACACCACAT TTCCCTGTCT GTATACAGTG CCTAGCAGAT TGGAAAACCT GAAATCAGAC 540  
 TTCATGTTAG TCCAATGCGT TGCTTGCTT GATCTTTCAG TGGTGTAGCT CATCTCATCT 600  
 CGAATTAAAT TTTCGTACC ACCCAAAAA ACANATCTC CANCTGCATC TCAAGATTAT 660  
 50 ATATATATGT TCGAAAATTG AANATCCACT CNTCTAAATG GTACACNGTC ATATGAATGT 720  
 GTTNTTTTGC TCCANTATCC CNACCATTAC CCACTCCAGA ATGGGAATAT ATGCCAGGAT 780  
 NTCCGCCACT TCACCTGTG TTGACANAAT TCTTGAGNTG CTGACAGCCG AGAAAAAGG 840  
 55 TCAAGGTAT 850

## (2) INFORMATION FOR SEQ ID NO:512:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1360UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

GATCGATGCA AACCAAGGACA ACTACTTAGA AGAGTCTTG AAAATTAAAA GGTATTGAG      60
TGAATTTGAA AATGACGTAC CGGATAAGAC AGATATCAGA GGAGTTCTCA ATCCGGTTGC      120
AATTGTTGGT TCCCGTGAAC ATGIGTTCTC TGAAAAAACC GGTGATTGG GAGATCTCGC      180
GGCTGGAAAG GAGCAAGTAT TCGGAACATT CTTTGCACTG ACCCTTTGGT ATATTGGTGC      240
AAAGTTACAC TATGGCCATC CTGATTTTGT TAATGCTATA TTGTCTACTA CCAGAGGTGG      300
TGTATCGAAA GCTCAAAAGG GCTTACACTT AAGCGAAGAC CTTTTTGTGT GGATGAGTTC      360
CATATTACGT GGGGGTAGGA TTAAGCATTG CGAGTACACT CAATGCGGGA AAGGCCGTGA      420
TTTAGGATTT GGGTCCATTT TGAAGTTGCG TACTAAGATT AGTGCGGGTA TGGGGGAGCA      480
AATACTCTCA AGGGAATACT TTTACTTGTG TTCAAATCTC CCACTCGACC GTTCTAGTT      540
TCTACTATGC ACATCCGGGA TACTACTTGA ATATGTTTCC AATATCCCTT CTAACCCCTT      600
AATTANGNAA TTTANTCCCG NATTAATGGC GGTCTGGTTC AANCCNACCA AAAATNINNA      660
NATTCINTTA ACCCCCCAAN CTGCAAAATT TATTGTGTGC ATTNAACCCN TAACCAAGGT      720
NCCCCNINC NCNTNANCA TCCNINTCC NCCGGINOCC TTCCAGTTT TGNAGAAAA      780
ATTTAAAAAC CNACNCCGGG TTNCCCCGAA AATGAAACTN NTANAAGNGC CCCCTTTCAA      840
ATTTTTTTTT C                                                                851

```

## (2) INFORMATION FOR SEQ ID NO:513:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1362RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GATCATAAGC TATTGGGTAC CCGTTGTAGC CTAGCCTTAA AATAATCGAC ATTTTGAAT 60  
 TTAGTTATTG CGTGGAAATA AGGTATATAT ATTGCTTCCA AGTTTAATGT CGCTTTTAAC 120  
 5 TCACTAAAAT ATGGATGTAA ATGTCTCAA TTGGACTTTC ATGTTCTATC TATACACTAA 180  
 CTGCGATGCG ACTCATGTG CTTCAGTATT CAAAACATGT TTTATATATG TAATATGCGG 240  
 ACGTAGAAGG CAACTAAATA TGAGAGGCAA CTTAGTCGCT GTCGCTGTG CTGTTTGAAT 300  
 10 CGCTGGAATC TTTTTCATAC ATGATCTCGT CGCATTATC TTCTTTTAGA ACGCTAAGTT 360  
 CCAAGTCCTT ATGAGATTCC TTGTTCTCTT GAGAGACCTC GTCATCAAAG ATGATCTTGG 420  
 TGTTGGAAAC GACAGGCAGG TTTTCTGCTT GCGACCTGTG ATAGCCTTCA CTTAGCAGTG 480  
 15 ACCCCTCGAG GGACACCATT CTGCCCAG TGTAGACATT TTTAACAGTA AATTGAGTT 540  
 TTCCGTCCAG CTGCTTACCG TTGCGTCAC CCAGTGGCCT AGAGACCGGG CCTGCGCAT 600  
 CCTGTGGAG AATCGTTTCG CTGCTCCCGT TGGTACTCTC TTGTTATGA ATAAAGTCCA 660  
 20 ACCATCGGA ATGTTATTTT CTAATGAAGC GTTGAACCTT CGTGATCCAN CAACCATNTT 720  
 GTTGAGGTGA CNNTTGAAAT CCCCCNCA CNATCCNAT TTTNGGACA NCCNCAATTT 780  
 CCGGCCCCN NITAANCCAG GNTATCTGNT CCANTGANTA CATCTCNCIT T 831  
 25

## (2) INFORMATION FOR SEQ ID NO:514:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1362UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GATCATAGCT GCAGGCTGCC AAGCAGACAT GCTGACATCA TACAGCCAAG AGAGCAGCTA 60  
 CGCTGTACCC GAGCTGGAAC AGAGGCTAAA CGAGTTTCGC ACTAAATGTA GAAAAAATGC 120  
 AAGCCACTTT CAGGCACTAC TTTCAGTGGT AACTGAGATA GACCATCCCG ACAGCAGCCG 180  
 45 GCTAAGTCAC CGTACAGTAG TCTTGACATA CATGGAATAT CGCTAAGGAA GGAGGTGTAA 240  
 TAGGACACAA AATCATGAGA AGAGTATTGG CTTGTGCAAG ATGCGGTGGG CACAAGATCA 300  
 AATGCGTGCA CAACAACGAG CCACCCTGCT CTTACTGCCA GCACAAAGGC ATAGCGGAGA 360  
 50 AATGCGTGTT ATCATTTCGG CCCAAGAAGA GGCGCAAGAA GCGGGAAGTA TACTTAGAAG 420  
 GGGTTGCGAT GCGCTGGGC GGGTATCCGG TGCAGCAGTT GGAACTGCA GATCTGCAAG 480  
 AGCATAAAGC CAGAGCGGAC GGCCTGTATG AAAGCCAAGC TCCTGTGCAT GCGCAGGACT 540  
 55 ATACGATCGG GAGCAAGCTG CGCAGATGTA CGAGCTGGCC AGCAGATGTA CTACGCTGCG 600



CCAGGCGTAC TCGACGGTTA TGTCGAGTAG TGCGAAGGTT CCCAGGCGGG TTGATTCTCC 660  
 CGCCAATTGC CACCCGGATT CTAAACCGAA ANAATGCAAC NCATGGAACC NGCCNTACTT 720  
 5 TMTGGACTG TCCCCAGTGC CCNATGCATN GTGCACTTGC AINGAGANNI TGTCATCCTT 780  
 CCCCAGTGGG NIGTTTANAT GANACCNCCC AAGAATACCC CCTGACCGTC TTTGGTTCCT 840  
 TTTGCCCCCC NCCT 854

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 853 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 20 (A) ORGANISM: PAG1363RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

25 GATCATTATC AGCATTAAATC TTCAACTCGG CATTGCCCTCT TAAACCAATA ACAAACCGG 60  
 CAGATTTGCC TCCAATTGCG TAAGGATCCT TTAACCCCTT GAGGGATACT TCAAAAAGGC 120  
 CTTCACTAGG CCAGCGAATA TTAATCTTGG CATGGAACAT ATTCTAATT TTATCCGAGA 180  
 30 AGCCTATTTT CTGGATGGA TCAACTGGAG GTTTCGAAAA ATTGTCTAAA CAATTCATGG 240  
 CCTGTGTAT AGCAGCTTCA TAAGAGCCAC CCCATGTCAC CATGTGATG TCTTTGAGT 300  
 GTATATCCAT TGTTACCTGA CTGTAAATTT TAATAGGCGT TAAAGACCGG CGGAAGCGCA 360  
 35 ACGAATAATA TAGGTCTATC TCAGAAGAAG TAACGGAAGG AACAAGCGGC ACAAATATCG 420  
 TTOGTAGCTC CTGGTTGAT TGAATCATAT CCTCCAGTAA TAAAGAGGTC ACCATACAAA 480  
 TGTATAGCGG GAAAGAACC TTGTTGGGAA GGCATAGCTT CGGCATATGG ACTAACGGTA 540  
 40 GTINGGGTTAA CCTTNAANA GCCCCCTTAA TTCACCCANC TTGGCTTCCA ATNTAAAAGG 600  
 GAAGCCNCCA NPTATTCTGG GTTANITTTG GAACCCCNIT TNCNCNCAAN TTTAATNAAT 660  
 TNCNNITTT ACCCTTCCCA CATNANGGCT TAAANTNNCA TGTTTTACCC CCCCNGCCAA 720  
 45 GANNTCNCC ATTTTGGAAA TGTTANANIC CANACCCCT TINCATNTIN NAGGANCTTC 780  
 AACTGTCCNT TTNCCCCAAA AANITAAATC CCNAAAAAT TCTTTCTCTC TGGGNTTTT 840  
 CCCCCCTTAC CNT 853

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 858 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

# EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1363UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GATCGAGGAT	ATTTCCGTAC	GCTGGATGTC	GCTCGATGTC	AAGTACATGG	GTGATCGGTT	60
GGCCTTTTCA	GTGTGCGTTC	AAAATATCAA	GCACAATAAG	GTCTGTCTGC	TGAAGTCTGG	120
TGCGCTGAG	GTTCCTGGCT	GTTCACAAA	AGACAGTCCC	TTGGACTAA	CATGTGTGA	180
ACTGAGTGC	AAGTTTCTTC	AATCACAGT	GCTGTGAGT	AACCTACTAG	CACTATTTAC	240
CTTGGGCAAA	GAAGAAGATG	AGGACGTGCA	AGGCTTTGCT	CGTAATATTT	TOGATGGCAT	300
GACCGAAGAT	CCACAACCTGA	ATGCACAGAA	TTGTGTGGAG	ATGATGAGAT	CAAGAGTTAC	360
CACGTTGCAT	AGCTACTTTT	CCCATCTAAC	TAAGGTTGAT	TTTTTTGTIG	ATAAGGTTAA	420
OCTGGCAGAT	ATACCACCCA	GCTTATTGCC	TGAGTTGTCA	TCTGCCGTGIG	AGCCTTTGAA	480
ATACGAAGTT	GCGCTTTCTA	GTTTTACTTT	TCAAGTCACC	CGTTTTAGCA	CCCGAACAGC	540
CAGGTATAGT	ATCCTTTTCA	AAAGTCTGAT	AGACCGTAGG	GTCCGTATCA	CATTGTTCATC	600
GTTCGAGTGC	GCTCTCAGTT	AATGCCCTTA	AAATCCCTCT	GAAAAGGCTC	CTGAATACAT	660
CCGGTTTTTTG	AAGTCCCAN	TTATATCCAT	ATGGTGANAC	TATACTTTTC	CTGAAAATTT	720
GACTGGTCCA	CGCTGTTTCT	GANACAAAGT	CAATGGTGGG	CAGTTTCTCC	CCTACCNIAA	780
NATTGAAATG	AAACCCCCAN	CTTGAACCCC	GTTCGCAATA	CTGTANGACT	ATTNTTCCN	840
CANAACCCCN	CCACGNAN					858

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1364RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GATCAGATCG	ACGTACAGTT	CCGTGCGCTG	GGCACACCTA	CGGACAAGGA	CTGGCCTGAG	60
GTCTGTCCTT	TCAGCGCGTA	CAACAAGATC	CAGGTATACC	CGCTCCGTC	GCGCAGCGAG	120
CTGGCAGGCC	GCTTCATGCG	TGCAACTGAG	AATGCCCTCG	ACCTGATGTG	CGGTATGCTG	180
ACGATGGACC	CGACAAACG	GTGGGACAG	ACTCGTTGCC	TGCTCAGTCA	GTATTTTGTA	240
GAGCTTCCGG	AGGCGACACC	TCCTACGGAA	CTTCCAAAAC	TAAATAAGTA	ATGACTATGA	300

5 TAACCTAGAT GGTATACTCG GACGTTTTGT GTTTGTGCTT TGAGGOGATG ACATTGGCCTT 360  
 TTATGGTATC GCAGACGTTG CCTGAAAAAG ATTCAACGTC TGGTAACAG ATTTGCGCAG 420  
 ACTACTTGTT GAAAGAACAA AGACCAGAGC GCTGGGATGC TCACCCCAAT GACGAACCCA 480  
 CTCGGCCTTA TTGGCGCTGG CTGCAGGTTT CTTAGCACCA ACAATAGGCC GCGACTGCAC 540  
 AAGATCTTTC CCTCCAAGAA GCTGGTGAAC AGGATGCTGT TCCGACCTTG ATAGCGGACT 600  
 10 GACCTTCCGG AAATTACTTG CCTTGATATC GAGCAGTTGT ACACCCAATT AGACAGTTAT 660  
 TACGGGCAAT TTGTATATAC CCNCGNCTTG ANGGCNCGA CMTTNTATCC TGAAAAGNTG 720  
 CTNGAAAAAA TCCCCGCNAA NGAAAANNCC ATGGCCATCT ANTTGNCCTG AAACAACTGC 780  
 15 TTTACTGCTG CCAATNGAN ACCAAAATCN CGGCGGTACC TTGAOCTTNT CACCGCTTNC 840  
 CT 842

## (2) INFORMATION FOR SEQ ID NO:518:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1364UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

35 GATCTAGTGC TTCACAAGCT AGAAGCTCCA ACCATGAAAG AGGATCGAT OCTGAGAACA 60  
 CTTTTTCTGT GGAGGCTTAT CAATGCTCTT TCTATCCGCA GCTTCTTCCA GGCAGATGAA 120  
 TACTGGCAGT CGCTGGAGCC TGCGCATGTT AAGGCGTTTG GATATGGTGG GCTGACTTGG 180  
 GAGTGGCAGC ATGGGCTGGG CAGCTATGCA TTCCCGATGC TCTTTGAAAT GTCTACTAT 240  
 40 GTGGCGTGA TACTGGGTGT GCGCACCCGG ATGGGCTGC AGGGGTTGGC ACATGCGAGC 300  
 GCGCTGTGTG GGGGGTGGT GCGGAGCGC GCGGCGGGCG TGCGCGGAT GAAGGCGTC 360  
 TGGGAGCTGC CGGAGGCAGC GCAGGAAGTGT GTGGAGTACT ACGGGTATT GTACGGGCGG 420  
 45 CGAGTGGTGA TGGCGGCGGT AGCAGGTGTC GGGGAGTTCT ACAGCGTGCT GCTGGTGGC 480  
 AAGCTGTATC TGGAGTGC GGATAAGGGG GAGGACCCAG AAGGGGAGG CGGCGCGGT 540  
 CAGCGGTTG GCGCTGAATG CTGACCATGA CAACTTCTT CAACTGTTTC TTGCGAAG 600  
 50 CAACGTTTAT CACTCCINCA AAATAACCCC CACNGCGNVC CCTCTAACC NATTTGGATT 660  
 GGANCCGGGG CCANCTTTG GTTCTCTTGG GCTTCCACCN CAACTTTTNGC GSTGGCTGCN 720  
 TTTGCGTGC CTGCAAGGCC NATACTTTTT ATCTTGGCCT CCTGCGCTGT TCTTGTGCCA 780  
 55 ACCTGTGTC CACCAAGGT GCACTCNVIT ANCTGTCCC TAGGTTGCC CCGGCCCCGC 840

GGGTTTTTCN ATACCANTNA NACNCTCCT

869

## (2) INFORMATION FOR SEQ ID NO:519:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 839 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1365RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GATCTGCGGC	CGCGGGAAGA	CGCAGAGGAA	AGCGAATCGA	GCGCGGGAGA	GCGCTACTCG	60
ACGGACAAAA	GCAGTTACGC	GTCTTCGGTG	CAGGCGGTGC	TCAGAGCGAG	GACAGCGTCG	120
GCAGCCAGCG	CAGATACAGC	AATGAGCAGT	TCAAACGGCAG	CCAGCGATAG	CGCGGGCGGC	180
GCTAAGATGG	ATGCAGCCGA	CGCAGATGAC	GCGACGGCCA	GCTTGGAGCT	GCGGCTTGCA	240
GCCCTCGCCA	CGCAGGACCC	GGCTGTGGAC	AGCGCAGACA	CGCGAGGGG	CGCGTCGCCG	300
GCGTCGCCCG	CGCGCGCGCC	CAGCCCGCCG	CCCANCGCGG	CGACGGAGGG	GTCCGACGAG	360
GCGCGCGGCG	CGCTGGAGGT	GCCCAAGCAG	CGCGGCGACG	CGGCAACGGC	GGCCGGCGGC	420
GAGCCGGTGC	GGCGGCGGCC	CACCAACCCC	TTCCGGGTGA	TTTCGGTGGG	CGGCTCCAGC	480
ACGTTCAAGC	GCGCGCGGGG	CGCGGACGGG	CAGGCGTGGC	GCACGTGGTC	CGCGGGCGAC	540
AAGGCGGCAC	CCGTGTCCGC	GAACGAGCAG	AGCATGCTCA	AGTTGCCCGG	CNAGCNCANC	600
TACCCTGACC	ATGAATTCNT	CNACTGTTCA	AAGANATTAA	TTTCCTGANA	ACNTGAANAA	660
ANCGTCCCT	GTNCTTGAAG	AANCCCCCN	ANTAACNACC	CCCTNGACAG	CTCNGATTTC	720
CTCNCCTTA	TINTAAAAAA	TTTCAAATNC	GGGTGGINCT	TCCCCNCNTN	CCCAACNTTT	780
TAAAANGTTC	CCACGGCNIN	NIGNNCCCN	NATTTGGCCC	CCGTTCCNT	TNCCNGGT	839

## (2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 851 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1365UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

EP 0 866 129 A2

GATCAAGTGA CGTTCATGGA GGTGCAGCA CTGCAAGACA GCGAAGCGGT GGTCGGGCGG 60  
 ACGCGGCGGG CGGCGGTGCA GCTGTATGTG GGGCCCGGGG GGGGGCTGGG GGGGGGCGTG 120  
 5 GGGGAGGCGC TGGACGAGTT GCTGGGCGGA CCCTTAGCGG CGAGCCCACT GGGGCCGCGG 180  
 TGGGATGTGT ACTTTATGCA GCTGGGCGGG CTCGGGGCGT CCGGTTCCAA CTGCATGAAG 240  
 CGGCGTGTGG GGTGCGTGAT TGTGGGCGCC TGCCGGGTCA TTGCCACCGG GTATAATGGG 300  
 10 ACGCGGCGGC ACTTGCGCAA TTGCCACGAC GCGGGGTGCG CGGCTGCAA CGGCGGCGGC 360  
 AGTGGCGTGC ACACCTGTCT CTGCTTACAC GCGGAGGAGA ATGGGTTACT GGAGGCCGGG 420  
 CGGGAGCGGG TGGGGGAGGG CGCGGTGCTG TACTGCGACA CCTGTCCGTG TTTGACATGT 480  
 15 TCGGTGAAGA TCGTTCAGAC GGGGATCAAG GAGGTGGTTT ACTGCGAGAC CTACCGGATG 540  
 GACAGCGACA GCTTCAAGGT ACTGCGGGGG GCGCGGTGCA GGTCCCGGCA GCTACAGGAC 600  
 GCGTTCGGCC GCACCTTTTA TTATATNNGC NGGCGCTTT CCNGCAACN GCTAAACTTG 660  
 20 CTGTTTTTNC ATATAAGGNC CCGCGGTGNC CGACTNCAA GNAATNCCNC AACCTTCTT 720  
 TMTTCCGAG GCGGGGAAT TTTCCCGGA TMTNNGGCC CCCCCGTNN TGCCGTTACC 780  
 25 CANTTCCCT GCCCAATCT CCCCAGGAAN CCNCCNCAA CGTCTCGNN TTNCTCCACC 840  
 CGNCTGNCC T 851

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1366RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GATCCAACGG TCAACCAATG CCTCCGAGAT TGCCGGCATA GCGGATGAGA TTGCCAAAGC 60  
 GGAGAAGCAG GACAGCTCCG CGCGGTGTG TGCCATGGGT GCGTCTAG GGCATGCAGC 120  
 45 GAGTCTTTTC GGTGCTTTGA ACGTGCTTAA CAGTTCTGCC GAGCTCTTGA ACCAGCCGGG 180  
 AGCAAAGCCT GCTGCGGTG CTCTCAAGGG CATGATGGAG GCTGGGTCTA ACACGACTAA 240  
 GGCATTTGAC TTCAATCATG AGCGTGCAAG TCATCCAAAG GCTGGGCGGG CAGAGCAGGT 300  
 50 GATGGGTCTA GATATGGTAC TCCAGAATGC CGTGAAGTCA AGCGAAACCT TTGCAAATAT 360  
 CATAAAAATG CAGATGGCAT CGACCGAGGA GTCCGAGAAG GCGCTCCCAA GTTGTGTTGG 420  
 CTTGTGTGCG TACTCGACTG ACAAGATCGA GAGCATGAAA TCCGTGATTA AGCTGATAGA 480  
 55 GTTCGGTGAA AAGAGCCCTG ATGTATTGAA TCCTGTCTTA GAAGTGCTGC AAGCTTCCGT 540

GAAGGTCAAC AGATTGATAC CCTCCGAAAG AATTTTNGAC TTACACCCAC ATCCTGGAAA 600  
 CTTCATNTTT GCTGCGAGTT ACAAACGGC ATTTCCCAAT CTGCCATTIG TTCCCTTAAC 660  
 GGNCCCCAAA GGTITGCACA CCNCCNTCCT NCAGGNTTCA ATNCTACTC CTNNNCCNA 720  
 CCNANGAATC CNNTTGGCCC TTNTTTAANN CAAATCNGNC CANATNTACC CCCAGGTTTT 780  
 TTTTGGAAAN CCTTTTANA CCTTTCCCCC CCTCCTTTIN NAT 823

## (2) INFORMATION FOR SEQ ID NO:522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1366UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GATCTTATCA GGATAAATGA TTTGCTCCCG GAAAGTCGAT AAATTGCTCA TATATGCCCT 60  
 CTGGGGGAGA TAATATATCG GACTTTCCGC ATTTTCAGCA TTTCTACGGC GCATGATTAG 120  
 CTTCGTAGGC TTCTTAGGGT TAGTAAACGA TTGCAAAACA GGOCACAACC CCCAAGGAC 180  
 CCTGAAAAGA GAAGACTTGC CGCAGCCATT AGGAOCTATA ATCAATAGAT GGTACCATG 240  
 CTTCAACTCG AAGTTAAGTT CGGGGATAAG GACCTGATTA GCAGGTGTCA CTAGTGGAAC 300  
 ATGAACGAAT TGAATCTTAG AATCGTCGTA TTCTATAATG ACCTTTTTC CATCAGTCTT 360  
 CGAACTACTT CCAGCGTCTA GCTGTTCATT GAAATTGTGTT AACCGTAGGG CCTCTCCCTT 420  
 TAGCTGCTGG ATACTACGGC GCAGTTGAC ATAGCGGCCA ATAGATGGGG ACCCAGTTAG 480  
 CAGTAAACGT CTGTTGGTGA TAAATCAGC GGTGACATCC TCAGCCATAT TAGAACGAAA 540  
 GAAGACGGGG ATAGAGCATA ATATCAAGCC CAGCAGCGCC CCAGAAGTAC TTCACCACAA 600  
 AGCTAGTACA ATTCTGACAG TGCTCTTAAA TTTATCTCCC CCGGCTNAGA ATAAGTTACT 660  
 GGTTANAAAN AAAAACCCAA TCCCATATTC GGTNTTGTAC CNTGAATAAA CNNTNCCN 720  
 TTGCTTGACC NCACTTGAAT TTATGACCGA ATTACNCCA TTTTCCCTG ACATACCGTT 780  
 CAATTGNNNG TTTGACCTCC CACTNATTAT GATTNAAATC AACCCATCCN GTCTTCNGC 840  
 TTTCCCTGGN GATC 854

## (2) INFORMATION FOR SEQ ID NO:523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1367RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

10	GGATCGCCCC CGGTGCGCCC CGTGTGGCCC CGTCCCCGCC GCCAGGGCCT GCGCGCGCG	60
	CAGGCCACC GCGCTCCGC CGTGTGCCC TAGCGGATG TTCATTCCCT GTGTGCTC	120
	CTGACTGTCC ACTCGACTC TTGTATCCG ACCTTCTGC CAAGTGGCC CCAAACCTG	180
15	TTTTCTGTC TGTCAGAGT TTCGCTCTT GCTGGGCTA CTGCTACCT GCGTTTGGT	240
	ATGGAGGAGA AGTGTGTGTG TATCTGATTT GTTATCTGC TTCTCTCTC CTATAAGCTT	300
	TTTGTAAATGA AAAAAATTAT GAAAACGGGA AATCTGTGGA ATTTGGAAT GCTGCTGGG	360
20	CTGCGTGTGT CAACTTCCAG CGCGCGGTC TCGTCTACT GCTCTGTCT TGGCTAGCT	420
	TTGGTATTT TTTCTGCTG GTTTCGCTT TTTTCTCTG AACGCAAGG CGGCTGGT	480
	GCCTGAGGTG CCAGGTGGCT GCACAAGTGC GGGCGCCCG GAAOGAGCC GGTAGTTAC	540
25	CGGGCAACTC TGCGCGCAT CCCCTGCGGA GCCTTACGC AGGCTTATT TAATTGTTAC	600
	GTAAGTCACG TGGAGCTAGC ACGTCTTGG CAGCTCAGC GCACTCAGC TAGGTGTGA	660
	CTAATCGCG CGACTGGTG GGTAAANGA CCGGTACNC CGTTAAGTG GAAAGCNC	720
30	AATAAATTAC NTACCNNTA AACACACGG ANAAAAANAN NCCCGCNC NAAGNANTT	780
	TTGCCCTTGA AGCGCGTGC CCAAGCCCG GNCNCCCCA GAAN	824

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1367UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

45	GATCTTATGG GTGTTCTCT AGGCTGAAA GCGGATATG GACAGTCGAA ATGGGCAGCA	60
	GAATTTATTA TAAACGTGC AGGTAGCGT GGTTCAGCG GTTGTATATT GAGGCCAGC	120
50	TATGTACTG GTTCCCTTC TACAGGAGT TCTAACGCG ATGACTTTCT GCTCCGTTT	180
	CTACGGGGAT GTGTCAGTT AGGCAAAAT CCTGATATTG AAGGAACGT TAATATGTA	240
	CCAGTTGATT ATGTGGCAG GTTAGCAACA GCGCTTCTT TCTGTGATC AGGCAATACA	300
55	CATATGATGG TTGTAAATGT CAATGCGAAA CCAAGAATAT CATTCAGGA CTATCTACTA	360

EP 0 866 129 A2

GCACTGAAGG AATAAGGGTA CCAGGTAACA TCAGTTCTTT ATGACGAGTG GAGTAAGGCG 420  
 CTTGAATCGT CGAGTGATGA AGAAAATCCT TTGTATCCGC TATTGTACCT TGTCCTAGAT 480  
 5 GACTTGCTTA AAAACTGCGC AGTCCTGAAC TCGATACTAC TAATGCGAAA TTGTGTTTAG 540  
 AAGAAGATTT TGGCGGACG AATATTGAGC CAATTATCAT TACTTCGGTG TCATTAGAGT 600  
 TGTTGGTCCC CATATCTCAT TTTTGCATAA TTTAGCTCCC NANAANAACC ACCTAAAGTT 660  
 10 CCCAGCCCTT GGCNATATTC NCCTCTCCGA CGAACAAATT CCTTAATANC NCATACCNC 720  
 GCNCCGAACA TACANCAACC CNTAAATACC NCAAAATGTN GACAACATGA NTGTTTATTT 780  
 TTTTATATTT ACAACCTATT ATTAACCAAA TTINATCAC GATCCTCTNT GACGCCCTCT 840  
 15 CTGACAAATT 850

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1368RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GATCATCTGA AGTAATATAG AATCTGCATG GCGCAAAACC GTTGGGTTCC AATGTAGCGC 60  
 CGGTGTAGCG GCCATCGGTA AAGGTGAGCA ACGCAGGGCC ATCCCATGGT TCCATCAAAC 120  
 35 AGGGGGCCCA GTCAAACCAA GCCTTCAGGT TAGAATCCAT GTCTTGTGG TAGGCTTCTG 180  
 GAACCATCAA GCACATCGCT TCGGGTAATG ACAGAACACC ATTTATCACT AGTAATTCTA 240  
 GCACATTGTC CAGCGGGCA GAGTCGGATC CGCTTCTTC GATAATCGGA TAAAGCTTCT 300  
 40 CCAGTTGGTC TTGGAAAACG GCGGATGCCA TGACACCTTC CTTGGCAAGC ATCCAGTTTT 360  
 TGTGCTCTT TAGGGTATTA ATTTCAAGT TGTGTGCAAG CCAGCGCAGA GGCTGGGCAC 420  
 GGTCCTAAGA TGGGAATGTA TTGGTTGGAG AAAAGAGAGT GTACCAAGGC CAGGTGAGAC 480  
 45 TTGAAATGAG CATTTGTCAA GTCTGTGTAA TAATTATACA CCTGGCAGG TCAATTGACC 540  
 TTTGTACACA ATTGTCCGT TATTTAGGAG CACACAGTA ACAGTTCTGA TACCGATGGC 600  
 CGTTAAACCC NCTTTCTTT AAATNTAAA CTGGCATCCN GAAGTCTCTC GTNATTANCC 660  
 50 TGAATCTNCN CCCGATACTC CTGCCATAT TTCTTTNCN CAACAAGTT TTTGAAATGG 720  
 TTTCCCAAAA CCAAGGAACC NAAAGAAATN CTNIGGACNC CTCCAACCN AACCCNNATT 780  
 TAACAATCGG TACTNGCAA TTINTCAAG CNNAACCTGT NNNCT 825

(2) INFORMATION FOR SEQ ID NO:526:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 839 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1368UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

15	GATCGTGACG ACTTTGTGTT TTACTTCAAC CGTATTGCAA CGATCTTGGT TTGCGGGGCT	60
	TTGGATGACA TTGCTATOGT GGGGATGAA CTGCCATTGG TGACTGCATC CGGATATCAA	120
	CTGGAGAAGC CTGTTTCATGT GAATTTTGAC AAGATTACGG CTGIGAATAT TGTGCGCTCT	180
20	GGGACTGTT TCATGGCTTC CCTACGCAA ACAGTGCCAA ATATATCCAT CGGTAAATTG	240
	CTCAITCAGT CTGACTCTCA AACAGGTGAG CCGCAGTTAC ATTGCGAGTT CTTACCAGTG	300
	AACATTGGCG GCTCTTTTGA CCAGGTCTTA TTGATGGATG CACAAATAAT CTCAGGCGCA	360
25	GCAATTATCA TGCTATTCA AGTGCTAGTT GACCATGGTG TTGAACTATC AAAAATAAAG	420
	GTTATTGTCT ACTTAGCCAC TGAAATTGGA ATAAGAAGGA TAATAAATGC CTTTAACAAC	480
	AAAGTATCAT ATATGCGGGC GAAATTATAT CAGACGAAAG TATGACAGAT GGCCAATGTA	540
30	CTGGGCGAGG GTGAGATTCA TCGACTCAAG ATACTTTGGC TGTGACTGAT TCAGAGCTTT	600
	TGCTGCCCAN GCAGGAATTA ANAACTTTTG GTGCTATTGC ATGTTACAAT ATTAGCATTT	660
	ATCATCCATA CCATAGCTGC TTTACNATAG CAINTAATTT TACTATCTTT NAACCCACCC	720
35	AGACTATTTT TCCCCCNCTA CTTTACNAN ANTTTAANCA ACTGACCCCC CGNTATAATT	780
	GCCATCCAA CCCCCCCNC CTCNTAANAA ANACCNACTT GGAACGAGTG GGAACCNCC	839

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 851 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1369RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

55	GATGCGCTAC TTGTCTCAGG AACTTGTTAT CATGAGAGAT GATATGTGCA ACAGGTTTAA	60
	GCGCAATAGC ATTATTTTCC CAACAGTGA AGAGGAACAG AAACAGGAAT ACATGCTGTT	120

ACAGCAGGAG CTCAGGATG ATGAACGTAG TTGGATCTC TCATTAGTC AACTGATTAA 180  
 GTCCAGGGAC CAATTGCGTG CCACTGTCCA GGAGTCCAGG AAGATAGTCA AAACCATCCT 240  
 CGATCAGCAA CACCTTTCCG CCTTTACCTC GCAGGTGGCG CCTATAAGT GGGACTATGA 300  
 CTACACGTTC CACCTGTCC CAATACCCCT CACTATGATC ATTTGCGACC CAACTGCACC 360  
 GAAATATGAT GTTACTTACA ACGGCTGCAA GAGTATCAAT CCAGGCTCAT TTCTOCACAA 420  
 GCGGAGGGTC AACTATACTG AGTACACTOC TTGGTTACGG AAAGCAACAG AGGAAGAAAT 480  
 TGTCGTGTAG GACTTTAAAC TTACATATAA TGTCAAATAT AAAGGTTTCA GAAGTCGTCA 540  
 TGTTCGTAT GGATATTTCT TGAAGTTTTC CGTAATATC GTATGGCATA CAGTAGAGGG 600  
 GGTCAATNGG AACCAACCCG CGTGCTTCTT CAACTGGNC CCCANCAAT CCCAAAAAT 660  
 TGTGAAAAAC TTCCACCTAG ATTTTCTGGC CATGCGGAT GCGCNCCT CTTTGATTCC 720  
 TNCANCCCCA GANNAATCNC CCNCTTTCTT GTCATCCAT NOCNNTNGC CCAATTCNA 780  
 NCGTTAAANG CCCCCCNC TTTCACCTT TNGGATTTN NINGTTTCOG TCGCNCNC 840  
 CCGTNCAGAC C 851

## (2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 858 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1369UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GATCAAGACG AAGCAGAAGA AGACGGGTA CGCATGTACG TGCCACCTGG TGCGGTGGGA 60  
 GCGGGCCAAG GCGATCGCTC TGGAGGGCGA CAGCGGCTG GGGCTGGTAA TATGGGTGGA 120  
 CCGACGGTG GACACACGGG CGCGCACAT ACAGAGCATT CTGGGCGAGC AGCAGAGGAA 180  
 GTACGGGGCG ACGGTGCCAA CCATCCGTGT GCGGTGATT AATTGATCG AACATTGCGA 240  
 GTTGTTTTTC GGCAAAACGC TCGACCGGAA CACACGGGAC TACCTGGTAA ACGTGAGCGC 300  
 TGCAATGGTG GTGTGGGCG ATGTGGTGGG GACCTGCGG CCGACCTGA GGCCAATATA 360  
 TTGCAAAAC CTGAGGTACC TGATAGACTG GTTGGATACC CCTGAGAGGC CATGGCCGTT 420  
 GCGGACTTTC TATCCGTGA AGGTATACAC TGCAATGGAC GTGGAGCGCT CGCTCTGAC 480  
 CGAGGTGAAA TACTCCCCAG AATAATGACT CCCTGGAGG ATGCGTTTTC CCAACGGCAA 540  
 GAACTTACC ATAGTTCCNT GGACAAAGGA ACGGTGGAAA TGCGCGATC TCCCTACTAC 600  
 CCAATAAGC GTTTTGAAAA ATGACTACAT TNGAATCCN CCNACCAAAA TTGAACACTC 660

CCCGGAANNA NCATACNAAN CCAAAAGTTT GCTAAATATC TCTTTCCNIN GTACACTGAC 720  
 CCNACTIVTT GCAGGGAAAG GNCITGTTTT AACTTCCAC TONGACTINA TTTTACCCCT 780  
 CCNGCATOC ACCNAANCAA CACCTNITON AOCATAGAA CNVITTTCTT TTTAAAACAC 840  
 TNAGAAGCAT TTNAAAAT 858

## (2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 834 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1370RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAICTTGTAC AACTGAGCCT AGGICTTGTT GTTGAACGGT AACCTCCACA TTCATTATTG 60  
 GCTCCAATAT GGAGAACGCC GAAGTTGGTA AACTOGTCAG TGCTGATATG ATTAAAGGAC 120  
 GCACAGTCAG CAGAATGGAT GCAGCTGCTG CGCAGTCTAG CGGTAGCGGC CAGCGTTTAA 180  
 CATGAATCAC ACACGAGTGT AGAGGAAAGC CTGCGGTITT ACCACCTCTT TGCAAAGCCA 240  
 CTATGCAACA CGAGATGATA GAGTTCACGA ATGCTTCATA TTTCATGGA AATGGCCAAT 300  
 TGICTTCGTT AAAGCGTGGG TTGGATCTA TGACAAGATA GTTATTATOG CTTCCCAAGG 360  
 GGTACCATCC GTTACTGAAT AGTACTTTAT CTCTTCATT GTATTGCCGA ACTTCGAGTT 420  
 CGAACGAATA TCATCATCT GTTTCAGAST GCTTCCTCTC TGTAGCAGTA TTAATGGITT 480  
 CCTTGATGA AACTGCTACC TTGCTACTC TTACAGGCGC CTTAATTCA TTGAGCAGCC 540  
 GTCGCTGCT ATTTCCAGTG CATTCOOCC ATCCATTCA TCACTGCTG ACCAGTCTCC 600  
 TCATCCCTCA CNAATACCAC NAGGTTCC CACTCGTTAG CTGCNCCANG ATCACCENAT 660  
 ANOCTTTTNT TCCCAANIT CCGCGTCCN NCANCGNCT AAAANGGTGG NGGTANTCAT 720  
 GGTNTTTCC CANITGNANT TNGCTTTTG AAAACAATC CCTTTTAAAGN TNNAAGNCNA 780  
 AANGGGTCC CTCTAANIG TGTCCTCTG GGCNCNCCN CCAATNCCG AGAT 834

## (2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 840 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1370UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

5 GATCGCAGAG GAGGAGCCCA TTCGACGCT TGCATGGAAG GAGGACACCT TTGAGAATTT 60  
 TCTGCGGAG GTGACATCCG ATGAGGCGCG CGAGACGCTG GTTTCGGAGG AGGATGCGCG 120  
 CACCTACCTG GCCAAGCTTT TATGACGGCT GTCCGTGCTT TTAAATTGTT ACATACTGTA 180  
 CATAITGCTT TTAGTCGTAC CACATTTTGA TCAGCTCTTC GGAAACCGCG CTGGGGGTCA 240  
 10 GCACGCCAG GTCTGTGATC AGCGCGTAA TGTGCTCGTG CGAGGTGTAG TCGATGGAAG 300  
 GGCTTAGCAG CTGCTCTGAC TGTGCTGTC GCGAGAAGTC CAGCGGTCA CGCTCCATGG 360  
 GCAAGTGTG GGGGAAAGC GGAACATCC TTACAACTT GTGGGATTG CTTACACGT 420  
 15 AGAATGGCTT GGTGCGTTC TTGGCGAGGA CCGCTACCGT GTACGTCCCC ACGAGATTTA 480  
 TGATGCGCG GGAATGCGC ACGCGCTCG CGCAACCAG CACTGTGCGA TTTTGTGTAT 540  
 GATGGACCA CCGCGCTGTC CACGATCATC GTCACCGAT GCGCTTTGCT TGCAGCAGGT 600  
 20 CATACAGCTG CTGCGCTGTC CCGAAGCGC CGTCTCGT CACGANACAC CGGAAGCAAT 660  
 CACTCTCAC TGTACTCAC ACGAAANCG CCGCAAACC AGTTCCAAA AAGTCTCTC 720  
 TGTTAGATCC NCCATCTTT GTNCITTTTIN TNGACGCTG CCGAANCAA AAGTCCNIT 780  
 25 CCNCGTTC TGTGNACCC CCGTCCANA TMTTTTTTCC CCCCCNCCC NATTTCTCT 840

## (2) INFORMATION FOR SEQ ID NO:531:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 835 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1371RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

45 GATCGAGAAC AACTACGACA ACAGCCAGC AGACGGGCG GAAGCGCTCA AGCCGAGCTA 60  
 TATTTTTGAG TACCTTGCTT CGCTCATGTA CCAGCGCGC TCAAAGCTGA ACCCGCTCTG 120  
 GAAGGCCATC ATGTCGCGG GGTGCGAGGA CGGCCAGGC TTCTCTCGTT ATGTGGACCT 180  
 CAAGGGGCTC AAGTACTCG CCCAAGCTT GGCTACTGGC TTTGGGCGCC ATATGGCCAT 240  
 50 TCCTCTCATG CGTAAAGTC CAGATGCGA AAAAGACGTC GCGGGGCTG ACCTCTCAAT 300  
 TCGCGAGCG ACTATCCTGG AGTCCATGAA GGTGTATTTC TACCGGATG CCGTAGTTC 360  
 CCGTGGCTTC TCGCTGCGA TCATCGACAA TGATGCCGGT GTCAGCATGG AGCAACTGGA 420

AGTGGAAAAC ATGACCTGGG GGTTCGCCAA GGATATTTCG GGCTATGGCA CCCAGAATGT 480  
 CTGAGTACCG GCGGCAAGC GCGCACCTG TATACTATCT TGTCGGGGCT GCTCGCCAAC 540  
 CGCTGGCTAC TCACATACAT ATCAAGATGC ATAATCAATC TGCTCATGAA CGCACTCTG 600  
 TTTTGTGGAT ACTCTTCTCG CCGGTATCCT GAGTACGCTG GAGTGCAAAA AGAGCCACTT 660  
 TGAAACAACA CGAGTCGCAG CTAAGNGAN ATCCGANTAA NCAACNCACA CTTCAATTGA 720  
 CTTATGAAAT GCCCAAGGTT GATTGAACCTG ACGTCCTTGG AACNNITGGN CGTGGAAACG 780  
 CCTCTTCAN TTGAACCAAA GTCCACAANN AGGTATTTNT TTNAACCGTT CCGCC 835

(2) INFORMATION FOR SEQ ID NO:532:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 850 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1371UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GATCCATGT GGGTTTGGAG GTCACGCCAC GGAGTGGAC ATGTAAGTGA TGAGCTTGA 60  
 CCGGCAGCTC TTCATTCTGT CCGCACGCAA GAAGCTTGAG TTCCCGAAGT CTCGGGGGA 120  
 GAGTTGGGG TACCTTGGGT ATTACAGCG ATACAAATTC GAGGCGATGG CGCTCTGGA 180  
 CGTCCGGTG GCGGAACTC CCGCGAGGT TCTGGAGAGC CCGGCAAC AGGTGCTCG 240  
 CAACGGTCG CAATACAGGA CTGTGATGAG AACCGGCGTC GGGGAGCACA AGCTGGTGCT 300  
 CGAGCTGAG ATCGACGCA TCATTGACTT CCGCGAGCTT ACGGGGACA ACCTGAAGCA 360  
 CTACGTGGAG CTGAAGGTGT GTCAGAAGAA CCGGAAGTTC TCAGAGAAAC TTTTCTCTTC 420  
 TTGGCTGCAA TGCTTTCTGG TGGCATAAA CAGGGTTATT ATTGGATTCC GGGATGAGAA 480  
 ATTCGTCTG AAGAGCGTG AGGAGTTGN TACGTACAG ATCCACACC TGTTAAAGGG 540  
 CACGGAATAT TCCAATGTAT GTGTGAGCC AATAGAGTG TATGGTGCTC TTACGAAGTG 600  
 GCTATGTGAG CTCGGCGGG CCTGAANACA CTTCAACTGT ACAGCTCTCC NGCTCCNIG 660  
 GTGCTTACGT NIGCNCCCT GCCNACAAT ACTCCCNAN NGGACNATT NTCTGTTTG 720  
 TTCCCAATT GCGCGGGCC CNATATAANN CANATTCCN CNTINTTTC CTNTGNTTT 780  
 TAAAAACCN TINTTCCAC CNATTNCCC AGANNACANA GGNNTCCCC ACCANNCTN 840  
 CCANCCNCA 850

(2) INFORMATION FOR SEQ ID NO:533:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 835 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1372RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GATCTTAAAA	TAAGATAGAA	TGGTAATAAA	TATCATTCAG	GTACAATAGA	TGCTGGTGTT	60
ACTAAAGGAT	TACCTGGAAT	ATAATTATCA	GGATGTCCTA	AAGTATTAGG	TGAAAAGAAT	120
ACAAATAATG	AAAAGAAAAT	TATAAATACA	AATACTGTTA	CTAAATCTTT	AAAAATAAAA	180
TAACCATGCA	TIGGTAATCT	ATCTAAATTA	CCTGTAATAC	CTAATGGATT	TGATGAACCA	240
TGTACATGTA	ATAGCATTAA	ATGCATAATT	ACTATGCTG	CAATAATAAA	TGGTACTAAA	300
TAATGAAATA	GAAAGAATCT	TATAATAGTA	GGATTACTAA	CACTAAATGA	TCCTCATAAT	360
CATAGTACAA	TATCATTTCC	AATAAATGGA	ATAGCACTAA	ATAAATTAGT	AATAACAGTA	420
GCACCTCAAT	GTGACATTTG	TCATATACT	AAACAATAAC	CTAAGAAAGC	TGCTGCTATA	480
GTTAAAATAA	AGATAATAAC	ACCAACTGTT	CATACAATAA	CTCTAGGTGA	TTTATAAGAA	540
CCATAATATA	AACCTTTACC	AATATGAATA	TACATACAAA	TAAAGAAGAA	TGAAGCACCA	600
TTAAGATGCA	TATATCTAAT	TAATCAACCT	AGTTGTACTC	TCTCATAATA	TGTTCTACTG	660
ATGANAAAGC	TAATCCATAT	TANATGAATA	AGCAATNCTA	AAAAATACCN	GINAGAATTG	720
AATACTAACN	TAACTTATAA	AACCNAAATC	NIOCATATAA	TGAGAAGGTG	AGGGAATCAT	780
ACNACTATAA	CNATTTAATA	TATTGATTCT	ATTNCCATTT	TNTTININAAT	TTTTTC	835

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 854 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1372UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GATCTAGAAT	TATTAAAGTCA	ACTATTAACT	AATATCTATA	ATAATAATGG	TTTATCATT	60
AAATCATTA	AGATAATTAT	TAATAAATTA	CCATTTAATA	ATGATATATT	ATTATCAAAA	120
AATTATGTTA	ATAAAATAAA	TAAATATAAT	TTACTAATTA	ATAATAATTT	AAATAATAAT	180
AAAAAAGATT	TAATTAATTT	ATATACTTTA	GATAATAAAT	TATTAGATTT	AAGTATCTT	240

AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTAAA GGTAGACTA 300  
 TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT 360  
 5 TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT 420  
 ATTAATAAAC TTAATAATCT ATTTATTAAAT AAAAATGGTA TATTTAATAT TAAAATTAAA 480  
 TTAAATACTA TTTAATAAAT ATTCTAAAGT AATTTCCTAT TTATTTTATA ACATTTTAAA 540  
 10 ATGTTTTATG TTAAATAGAT AATAATCAAT TAAATAATAA AAATTAAGAT GCCACAAATA 600  
 ATTCCATTTT CTTTATGAAT CAATTAACCT ATGGTTTCTA TTTATTTTAC NATTTATCNC 660  
 ACTACTNATG TTTTTTTACC NVIGAATTIN ANAATATATA CTCNCNANTA NATATTNCA 720  
 15 AATTATAATA TTAATTAAAT TTAATTAATC TATTATGATC CTNNNTNTAA ANATATCAGA 780  
 ANAATTTAAT ATATATATNG AAATATNITT ATCCCCNGG NCACTTGAAN AAAANTATAG 840  
 20 TTTCTNCCCC ACAT 854

## (2) INFORMATION FOR SEQ ID NO:535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1373RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

35 GATCTTAATT TAAAATTTTA ATTAACATTT TATAATTTAG AAATATATAA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180  
 40 ATTTTATTTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300  
 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
 45 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
 TTTTATAATA TTTATTTTAA TTAGTCTAGT AATATCTAT TTAATAGTCT ACCCTTTAAT 480  
 TGGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT 540  
 50 AATAATTTAT TATCTAAAGT ATATAAATA ATTAATCTTT TTAATTATAA TTTAAATCAT 600  
 TATAATAAGT AAATATATTA TTATTTTATT AACATAATTT TTGATAATAA TATACCATTA 660  
 TTAATGNNN TTATAANAAT TATCTTNAAG GATTNNNTGG AAANCCTTNN TTTTAGAAAT 720  
 55 TNGGTAAANG TGNNCTAAAN NCCAATCCCN AATTATTAAA TTAATTTAAN AANAANNANC 780

CTTTTNTINA ATTAGTTTN AATTTAACC NCTCCCCINT TTAANAT

827

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1374RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GATCAATGAT AAATCGAAAT AACTGATAC TATTGTAGCC ATTTTCTGA ATTAGCACT	60
GGAAACACTT TTTAACCTGT TCGGAGTGG TCTCTGACTG ATTGGAGTTG AGCGTCTGC	120
CGGTAAGTGC CTCTGCTGTC GTCTTAGCTC CGACGTTTTC CACTGCCCCG CGCTGGGTGC	180
CCACAGCGGT CTCTTCTGA ACTGCGAGTG GCCCCAACAT GTGGTCCACT AGCGTTGGTG	240
CGCCGCCAAG TTGCTGGAAT AACGCACCA TCTTAAACCA GTTGAAGTGT GCAAAATCTC	300
CATACGCTTC GAATTGCCTG AGATAGGAGT TCGCTGCAT GCTCTGGCGA AGAGCAGCAT	360
CCGCATGCTG ATTGGTGCTC TCATCTAGAG CGTCGCTGGT AGCATCTCCA TCATTTTGA	420
TGCTGTGCTT CTGGGTATTG CTAGCATCGT CTGTTTCGG ATACATAGAG CCAGGTACAC	480
TCACGTGATT CAACTCAAGG TAGTCTTCCA GCAGAAACCG CTTGGCCCCG TTGACAAACT	540
CCTCAGGGCT CAAAAGCTTC CCGCATTTG TCAGTTTTCG ATTGCGTATA CTCAGCTTG	600
CAAGTCGCTG ACGCTCATCA CGGCATGCGA ATCTTGGGCA AAAGAGAATT GACCTCAGTT	660
CAATCGCCCG CCTTGCTTTA AAAACATATT AACTCTCCCN CGCNCNCAG GANAGAATNC	720
TCCCGTACTT CNANGNAGNC ANCTINIGCC NTCATCTCAA ATTGCGNACC TINGINANTG	780
GANCCNPTCC CGAGCCCTC TGCCCCCTA TTGANGVICG NCCCCGTTG A	831

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1374UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:



GATCTTAAAG GGGATATAA AAGCTGTACA AAAGAAGATG AACAAAGCTTC CAACGCTTCT 60  
 AAACCTTGAT ACTTCCGCCA TTGCCTTGGG AGATGAAGGC GAAACAAAAG AAAGTACCGA 120  
 5 ATTTAGGGCT ATTATTAAAG AGTTTGAAAC ACAAATAGT TTCCAGAAGA TTTTATATGG 180  
 GAATTAATAG ATAAGACTAG CATCTTTTGA AAACCTTTATA TAAACCAGGC AGATTAGCTA 240  
 CCTCTACAAT GTCTTCAGA AGTCTCGTCG ACGCTAGGAG TCGCCTCTTT ATCGTTGGGA 300  
 10 AAACCACTTG TTCCAGAACT GTCCCAATAT GCTCTGCCCT GGAAATATAA TAAGCGGAG 360  
 CATCGCCATC GATTGTGTG TOGTTTATAT CTACGTGCTC AATAATCTCA GGAATATAGA 420  
 ACAAGGCAAG TTGTGGAAGG ATTCTTCTA GGCCTCCTT TTCCGACGAC CAATCTACCT 480  
 15 TAGTTCCCAT TCTGTAGAGG AAAAATGGAA GTTTAGAAAG AGCGGGGACA TAATCCTTTA 540  
 AAAGTAAGGG TACACTCTTA ATGCGAACGT TGTICAAATC GGTCTGCTCT CCACATATTT 600  
 CAATCGASTA ATAGTTCTCT AGCATTTCTCT CATGTCCACA CTGTTGAGTT ATTCCAAATA 660  
 20 TCGAATGCGA CGCATTTATC ATCTTAGATA NGTTGGTAT ATCGCTAACT TCGCAATCT 720  
 CAACCNANC CTNGATATNA TTTCCCGAAN TTTGNNAATN NNNATCCCAT TGANAAAATT 780  
 CCTTCCTTAG GACCTATCAC CCAAATANIT AACCGGNTT NANGATCCT GNTTGGTCAC 840  
 25 AACCNNGGT CTNNN 856

## (2) INFORMATION FOR SEQ ID NO:538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1375RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GATCTTAATT TAAATTTTA ATTAACATT TATAATTAG AAATATATAA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAATA 120  
 45 AATAGAAAAC CATAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180  
 ATTTTATTA TTAAATGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTIAA TTTTAAATTT 300  
 50 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATIAA GTGATATATA 360  
 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
 TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480  
 55 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540

TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTATTTAT TATTTAAATT 600  
 ATTATTAAATT AGTAAATTAT ATTTATTTAT TTTATAACAT AATTTTTTGA TAATAATATA 660  
 5 TCATTATTAA ATGGTAATTT ATTAATAAATT ATCTTTATGA TTTATGACAA CCATATATTA 720  
 TAGANATTGT TAATAGTTGA CTAATATCCN ATCCAACCTN TATTNATTIA NAGATCATAN 780  
 10 ACCTTTTATA CAATTATTTT NATATAACAT NTACCTNATT ANAATATN 828

## (2) INFORMATION FOR SEQ ID NO:539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1376RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GATCTATTTT GCCGACTTCC CTATCTACA TTATCTATC AACTAGAGGC TGTCACCTT 60  
 GGAGACCTGC TGCGGTTATC AGTACGACCT GGCATGAAA CTATTCCTTC CTGTGGATT 120  
 TCAAGGGCGC TGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG 180  
 30 ACCCATCTC CGGATAAACC AATTCGGGG TGATAAGCTG TTAAGAAGAA AAGATAACTC 240  
 CTOCCAGGOC TCAAGCCGAC GTCTCCACAC TCAGTTACGT TGCCGTGAAG AATCCATATC 300  
 CAGGTTCCCG AATATTAACC GGATTCCCTT TCGATGGTGG OCTGGAAAAT CAGGCCTTTG 360  
 35 AAACGGAGCT TCCCATCTC TTAGGATCGA CTAAOCCACG TCCAACGTCT GTTGACGTGG 420  
 AACCTTTCC CACTTCAGTC TTCAAAGTTC TCATTTGAAT ATTTGCTACT ACCACCAAGA 480  
 TCTGCACTAG AGGCGGTTG ACCAGCTTT ACAGCCTAGG CTTGCTCACT GACTCCACGC 540  
 40 CTGCCTACTC GTCAGGGCGT CATATTCTGC OCTGACGGTG GAGTATAGGT AACACGCTTG 600  
 AGGCCATCC ATTTTCAGGG CTAGTTCAIT CGGCCGGTGA GTTGTACAC ACTCCTTAAC 660  
 45 GGATTCCGAC TTCCATGGCA CGTCCCG 688

## (2) INFORMATION FOR SEQ ID NO:540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1376UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

5	GATCCAAGGA ACCTTTCCTT CTGGCTAACC TAGGGTACTT GTACTCTAGG CGAACCANGA	60
	CTTTTACTTT GAAAAAATTA GAGTGTCAA AGCAGGGCA AGCTOGAATA TATTAGCATG	120
	GAATAATGGA ATAGGACGTT TGGTTCCTATT TTGTTGGTTT CTAGGACCAT CGTAATGATT	180
	AATAGGGAAG GTGGGGGCA TCAGTATCA ATTGTCAGAG GTGAAATTCT TGGATTATT	240
10	GAAGACTAAC TACTGCGAAA GCATTGCGA AGGACGTTT CATTAAATCA GAAACGAAAGT	300
	TAGGGGATCG AAGATGATCA GATACCGTC TAGTCTTAAC CATAAACTAT GCGACTAGG	360
	GATCGGGTGG TGTTTTCTTA TGACCCACTC GGCACCTTAC GAGAAATCAA AGTCTTTGGG	420
15	TTCTGGGGGG AGTATGGTCG CAAGGCTGAA ACTTAAAGGA ATTGACGGAA GGGCACCACC	480
	AGGAGTGGAG CCTGCGGCTT AATTGACTC AACACGGGA AACTCACCAG GTCCAGACAC	540
	AATAAGGATT GACAGATTGA GAGCTCTTTC TTGATTTTGT GGGTGGTGGT GCATGGCGGT	600
20	TCCTAGTTGG TGGAGTGATT GTCTGCTTAA TTGCGATAAC GAACGAGACC TTAATACTA	660
	AATATGCTGC TGCATTTGCT GTTGGCCCTC TTAAAGGACT ATCCGTTTCA ACCCANTGAN	720
25	TTTGAGCATA CAGTCTGTGA TGCCCTAACT TCTGGCG	757

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 821 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1378RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

40	GATCCTTATA AAATGGGCAA TAGACGTGTT ATAAATATAAT ATACAAAATT ATAAATAAAT	60
	ATTAAATAAA ATATAAAATT AATAATTAAA GTATTATAAT AATTAAATAA ATTATTTATT	120
	AATAAGTATG GATTTTTAAC TGAAATTGT TAAATGAAA TAAGAATTGC TAGTAATCTA	180
45	TTAATAAGAA AGTAATGGTG AATACTCTAA CTGTTTGGCA CTAATCCTC ATCAGCGGTT	240
	GAAACATATA ATTAAATAAA GAATATTAAAT TAATTTATTA ATTATTAAAT ATTATTAAATA	300
	TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAAATGC AAGTTGAAAT	360
50	ACAGTTACTG TAGGGGAACC TGCAGTGGGC TTATAAATAT CTTTAATATT CCATTTTAT	420
	AAAATAAATA TATTTTTTAA TATATTTTAT AATAACTATA ATTAAATAGT TAAAATTTAA	480
	ATTATAATTT AATAATTTAA TAACTTATTA ATTAGAGAGT TAGGGTACAT OCCCCCTAAT	540
55	GCTATGCATT ATGGTTGGTA CACTCTAATT AATAACTAT AATAAATAAA TACTAATATT	600

TTATACCAIN AATTATAATT ATTTTAAANA NATTTAATAT TATTAATGAA ATATATAATA 660  
 AGTATININA TTTNATAATA ATAAAAATGA NAAAAAGACC CCTAATAATA ATTTGCATTT 720  
 5 ANANTTACCC TTACACCTCC CNITAAATTT TTACCCINAT ANCCNINITA ATTAAGGANG 780  
 GNGNCCCCN TGCTCCCCNN TGCCCCCCC ATTNANNTTT A 821

## (2) INFORMATION FOR SEQ ID NO:542:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 852 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1378UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GATCCTTGCG TACTAAGAGT TAGACTTTAA TTAATAATAT TATTTGTAGA AGATAGAAAC 60  
 25 CATACTGACT CACGTCGTAT TTAACCCAAC TCACGTAACC TTTTAATTGA CGAACAGTCA 120  
 AACCTACTTT AGCTGTTTACA ACCAAGAGGA TAGGTTGAGT CGACATCGAG GTGGCAACA 180  
 TAACTTACAA TAGCTACTCT ATCGTTATAT TACCTGTTT AATTTTGTGA TCATAATAAC 240  
 30 ATTTAATTAT TATTTCAATA ATTCTCATTA TTGTTTCAGAC TATTTTCATTA TGTATTATTT 300  
 ATTAATTAAT ACATATTGGG CTTTCGTGGA TATAATTATT GTTAATCCTA CTCATATATC 360  
 TAGTCGTGTA ACGTTCCTAT AACTTTATAA AAAGGATTGT TATAAGCTTC GCTGCAGATT 420  
 35 GTCCCTTATT ATTATAAAAT AATATTAGGA GTTCTTTGCA ATTAACCCAA TTTACTCAAT 480  
 ATATTTAAAT ATTGATAATT AAATTTTACA ATTTAATGGG ACTATTAAAT AACCTAGCG 540  
 TAACTTTTAT TCGTTATCAA ATACCATTAC AATATGTATA TTTGTTCAT TATGCCAAC 600  
 40 TTACGTTATT GTTCTACTTG TAGGTATTAC AATTATAGCA CAGTTATACC ATTATATTTA 660  
 TTTATATATA TOCCATATAA GTTTTATTA ACATATAAAC TGTCATTAT TTATCINTTT 720  
 TATATAAAAT ATNATTATAT TAATNATTTA TTAANATTTA NACCCNATA TTAAATATAA 780  
 45 TCNTTTTTAA TAATAAATTA TTAAGGACTN TCCAACCTTT TTGAAAGACC CCCCCTNCC 840  
 ATTAAATGTC NT 852

## (2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 845 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1379RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GATCCAATTC TCTGGTAGT TTCCTTCCAT ATAGAGACTG ATCAACTAGC CACATTCCCA 60  
 CAACAAAAGA GTTCTATCT AACGTGCCAT CGGTCCTTGT ATCTACCATG TCGTAGATTT 120  
 GAGCCAAAGT ATCTTGAGGT AGATTGCTTC GAGACCAGAT ATCTGTAACA ACTAAGTICA 180  
 ACATTAGACC ATCCTCTGGC ACCTCTCTTG TCTCATCGTA GTTACCGTTA TTCCACCATG 240  
 GGAGCAAGTC AAGATAAGTG TCTCTATTGC TGACCCACAT TCCCTOGTAA CGCTTTCTTT 300  
 CCCTTTTCAGT TACGTACCCA ACATCAAGGT GCGACTTCCA AGGTTTGCTCT TCGTTGAAGG 360  
 AATTACGGTA TCGAAGATTT TGAAGTATCT TCTCGCGCTT TTTGCGGAT CTTCTTCTTG 420  
 GACTTCGACT ACGGGAGTTG CGGTGCTTC CGTAATCCTC TTCAGAGTCT TCGCTGTCAT 480  
 CGCTTAGTTG ATGGGCTCT GAGCTGGAAC TGTCATTAG TATACCCCGC ATAGTGGTTT 540  
 TTAGCCGCAC ATGCAATTTA CTCTGCACGA GAGCGTTATC GTTCTGGTA TATATATGTG 600  
 ACGTTGGGG GTGATTCCTG CTGGGGCCTA GCGCAGTTG CCGATGGGCG TTGAAAGCTT 660  
 CATCCACTTG GANIGCTGCG TTGANANITT GGTATTAAATN CAGGAANATT CCTCCGTAGT 720  
 CCAGTTCATA GGAATTTGTT CATGTCAATT ACAANCCTTC NACGGGAATC TTTTGGGACT 780  
 CNIGTCAAGT CGANGNATNT GTCTCCGTA CANCTCCCGA TNCNCCAAAN TNNCCNCATT 840  
 CNCNN 845

(2) INFORMATION FOR SEQ ID NO:544:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 855 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1379UP

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GATCCGGAAG TTAACACTGC CTGGGATTCA TAACTTGGCA ACAGCGTATG TCGGTGTGAA 60  
 CATAGTCGAT GGAGCACATG AATTGGGGTA TCAATACTGA TTTTATAATG CTTTCTGGAG 120  
 CCATTGACCT TCGGTGACAA CCTCAAACAT ATTTGGAGCC AATGGTTGGA CTTTATGTGG 180  
 GGAGATGCAG TATTGGATG TATGCACTGT TGGTAGTTCA ATCTTTGGG GACAAAAACC 240  
 TGGTAAGTGA ATTGTCTCTT TGAAGCGCCA CCGCTCCAT CATCCAGCAG GTTTCCTAAG 300

55

TTTTTAGCAC GCGAAAGGCT CGCGCCTTCG TGTATACCCT TAAGTGGTGG TGCTTTGTGC 360  
 TOGACCAGCA AGAAGCTTCTT TGTAGGCTCC ACTCGGTGTA CTTTCGGACC TTTACAATAA 420  
 5 TACTCTAAAG TTTCGGTCAG GAATATTCTA ACCCTGTGGA GCACGAGATT AGCCCGTGGG 480  
 TTTAGCGAGA GCGATATTGG TAGAAATGCG TCCAAAATA TATCTTTTGA TGCAATTACG 540  
 ATTTCATAAC TCAATTCTTT TTCCAGTCA CGTGATATGA CTATCGGTTC GGTATCTTCT 600  
 10 ACAGAGTTTC GAGATAGTGT GCGGATAAGT TAATCGGAAC ACGACGTGGA CATTGGACTT 660  
 AAGGTCCTAT GCGCTCAATG TCACTCAAGC AGGTATTTAC GTTCCCNATG TTAAGTAGAAT 720  
 CTCTTGCTC GACNCCGGAN TNGANCCCCA AGAAAAATA TCCCCGCCNG AAAANAATTT 780  
 15 CCTGGNGTG ACGTGTGNAT NACCCNACGA AAACNCTCTC CTTCGAANGT NOCTTATATT 840  
 CNNTNAAANA ATANA 855

## (2) INFORMATION FOR SEQ ID NO:545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1380RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GATCGCATCG ACCTCGCCAA AGTAAGGCAG GCTCTGAGC GAGATCCAGT CGACAAGGTG 60  
 35 AGGAAGCGTG GTGTCTTAC CCTCGAACAC AATTGGCTCC TTCTGCCCCG GCAAGTGGAC 120  
 CGCCAAGGTC GGCTTCTTAG TTGGGTACTG CACAAATACA AAGTCGTTC GGAGCAGGTT 180  
 GGCCAGTTTC TAAAGGACT CGTTCAGGCC CTTCACGCCA CCGTCAACCA CCACTGGGGT 240  
 40 CTTCGACTCC GCAAGCAGGT CCTCCAGGTC CTGGGGGGCC TCCTTGCCCT CCAGCACCGT 300  
 CACGGCCGCG TCGGCCTGGC GCAGCATGTA CGCCACAATT TCCTGGGCT TGGTGGGCC 360  
 CGTGTATGCG ATGCCCCCTCT CTGACGCCCC ACTGTGGAAC ACCTTCAGCG TGGGTACCC 420  
 GCGCAGGTC TGGCCCGGCG ATAGATCCAG CTCTGCTCG CAGTCCACT GCGCCAGCTT 480  
 45 GATGCCCTTC TCGCCAGCT CCCCAGCCGC CTTCAGTAC TCCGTGCCA GGTGCTTACA 540  
 GTGGCCACAC CATGGCGCAT AAAACTCCGC CATCACAAGC GGGTCTCTCT CTAAGAACTT 600  
 50 CCGAAGGTC TTCCGGTCA ACTTGACACT GCAGAGTCT CTGGTGCACT GGCATCTTGG 660  
 GCTGTGCAA CTGTGCCAGC AACCGCGAT GGACAACACA AACCGCTTGT CCAAAACNT 720  
 TCTGCTGGG TCTATCTTAC CCGTGGTTTN GTGACTCTG TGGGATCAA ANCCGNTN 780  
 55 CNATTTTTGT TTTACTGA TCCAGAATTC ACCCTTCTC AAAACNNTN CCNGAAAAGA 840

NCGNGTN

847

## (2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 860 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1380UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GATCTOGCCT GTGTGAGTG ACGCCGAGTT GCGCGAATTG TAGCAGTGCG AGAGGAAAGT	60
GCGACGGTA TCGTTTGCCA GCGGACAAAC GCGCAGCTG CCCAACCGA CCGCGTCCAA	120
CTGCTCTGG TACATCTTGA CCACTGCTT GCGCATGCA TCCTTGATGT TGAAGCCCTT	180
CGTCAGGG ATCAAAGTGC CGCTCGATAG CGATGTCTGC GGCACGGAT ACGAGAAAGT	240
AAACCCGAGC TTCAGTTGGC CGCCCTCGCT CTGGAGCACT TCAGAGTGGT AGCGCTTGAC	300
AAACGCCATT GTGCGCTTGG CGATGAAGCC GAACAACCTG TCTGATGTA CGTGTGTGTC	360
AAGGAGCTCC TCGGGGATCT TCGACTTCAA CTGCTCCAGC TTGAACGTGT GATCAACGTT	420
GAGACGCACC GAGCACACC GGAATTTGCT GCGGCAAGG TCGCGCGCA AGAACGTGCC	480
CTCTCAGTG CCATTTGGGC TGCCATCAC GTACGAGGG ATCATGGAA GCCACGGTA	540
CTCCCGTCC TCTCTCGTT CTGAGACCT GTTCATACA TTGATGAAG TACGGGTCA	600
ACTCGCGGAG TTTGTCTCC GTCACTCGA AATCTTACA TATTTGTCC ACTGCTCTC	660
GACTTTCCG CGTTGCGCTT GTGCAATCT TCNAAAANAT CCTGGTACTG TAAANATTAG	720
ACTTCGANAC GTTGGTCGAG TCTTTCNNGC TTNCCTACTC NCNGCCNTG TCNTANTATT	780
TTGANGGCGN TCCAATAAAA AACCTTTTNG GGGGTGCAA GNGAAGTCC ACCCTCTTTT	840
GTTCGCCNT CCNNAATGA	860

## (2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 835 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1381RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT 60  
 ATTATATTAA TTCGCCATTG GAGCAATTIG AGATTAGAGA TTTATTAGGT TTAACATCAC 120  
 CAATAATAGA TTTTAGTTTT ATTAATATTA CTAATTTTGG TTTATATCTT ATAATTCTTT 180  
 TATTAGTAAT TTTACTAATG AATTAAATAA CTAATAATTA TAATAAATTA GTAGGTCTA 240  
 ATTGATATTT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA 300  
 TTGGTGGTAA AGTATGAGGT TATTATTTTC CATTAGTTTA TACATTTTTT ATTCTTATTT 360  
 TTACTATAAA TTTAATTAGT ATAATTCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT 420  
 TTGTAGTATC AATAAGTATA ATTATTTGAT TAGGCTAAC TATTATTGGT TTTTATACTC 480  
 ATGGTTTAAA ATTCTTTGGT TTATTTTTAC CACTAGGTAC ACCATTAATT TTAGTCACCA 540  
 TTATTAGTAT CAATTGAATT ATTATCATAT TTTGCTAGAC TTATTCATT AGGTTTAAAG 600  
 TTATCAGCTA ATATTATAGC TGGTCATTTA TTAATTGITA TTTTAGGTGG TTTATTACTT 660  
 AATCTAAANC CACAAATATT TAACNITTIN TTAAGTTCNN CCNATGAATG CTATTINAGT 720  
 ATGINTGTIA GAATTINIAT CTTATACCNG CTTANINIGA AGININAATA CNOCNTATNA 780  
 AACTATTTAT TCTTATTAA ATTAACANTT NAACNCCNA TTANITNTIA TNCTT 835

## (2) INFORMATION FOR SEQ ID NO:548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1381UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GATCATTTGIC CAATATTCOC CACTGCTGTA TCATATAGAT ATTGATTATA ATTTCTAAAT 60  
 CAACGTGATT GTTCTAAGCT TAATTAACAA TTATGAATTT TTGGCTAGTT ATTATTTTTT 120  
 AATTAACTAA TACCTAAATC ATTATAAGCT TGACTTAAAA CAAATAATTA TTACATTATT 180  
 CTTTATTTAT TATTTAATAT TTAGTTAAAT TTTAAGTTCA TTATTCCTAA TTTTACTCA 240  
 CGAGTACACC ACTTATTAAT ACTATTAATT AATAATATTA ACGTTTGATT CGCATGTGTA 300  
 ATGTCCTTAG TTAGCGCTTA ATCTGAACCA ACATCATGTT CTCATTATTA TTAAGTATTT 360  
 TTAATTATTT TAAATAATTA TTTAATACGA AAGTTATAGG ATTGGAACCT ATGAAATCAT 420  
 AAAGATTTAT AATAGCTCAA ATATTACACT TTAAACCACT CAGTCAAACCT TTCTTAATAT 480  
 ATATACTTCA TATATGGTTT GATAATTTAC TTATAATATA TAGTATATAA TTTAATGATA 540  
 AACTCTTATC ATTTAGGTGC GTAGGGTTCA CCCCCCTATT GCTAGTCAGC AATATGATGT 600



ACCTCCTAAA TGATAAAGAA GTATAATATA TAAATATTAA TATTAAAGTA TTTAATGAAT 660  
ATTATTATTA TTTATTTAAT TATTATTTTT ATTTAGTAAA TAAATAAATA TTTCCACTTA 720  
5 TTGAAATATA GGTTCCTINGA TTAGAAATAA GCNATNATAA TGINOCATTG ACTATTAAAT 780  
ANTGIGCTCN CNGACTTCC CTATTNCCN NNGANAANTC NGAANATCAG AANANAGATT 840  
10 CCNANATNTT TAATNNNCCC CCA 863

## (2) INFORMATION FOR SEQ ID NO:549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1382RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

25 GATCTCACAC GTGACTAAAA TCACTAACAC CACGTGACTT CGTGACCGTG GCATOGTCCC 60  
ATTCTGTGCG TOGCTAGCAT TCTGCCCCGG CATCTGTGTC AGGCCACTGC GCAGCTGACC 120  
ACGCCGTACC ACGGCAGGCT TCACGACAGA CGGCAAGCTC AATOGCTATC TACGGTTTCA 180  
30 GGTGGAATTT CTTACGGGCA TCCGATTAAT TGCTTTTTTG GCTTCCTTTT GCCCCCTTTT 240  
TTCCAGIGGG TTGCTTCCTG AAAACAGGGA GCTAGCTTCC CGTAGTACGT AACAGTCGTA 300  
GAGGGTATAG CATCGCTGAG CTCGAGACCC GGTGATGCAA TGTCACAAAC CCTCGTCTGC 360  
35 GCAAAACGGG CACGAAGATT GAAAGTATCC AGGAGTGCAG CCCAGGGTCA TCGAGACAG 420  
AATGGGOCAG AAAAAGCGAA AAAATGGACG ACGCTTTTAT ATATATATGT AGCGAGGCOG 480  
GGCGTTCCCA GAACGGGACC CGACACAAC TGTGTAGAA TTTCTATCTG CAAGGAATCA 540  
40 AATACAAAAT GGAATCTAGA TTGGGATGGC TAACTOGTTT GAACTACGAC ACTGGTTCTG 600  
CATTGAGAAG AACTCCATCA TCCGACAAT GGTCTAAGA CCAACCACCC AGANACTTNG 660  
TGGANCTTAA AAAGGNGGGT TGAACATCCT GAGAATGAAC TTCTGGCNOG GTCTTACAAT 720  
45 TNCCACCATC GGTGNTCNAA NACCCNNAAT TCGAGATTNT NCCNGTTAAC NITGGCCTTG 780  
CTTTGAANCC AAGTNCCTGA ATNAAATGIN CCTNTCGAAA NITANTACCN TCCCCTACCC 840  
50 AAANC 845

## (2) INFORMATION FOR SEQ ID NO:550:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1382UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

25	GATCTATAAC AGGTGCCAAG TTGGCAGATT TGTTTCAGGG GCTCGACGAT GTAGAGTCCA	60
	GTAGAATGCT CTGTAAACCC AGAGCATACT TTGCGOGAAA GTCTTTATCT GTTGAAATCA	120
30	ACTGGGGTAT CCGCTTTGAT GCTGTCCCGG AGGTTCATGC CTTTCTTGAT CGCCTTGTC	180
	AGTATCTGGT TGGTAAGCTC AATGAGCTCC GCATGACCAC GTCCCATATT GTTTTGAAAA	240
35	TAGCAACGAG AAGCAGGGAT GCCCCATCG AACCCCCCAA ATACTTGGGC ATGGGTGACT	300
	GTGACAGTTA TAGTAAATCG TGCAGATTAG GTCTTGCTAC CAATATTCTT GGGTTTATAT	360
40	CTGCAGAGAT AAAGGCAGCT TTTCGCATGC TATGCTGCCC CGCAAAGGAA CTGGGTGGTA	420
	TAGCCGTTCA GTTTCTTAAA CTGAAGGAGG CATCCATTTT TCAAATGCCC CGTCAGCTCA	480
45	GGTTTCATT TGGTACAATC AGACCTTAA CAACTCCAAA GAATCGTATC ACAGCGTCGG	540
	TTACAGAATT GCCAAGTGTG GTTTATAAAA GGGCCACTCC TATTAAGGAT TTTTTTGACC	600
50	GGCACAAGAG GACTCAGATT CACCATCACC TGATTCACCT ACATGATGTC TCGGTCAGCC	660
	TTGTGCGAGT CATTCCTGGT GGATTACCTA CGATCTTGCG GAAAAATCCN AAAAAACATT	720
55	GACNATCINA AACCAGACTT CTTTNTGTCN ATTCCCAAAA AAATTGGGNN GNGCCGNGGT	780

TNNATCCCAN CATGCCCTTA AAATTTAGAT CCTTGACCTT ACTCCNANIT GNTNCCCNAA 840

5 AAAAAAATA TCAATGTNTN CT 862

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1384RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GATCTGCATC GCGTCCACCG TGGACTGGGC GGTGGTGGGC GGTACCGAA AACTCGGGG 60

ACTCGGTGAT GGTGCCGGCA AGCGTCTCGT AGCGGATGG CACGACCTTC GCAAAGTAGG 120

AAAAGAAGTG GCTATGGCCG TTCGGAACCT CCATGGGCGG GCCATTGAGC GGCCCGGGGT 180

TGCCGGCAAT TTGGGGCCCA AAGGAGAGAC TATGGATCAC GTGGTTGAAG GAGAGATGG 240

GGTGTTCCTT GTAGAAGGAA TCGTCGTGGG CGTGGCCCTT GCCAACGTGC GCAGAGCCCG 300

GGCGAAGTG AATGTTCCCG TGAACGCGGT TGAGCTGCC GGTGCCAGCG ACGCGGCATC 360

CCTCGTTGAT CTGCTCCTGC AGGCGCTCCG TGTAGCCCTC GCGCTTGAC TGCTCAAAGC 420

CTTTGCCATC GAAAGTGGCC CAGTTCATCT CTGGTACGC CGCGCGCAC TCCCGCACG 480

TCTGACAGCA CACGCGCTCG CTGCGCGGCA GGTTCCTGTT CTGGTCTGG TCGGTGGC 540

CATACACGGC CACAGTAGTC TTGGTGTCT GTAGACGGCA ACGTCTCGC ACTCGGAATT 600

CCTCCTTCCC CACGTCCGTC CNTGTTTGT CACCNITTTT CCTTGATCT CCTCCACNA 660

ATTCACTGTG CTCCTGTTC TCINTANNIC CATTTCATAC TCCCCCGGAT CTTGCAAAC 720  
 5 TATATCNAAC CCCACTCCNC TCTGCTGCCG TCCTTCAANC ACTGNGCGTC TCCCTCCCCA 780  
 NTCCCTCCT ANCAAANACN CGTTCACAAC ACCNCTATN CCT 823

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1384UP

(>i) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GATCACTTIG TTGTGTCTG CACGATAAAT GGCTCGGTA CAGAGTTTTA CGAGTGTTC 60  
 TTGGCTGAGA COGACAGGT CAATCTCAGA GTTTTTACTA TTCATTAGTG AGTAGATTGA 120  
 35 CGCGTAGTGA TTATCAAAGG CCACCGGGGA ATTGTTAAAG AAGTTGGAAA CAGATGATTT 180  
 CGACATGGTA TAGTTCGTGA GCTTAATTAG AACGGGCAGG TCTGAGCTCT CCGGACGGG 240  
 40 AGTACTGTTT TGAATGGGTG GCACAGCCAG TGGCGGTGG GCGTGACCA TGCCAAGCTG 300  
 TGGCCCCCT GTGAGGCCG CTGGTACTGG AGCGGCACG CTTATCGGCG GGTCTGCTGG 360  
 45 TGTOGGGAT TTGGAATAC GGTGTGTGCA CGCTGCTAGG TATTTTTCG CTTCCGCTGG 420  
 GCTCATCTTC TTCTCGGTCA AAGCAGGGTC GAAGTTCAGA ATACCCCTAC TCTTGTCTC 480  
 50 CTCTGCAATC ATGTGCAACG TTTGCGCGAT CTTCCCCAGC TTGTGGTGAT AGGGCGCCAG 540  
 GTGCCCCGAG TTCCGGATCA GCTGCGCTTT CATGCCAAAG TTAACGAAAT TCTTGTAACA 600  
 55

5 GGGTTCGACG CAGCGCTTCC CAAGCGGTAC CGCAGCGCAA ATCGTTTTCC TGCTGGTACT 660  
 10 TGTGTGTCNAT ATTGAATCNA ACAGGCCCCC CAATAANCCT GTCCACGGG CCCCCTTCCCT 720  
 15 GANNAAACCA GCATCACACC GCNAAAAAAC GGGCCCCACN CGTCGTGATC NAACTTACCC 780  
 20 CTCAGACTG NNTATCCANN GCATNCNCT TTTTINTCCC GTGTNCTGA AANTNCNAAG 840  
 25 CCCCCACCT 849

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1385RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

35 GATGACCTC GTTCATCATGG GCAAGCAGGC CACCGACAGC GACAACAACA ACACCGGGCA 60  
 40 GATGCTGGCG GGCTTTCTCA ACTGGCCGCA GGCCACCAAC GCGCGCGGTG TTGAGCTGGA 120  
 45 CGGACTGGC ACGGTGCGA CGTCACCGG CGAGGTGAG GCGGCGAGG AGGTGTCAG 180  
 50 TGCGGCGCTG CCACTGCTGG TCACCACGGA CCTGCGGCTC AACACGCGC GCTACGTCAC 240  
 55 GCTGCCCAAC AAGATGAAGG CGAAGAAGAA GCGATGGCG AAGCTCAACC TCGCGCGTT 300  
 60 CCGCGCGGTC GACTCCGCG CCGGCTCAA TCTGCTGCG TTGAGGAGC CCGCGCGCG 360  
 65 CGCGCGGCG ACGTGTGCG CGTCGTGGA CGAGCTGCTC GCCAACTCA GGGAGGCCAA 420  
 70 GGCGTTTAA CACCTATATA AACTAACAGC CCTATTTCC TCGCGGAGC CAGGTCCCG 480

CTCTCCAGCA GCCCCGGGG CTGCTTGCGC AGGTACGTCT GCTCGTACCA CGCTCCAC 540  
 5 TCCCCGCGCT GCGCCGGGC CTGCTGTACG CTCTTCAGC ACGCGCGGC ACTCCTGTC 600  
 CCACGCGCG AGGTTGCTCC CCGGTGCT GCGCCGGGC CTATCTTGA ACNCGCCAG 660  
 10 CTGCGAGTTT CCGCCGCC CCGGCATGT NCCCCNCAA CINCITTTTA CACNGGATNT 720  
 TNCCNITTG TTNCCNINN NTTCNCCC GTGGAANTGN TTTGCCNTTG CTGANAAIG 780  
 15 CTANCAACC CCCCATTG ATNGGCCCC CCAAAATNA ACTTCCACT TTGCGAGAC 840  
 CCGCCCTGT NCCCTTNTT AA 862

20 (2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 851 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1385UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

40 GATCCTGAG GCTTGTTC TGGCTTGA GCGCGGCC GAGGCGAGC TCGCGCGC 60  
 GCGCGGACC TACGCGCG CCGGCTGC CGAGTCAAC GCGCGCTG AGGACTACTC 120  
 45 TGGTGTCTG TGGCGCGG CTGGGTGCC CTGGTGGC ATGTGTTCG ACGGCAGGT 180  
 TGGGAGTGC GTGCCCCCT GCGCATCA GAGGAGCAC GAGCTGCGG AGCGCTGGG 240  
 50 GCGCGCATG ACCGACGCG AGGTGCAGC ATTTCTGGAG CGCTACCTGG TGTGCTACGA 300  
 CGTCTACTAT GCGGTCTGG TCGCGAGGG GCTCGGAC CTGCACGCG TGA CTGTGG 360  
 55

GCTGGAAGGA GACCGAAAAG TTACGTATGT TAGCCAGAAG AATATGTAAT GCGAGTCTA 420  
 5 TAGTTCTCTGG TCCGAGATGT CCTCCCAGGG GATGAGATAG CCGCTCTGGT GCGCCTTGTC 480  
 GCGCGTGCGC GCGCGGGGGC CCGCGGGCGA CGCGGGCTGG CGCGGGCCA TGCTGGGGGG 540  
 10 CCGCGTGGAC GGCAGCACGC TGCCGCGAG CTGCTCACTG GCGCGGCCAG GAAGGCTCTC 600  
 GTCTGGGCTT GCGCGGGGCT CAACGCTGC AGTGGGGGA ACGCTGCCA NCACTTCTGT 660  
 15 CCGCGTCTC ACTGCGGGG ACTTNTTAAA CACTCTGCT TTCTTGAAT CCTTGAACNA 720  
 NCGCTGTGC GCTTTCNAC TTTATGANC CCCCCAAC CCTTTCNG GCGTGGGGC 780  
 20 NCCCCCCCC NNNCTCTCG CCGGTTCG TGCTCTTAC CCTTCCCTT TNCNTTAAAC 840  
 GTTANNTIN N 851

25 (2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 857 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1386RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GATCGCACT CATTTTACCT ACAGGCTGGG CTTTGAAGA AGACGCTGC ATGGTACAAT 60  
 50 GTCTAGCCA GGATCCACC TGTGACCAAG TTGCGCAGAG AACCGAAGCT GCATGACCCA 120  
 GTTAGCGCA AGTACAAGG CGAGCTGGAT ATAATGACG ATAGATTAAA CAGAAACACA 180  
 55 GAGACGTACA AGACAGGCG TGGGAGTTC GACCGGCAGA CCGCGCGGT GCACAAGCCT 240

TCTAAGCTGC GGTITATCGA GGACAAGCTG CGGTGCTGT TTTTCCAGCA GCATCCCTGG 300  
 5 GAGCTGTGCG GGCCGAAGGT GCTGGTGGAG AACATGGGAA ATGAGCAGTA CGACTGGTCG 360  
 CGGATGTTGC AGCTAGGCAA GCGCTTGAC GGTGAGTCTG TGGTGACGG GACGCTGTAT 420  
 10 CTGCTGAAGT CCGGCGCGCA CCGGAGATG CTGGCGGCAT ACGACCAGG CCGGTTTGAG 480  
 TTCTATCGTC TGAGGATGCA GCAGGAGCTG GAGGAGCAAA TAGCGTACGA GGAGGCCACG 540  
 15 ATGGTTGGCG CTGTGTTCAA GACAACCGCT GTGGAGCAG GTCTGCAGCA AGAGCAGAAG 600  
 GTCTCGACA GTGGAAAGAA GACTTTGTG CCGGGTTTG CCTGATTTT GCNAAAAAA 660  
 20 ACTCTACAAA GCAGTCNIG GGCNAACCC ACCGAAGAAA AAGAAGAACC AGGACNNTGC 720  
 CGAACCCNAA GACNCCACT GTGNACTCN TTGCCAACTT TGTATAAAT TCTTACNNT 780  
 25 TTATTCCTT NGTACAATNC NANNTACTGT TGTGTGCCAT CATGTGCCCC AACAGGTTCC 840  
 CCCCNTTGG NAAANGC 857

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1386UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GATCCATGCC TCGTTATAAC TGAGCAGAAG TGTGCATCG AACAGAGGCG TTTCCTTGTT 60  
 55 CCTTGCCAGT TCCCCATTC CCCAAGTTGC ACTGCAAAAT GTGAATCATT GATGCTTGT 120



CGTCGCCATC GGTGCGCTGA AAGATGCTGT TCCGGTAGAC CGCATTCGTGT CAAGCGGAAC 180  
 5 TCTAGGCGGC GCGGTGAGAG TCCAGATGAT GAATCTGAAG TTGAGGCOCA GCACGTGTGC 240  
 TTAAAAGATT GTAATCGGGT GCTGCTTTGT GGTATOCACA TGTGCAATTA CAAATGCCAT 300  
 10 GCAGGCAAAT GTCTCCCTG CTTAGAATCA GATTOCAATG ACCTTATCTG TCCCTGTGGT 360  
 AAGACAATCG TACCAGCCCC TGTCGGTTGT GGAACAAAGC TCCCTGCGTG CACTCATOCA 420  
 15 TGTGAAACT CGCTGCTGGA TACTTGGCCC TCGGACACA GTCCACCTTC GCATAATTGT 480  
 CATCCCTTAG ATGAACCTTG CCCCATGTA CCATCACAGT CAAGAAAAC TGTGCTGCG 540  
 20 GTAAAAAGA GATCAGGACA TTCTGCTACA ATGATGATTG TGTGTTGA GACGTGTAA 600  
 GAAGCATGT CCTATTGCAA TCACTTCTGC CAATTNCTG TCATTCCGAT GCAATGCCA 660  
 25 GCAAACTTGT TAGCAAGCCT GTGGTCNACC ACCGAAAGCC GCACNTGTTT GTTAGGGAA 720  
 TGCNTGGCNT NCGNATGCTT GAATCCCTGT NNNAAAAA AANNCCGTC CGTTGTCCAT 780  
 30 CNCCACCAAT NIGCNTGATT TGCTGGAAGA GAANGTTCG ACACCNCCC GTCTGNAAG 840  
 AATGTCAAT CNNGN 856

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1387RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

EP 0 866 129 A2

	GATCAACCAC TOGTGTGCCT ATACATAGGA ACCAAAAAGC CTTCTGGCCT GGTCTCAAG	60
5	TAGTATGTGA TAAGTTTGA ATCCTTGTA GGGTTGCCT TCCGGCACC TTTCATATTT	120
	TCGGTAAAAG CCTCCACAAG GTTCCTATCT TTATCCTTGA AGTTGTCTCC ACAGGACTCC	180
10	CACAAGAAG CCCCAGCAAG CTTCTTATCT TTCACGTATT CCTTCCTTAT TTTCATTGAA	240
	TCCACATTGT CGTAGACGAC AAGAGTTTTA GTATTAGGAT CGTAGCTATA TGCAGAGACC	300
15	CAAACATTGT CAACTTCTC TGGGCGGTGA GCTAGCGGCA ATTGGTTGTA TAGCCACATA	360
	CCCGGTTCC CTTCTGATCC TCCGCCTACA CCAGAATATT TCTGGCCAAT TAGTTGTTC	420
20	CCATCGCCCC GAACGTTGGT GAAGCCACGG CCATACGCTG CCATGCGAG TCAATTTTTT	480
	CTGGGCTGA CCTTAAATTG TTCGGTCATC ATGAGTATCG CATCATGTGC ATTCAACTCA	540
25	TCAAAGTTGT CAATACOCAT ATCTTCATAC CGACGCTTAT CTAGGTGGA TTGTACGGCG	600
	AATTGTTAGC ATTGTACAAG TTGCTATGGT AGCCTGTTGG CTCTGACCAT GCACCGTGGT	660
30	ATCGTATGTC ATCATATCCN CATGCTGAAA ACTGTTCACT CNCAACGGGA AATGCAATNT	720
	CTGAAGAAGC NGGCTGCCAG CTINATTGAA CCGTCTGTIN TCCCCGGGCC CNANATNTTT	780
35	CCATCTCINT GTTNGCAGCG GINTTTTINA AACTGGNTC GNNCNCACCA	830

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1387UP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

5	GATCACCACA ACACAGAAGC ACGCAACGCT ACAGGACTTC CCTGTTCTTT TGCTTGACACA	60
	CGTCCAGCCC AGAGGACGAT TACACCGCCG TCAGGGTTGG CTAGTCTCCG GCAGCACAGG	120
10	CTCCTTATCA CATTTTGCAT TTTCACGCTC GCACATGTCA CAAATAACCA AATACATCCC	180
	CAAAGCAGC CTTTCTCTCT GCGCGTCTT TCTCATCGG TCAGACTTGG TACTCGCTAT	240
15	GAGCGGCAAG GGCACGCGCG CAGGGAGCTC ATCTACAGGC ATCGGGTGGC GCGCCAGCGC	300
	TCTGCAGCGG CTGCGGCAGC TCGTAGCGCA TCGAGATCCG GCAAGAGGCG CGTCAGGTGC	360
20	ACTTACGAGC ATCGAAGAGT TTACTAGGAG ATGACAGCGC CTGCAGGTCC CTGAGGCTAG	420
	CCTCCCGAGG CCGGCGGGCC GCTTGGTATA GGGTTTACAT AGCAGAATGG CACGAATATT	480
25	TGCTCTAGGC AACTGCAGGG ACGGAAGGGG CTTCATGCGA AATCCTTGCA CCGCCGGGTG	540
	CCGTATATAA GGTGACGCAG CTGCGCAGCT GCGGCGGGCA TGCTAACCAC GACAGGATGT	600
30	GGAGTGGTGC GCGATTATAT ACGACAAGCC GCGTGGAGG GTCGGTGCAC AGGCAGGACA	660
	CCTGGCGGAA ATCCCAANTC GTTGAACAAG GGAAGTGGTG CAGCGGGCGC AATCTACAAG	720
35	AGTTGTIGAN GCGGCGCGTC ACATTTGGCG TTNCACTGAC CCTGTCTCGA TCCANGAAGA	780
	GGNCTGGCAT NTCACANAAC CTCCCCACAG CTGTNGACTT GAACTCCNGC CTACCTTGAT	840
40	TTGCANNCCA GAAAAAN	857

(2) INFORMATION FOR SEQ ID NO:559:

45	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 821 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1388RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45

GATCCACCCA AATTGCTCTG TGCTGGACCA GCTTTCCCAA CAGTCTCCGA GGTAAATCAGG 60  
 CTA CTGCGTT CCTATTTTAT GGCTTCAAT AACTCTTTAT ACTTAATTTA GACGTTAACT 120  
 TCCACATCCG GTATTTTTC AATCTGAGAT ACTGGCAAGC ACGGCTAGCT TTAGGAGAAC 180  
 TGTATCCCAT GACTTGTGGA CAGGGGCTTT ATGAAAAAAC GCGTGTCCGT GTAAGGATAT 240  
 AGAAAACATA CTGAGATGGC TTTTGTGCT GAATCAGACA TTCTTAGGTT ACATTTTGGG 300  
 CCTGGCTGTA CAAGGCACTA ATATGAAGAT AGAGTTATAG CGCGTGAGAA GGAAAGGCTC 360  
 CACTGGGTGT TGCAATGGGAT TTCAGGGTCT TGATAATAAT GCCAGGCAAT CATATAGATT 420  
 ACCACGAGGG AAACATCAAC GCTATTTAAG GTCATCCTTT TTGACATCTG TOGAGGAAGT 480  
 GCGAATAGCT GTAAGGCGAA CTCTACAAGA TCGCGCCGTC TCCAAGACCA ATGCTAAGCA 540  
 CCACAACCTC AATGAOCTGA TTA CTGCGGA GCAATTCOGT CCTCGAAAGT TGGCAGCTCG 600  
 ACTGACTGGT TTTCTGCCCA GAGATCAATC NATTGATCCN TNATCOCTTA CATCNCCGGA 660  
 CTTTNGAAAA CCCAAATTAA AATTCCGNAN NCCAAAATCC NCGGATTGNC CACCCTTGAA 720  
 CTACCCACNC GGCCCTATTA TTTTATAATT GCNNACAANN CCGATCCCC CGNNAACCGN 780  
 GTAAANCGAA AACCCCCCGG NNITCGGACC NNCNTTTTNC T 821

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- 50  
 55
- (A) LENGTH: 838 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1388UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GATCCAGCGG CTGGGTAGCA TGCTGGCCGA GGAGTTCCGC TGTCTGGTT TTGCGGCTG	60
AGGCTCACTT ATAGGTGCG ACTTCGATTG CCACTTGTGG CCAAGACTTG CTTCTTTACA	120
TAGCTAAATG CCACTGATCA TATAGACTGC TTATTCCTGC TTAAGTGCT CAAAGTTCCA	180
TACCATCTCC GCGTACTCCT CTATGCAGCG GTCAGTCTG AAGAAGCCAA CGTTGGCGAC	240
GGACAGGATC GACTTCTGGA GCCAGGCCCG GCGTCCCGG TGGTAGACG GGTCAACGAG	300
AGCCTGGCAG GCTATGTAGG AGTCGAAATC GTGCTCACC AGGTAGTAGT CCCCCTGCTG	360
GGCGACGGAG TCCACCAGAG GTTGAATTC ACGCAGGTCC TGAGGGGAAA ATGCGCCCGA	420
GGAGAGCGTC TCCAGTACGC GAGCAATGGG GGCTGGCAAC TCTTGGCGGT GATACCGGTG	480
CCGCTAGCGG AGGTCTTGA CATCTTCTGC GAGATTACCA AAGAGGAAGA TGTGTCTTC	540
GCCGATCTCG CGTGTGATCT CGACGTGGC GCCATGACG GTCCCGATAA TGAGACACCA	600
TTTATAACGA ACTTCATGTT NGAATTCCN GAACCTCATT ACCCGCTGTC AAANGTGCTC	660
ACTAATCGGA ACNGGGANAA TATTCGCCCC GAANATGTAT CCGAATGAA ACCCTCAGA	720
AATACNATCC CTCTCTTANA CACNGCCNC TTATTACCTA TATNGCTGCC NTTTTACCG	780
GGCTTINCC CNAAAANACC TTGAGAAGNC CCCCINININ GGNCCCGIN CCNITTTA	838

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1389RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

5	GATCTTCTTT TTGAAGCCCA CAGACACAAA CTGTGATGGA GTGCTGGAGA CGCCAGCTTT	60
10	GGACGACTTC CTTTCTTAG ACCGGGAGT CTTTTCCTA GGTGTATGTC TTTCCTTGGT	120
15	GGCGTGTTG CTCACAATTG CCTTTAGCTC TTGACGACA ATCTTTGTGG ATAACCTTTG	180
20	GCCATCTAAT GAGCCCTTTT CAATGACACC TTTGATCCAA CATCTTCCAT TCCAAAGAT	240
25	ATTGGTCACC ACCAACATAT TAGTGGAGTT ATCTTTCCCC CATGATAAGT AGAATCTGGT	300
30	ATGTATTTC AAGCACCTC CCGAGGGTAC ATCTGGCGTC TTGTTATCT GCTCCACTAC	360
35	TATGTGAGAG TTCACATCGC AATGTAGGAT TTTTCTCTG ATCAAGCATC GGTCTGCTT	420
40	AGGACCAACA GGATTGTTTA ATGGCTTGAT ATATTCATAT TCCCTCACAT TATCTGAGAA	480
45	TTCAGACGGT ATAGCTGAAA TATTATGATT AGCCTGTTT TCTAATATCT TTTGCAAGTA	540
50	GGACGTGTCC TCACCAATA ACAGCTTGTA CAGACACCC AATGGTGCTG CGATGGAATC	600
55	GAATCATCAA CAATAACATC TCCTGGTTGC TCGTATAGGT GTTCTTGTG GGAGGANGCT	660
60	ACTAGGGCGA TATTNGTAAA TATTAAGANA CANTTGITGA CTGTTNGAAC TGCCNCGTAC	720
65	TTGATTNTAT AAAACCTCNC AATGTTACCG TTCNACNCT TNGAGANTIN ANCCCTCNAA	780
70	TCNMTCCNC GTGANITTC ATCTCCCCC NICTATACTG ATACNT	826

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1389UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GATCGGTGCG	ACTTTCAACA	TTGTGAAOGA	CTTCACACCG	GAAGAAGAGG	CTGOCATCCG	60
COGTGAGAAC	GAGTGGGCOG	AGGACOGCTA	GCCACGGCCC	GOCTCTATGT	ACCATAAGTA	120
GCCGATATCT	ACCGCTGCOG	GCGGGGGCCC	CGCCCGCGCC	ACCGTTGCGT	GCCAGGAGCT	180
GGTCTGCCGA	CTATCCGTGC	CAAGTAOGA	AAOGATGCTG	GTTTATGTGG	TCGCCCCGOC	240
GCTGGTTACA	ATTAACCGCC	CCAGGTCATC	GGTAGACCGA	GCTAGCTACT	CGTTGTCTCTG	300
TAAGTGAGTT	AACGCACAAG	GGGAAGTATT	CGTGTTGGTCA	GGCAGCAGAG	ACGCTGCAGG	360
ACATACTACG	AGTTATTTCT	CATAACTAAA	CATTTTIGAA	ACCTTTGTGTG	CGGGGGCCAG	420
GTCGTTTTCG	AAAAGGCGGC	GGAATAAACA	GGGAGGAGAG	GTAGATGCTC	TTCTCAGGCA	480
GAGGCTAGCA	AGGATGGCAG	AACAGCGGAA	GCGGTGCGGG	TGCTCAGAG	AGAGGCGGCG	540
GGCACTTTTC	AAGAAGCATA	CGGGGAAGG	GGGGGGGAA	GGGGCGGCG	ACAGTGCCAA	600
AGACGGTTAC	GACCCGAATG	GGGAACCGCG	GANCGGGCCC	GAGCGGTNAT	TTCAAGTTGG	660
CGCNGGGAAG	GCCCGANTTT	NAAACCGGTG	TNTAGACAAA	AACTTGTCOA	GTTCNCACCC	720
GTNGTTTACC	AANNNNNNAA	TCTCCNCCCC	NGGGTNGGTG	GCCNGAACCC	CCNCTGGCTT	780
ACGGGGNCCA	CATCTCTOCC	CCCCCTOCCA	TTAAANACCC	CGNCNCTTTT	TNTCTGNCC	839

(2) INFORMATION FOR SEQ ID NO:563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1390RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GATCAAGTAA TCAATCAGTT AATAATATTA AGAATATAAT ATGTAGACAT TTAGTCTAGT 60  
 CTATTAATTA TTAATTATTT TGTAATTTGT TGTTAATTGG TTGATATTTT ATTGATTTTG 120  
 TTGACATTTT GTTGACATGT TGATATGTTA TAAATATATA TTTAATATTA TTTTATATAA 180  
 TTATTATTAT TATCTAGTCA TAGACTCATA TAAATATGAA TATATTCCAT TATTAATTGT 240  
 TTAGGATAAA CATAAATTAA TATAATAACT TATTTTAAAG TTCAATAAAT ATGTTCATAT 300  
 TTATATGATT AATTCATAAC GTATTGATA TAAATATCTC ATACCCTTT ATGAATTAAT 360  
 TAAGCGGTAT TAAATTATTC TGATTGGATT AAGTTATTAT TTAATTTATG TTCCTAACAA 420  
 TTAATTGATT CCATAAATAT CGATATTTAT TATTATTTAT TAAAATATTA ATGATAATAT 480  
 TGTAATACTT CAATTATTTT ATCAAATGGC AAGTAATCTA TTAATCTTTT AATACGATTG 540  
 ATAAGAAAGA AAAGAATATC ATCTATCGTA TAATATATTT CAAGTATGAC CTCTTCAATA 600  
 TAATTAGAAG TTAAACTTGG TAGACAATTA AGAATTTAAT ATGAGTCTTA CATTAACCT 660  
 GATATGAACC TTTAATCTAC TTATTGTTTT AACCGTTGAA GAGAGAATAG TTAATCTNAG 720  
 TATNACTTAT ATATTGATAC 740

## (2) INFORMATION FOR SEQ ID NO:564:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1390UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GATCAACTA AGAAACCTAA TAACTAATA GAACCTATTA GATAAATTAT AGAAATTTC	60
CCAAATACAG GTTTTTTAGA ATAAGTTGAT ACAATATGTG ATATTATACC AAATAGTGGT	120
ACAATTATAA TATATACTTC AGGATGACCA AGAATCAAA ATAAATGTTG ATATAAATA	180
GGATCACCAC CACCTTGTC TCAAGAAT GATGTATTAA AATTCTATC TATTAATAAT	240
ATAGTAACAC CAGCTGATAA TACTGGTAAT GATATTAATA ATATAACAGC AGTAATTAAA	300
ATTGATCATA GAAATAAAGG TATTTTATGT AAGTTTATAC CATTAGTTCT TATATTTAAA	360
GCTGTAACAA TAAATTAAT AAGTCCTAAT AATGAAGAAA TAGTAGTTAA ATGTAAAGAG	420
AAAATAGCTA AATCAACAGA AGCACCAGAA TGTGATTGAA TAGAAGATAA AGGAGGATAA	480
ACAGTTCAAC CAGTACCTAG ACCAGATTCA ACTATAGTAG ATGTTAATAA ACAAATTAAT	540
AGTGGTGGTA ATAGTCAAAA TGAATATTA TTAATCTAG CAAATGATAT ATCAGAAGCA	600
OCAATTATTA ATGGTAAATA ATAATTACCA AAACCACCAA TTAATATAGG TATTACTAAA	660
AAGAATACTA TTAAATAAG ATGTCAGTA ACTAATACAT TAAATAATTG ATTTTGACCT	720
TGTAAATATT GTTGACAGGT GCTGATAATT CTATTCTAAT AATAAATGAT ATA	773

## (2) INFORMATION FOR SEQ ID NO:565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1391RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GATCTTTTTC	CTCCAGGTTA	TTCCCTTCCT	GGACACATTT	ACGAAGTGTA	TTTTCAGAC	60
CTGACTCGCG	CATTAGGTG	TTACGTTAAA	GCCTTTGAGC	TAGATGCOGG	CGACCTGTC	120
GCTGCTAAAT	ACATGGTGA	ATACTATAGT	GACCTGTGCA	ATTGGCAGGC	GGGGCCAAC	180
ATCTGTGACC	GTGTAATCAA	GAATGATATG	CATCTCAATT	CCGTCAACTG	GGGTACAGA	240
GTTCTGGGTG	TTTATTATTT	GGAGCTTCAA	CAGGAGGCTG	AATGATCGA	ATGTTTCAA	300
TCTGCTTTAC	GGATTGATTC	GTCTGATGTT	GAGGCATGGA	TAGGCGTGGG	ACAGGGTAC	360
GGCGCATGTG	GCAGAATCGA	AGCCTCGATC	AAGGTTTTTG	AAAGGGCATT	AGAGCTGTCT	420
CCAGAACATA	AGTATGCAGG	GTTATTCTCT	GCTATATCAT	TATGCCAGCT	TTCAGAATTC	480
GAAAAAAGTC	TCGAGGCCCT	GAGAAAACCT	GTGAATAAGT	ATCCACAAGA	AGCTATCTTC	540
AAAGAAAGAC	TAAGTGCAAC	GTTGGTGGAG	CATGCTTTGC	AGTTCCTTGA	CCAAGGTAC	600
CTGATAAAAG	CGGCAACTTG	CGCTGCTGAG	GTCATATCGA	TCATAGAAGG	CATTGTATCT	660
GAACAGGTAG	AATATACAAC	CAATATGTGG	ATTACTTTAT	CAAAGGCTTT	GAATATTTTT	720
ATTTCCACGC	GTTCTCAGTT	CGACAACTT				749

## (2) INFORMATION FOR SEQ ID NO:566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1391UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GATCGCCGCG CAGATTGTGC AGAAGTGCT TGCCTAGGG TCTCTTACGA CAAAGGACTA 60  
 CATGCAGTCG TTGGCTTCGG ATGTTTCTGT GAATGATGTG GCGTCCATGT TTGTGAAGCT 120  
 GGTGAACTA GGCTTTCTGG TCCCGCTTTC CAACGTGCAC TACATGCCAC TGGCCGATCT 180  
 ATGGGATGTG CTCTACAAGA AGGAATACAA TGCTATTCCA AAGAATTCCA CGTTGTGAGA 240  
 TGCCAAGAAA CGTGCAGAAA CAAAGCGGAA GACGAAGGTT CAGTTCAATA CGTTGCTGAA 300  
 GAATGTCGAA ATGAGCAACG TACTAATGAC TGATATGCAG ACTTCAATGA GACGTGTCCA 360  
 AGACAATCTT CCTCTAACAT TTAACCTCGG CCGGTACATG AAGCACCGGC GTTCTCGGCA 420  
 GCTTGTACAG TTTGCACGTT CCGGTGTGGG GAGCGTACCA GCCATGATCT ATAAGGTGGC 480  
 ACTGAAGATA ACCGAACAAT GTGCCCGTGC GCTTTCAGAT CCGCTATGTG AGACAGGCTT 540  
 AATGCAGGAA CTTGAGGAGC AACTGGCTAT TCAGGAAGAT ATGGCGCTAG ACGATGAGAA 600  
 GCTACCGGGC GTTACATTCA ATGGGGTGGG CATATCCAGA AACTTACCAA ATAACATGGA 660  
 CCTACGTGGC AACTGACTTT CTATGCCAAG AAGATCACCA GAACGTTGCA CGCACCAAGG 720  
 TCAATCCCAT AAGCGGNTGA AGGCTGAAGA TGGGATGGCT GTAGCAG 767

## (2) INFORMATION FOR SEQ ID NO:567:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1392RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GATCCCCACC ACCGTCAACC GGGTGCCCGG CACCACCCGG TTGTGAGGT ACCGGTCGCA 60  
 CGTCAGCAGC AGGTTGCGCG GCATCTCGCC GATCGGTACG GACTCCGGCA CCTCTCGGAG 120  
 CTTCAGGAAC TGCTGGTCTA CGAAGCGCGA GCTCTCGTGA ACGATCATGT ACGGGTCCTG 180  
 GCGCAAGGG TTCCCCCGCG CGCTGCCATC GTCATTGAG TGGTCTGCA GGCACGCGCG 240  
 CGGTAGCGCC ACGTTGCTCC CGCAAGCGA CTGGAAGTTG TTGAGGTCCA GCGCGTGGT 300  
 GTGCGGCAG TTGCGGCACA TCAGCGCAAC GTGAGTCGA CGTGACGTCA GCACCGACGT 360  
 TGACACCAG ATCCCGCTCA GCGCAACAG CCGCGAAAG CTCTGTGAGT CCAGCTGCGG 420  
 CAGCGCGTTC TCAGCGCGCG CGCTCTGCAG CTCCACCTGC ACCGCGCGCA GCGCGCGCGC 480  
 GTCTTCGCC CGGAGCGCGG CCATCGCGCG CGCTATTTCG GTCACCGCCT GCTCAAAGAG 540  
 GGGCACGTC TCACAGGCT CGTCGCGCAC AGTTTGTACA GCGCTCGTT GTACCAATCA 600  
 GATGCTCGGT GTTGACGCGC AGCGGTACG CCGCACCAGC AGGTTGTTGC GCAACTGCTC 660  
 GCGATATAAN NAACCGCGCG TCNAACGAAA CTCNGCACA AANNCNGA AGAGCGCACC 720  
 NCCTCGANC GGTGTTGCG CGCCCGCCTC CTC 753

## (2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1393RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GATCACGGAT TGCCCCAAGT ANTGGGCAAC AGTGTGCAAN TCTGACATAT CTCTTGCAAA	60
TGCTAGCCTC TGGGGGCTTG AACTAACCAT TACTTCTAAT ACCTGGCTAG CTGCTCCAA	120
ATCCGGATCC AAAAAAGCAA TATTTATACA TAACTATACA CGAAATCTCA GTTCATCGCT	180
AGCTAGCTCA TCGTATCCGG GACTGGGAGA GGAAGTCAAT GCTGTGGAAC CCTTGAATA	240
TGGCAGCGTC GGCGATGTTG ACCAAGGACT CGCTGGGOC AAACATGCGG ATGCCACNTA	300
GGTGGGTGTC TTTCGGTTC TCGTGGTTAG TCAAGACCTC GATGGGCAA AACTGGCACT	360
TGAGCAGGCC GTCGGAGGGT CGGTGTGCTT CGAAGGTGAA CTTGACCCAC CCATTGACTT	420
GCGGACTTCT AGGGTCTTGT AGTAGGTGTC GTCGGAAGGG CTGTGCCAG CGTATATGG	480
GAGCGTCTCC NANGTGTAGG ACTCATGAC GAAGAGGAG AAGTACATGG CAAGCTGGAT	540
GATGTCAACG CGCTTGCTGA AGAAGACGTC TATGGTGTGT GGCTGGGAGC CGTCGCTTTG	600
CCANAANGTG GCGGGTTAT CATCCNAAGG CGTTTTCAT GGGGTANCCG GCCTTGAANG	660
AAGAAGGCTT CCANTAGGCC AACNAAGTGA TATCNACTTA CCTGGTTCT CCAATGTTTG	720
CAAGCCCNCC TGTTATTTTG NCCAGAAAAG AC	752

(2) INFORMATION FOR SEQ ID NO:569:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1393UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GATCCAGGAT ATCATGCCCC AAATCCTTGA AGCCGCTGCA AAGCGCCTCG TGCAAATCAA	60
GAATCTGCAC ACGGCAGAGA ACTTACTCTT CGTATTTTTC TACCTGACTT CTATTGATGC	120
GCGGCAGACA GTGGACTTTC TTTCATCAAC GATCATCGAT GAAGGGGGCC GTACCGCCCT	180
CCAGGCTATC GTTCGGGTT GGTAGAAGC ATTGAGGTT CTCGGGGAG AACATAAAAT	240
CAAAGAGAAC ATTTTATCCC TTTCGAAGCT TTCTCTCTT GAGGATCCCC GTATAGCGGG	300
CATCACGGTC AATGGGGATC TGATTCCCCA CGATGGCGAC ATCATAATCA CCGCTCCAT	360
GGCCAAGAAA ATGCGTGATA AGTACACGCA GATCTCCGCG GCGAGAAGA TAGTCAAGCT	420
CTTTGTTGCA GAACTAGCCT TCAGCAAAA CCAGCTGAC CCGGGCGTT ACCCTAAAGA	480
CGGTCCTGGC CCGCTGACC CACATGACTC CGAGGAGAC TCAGTGATG AAGACTGGGA	540
GGATGTGAT GACATCCTTG ACTACGAAA ATTGCGGAG TACGGGATG ATAGTGACAT	600
TGACGACACG GTGACAGCCT TTTATTACCA AGTAACATCG AAGAGGATGT AACCCTCTG	660
CTTACTCAAT TCTTCAAGGA AGCGTTTGC AGAAATGCCT CTGGCTTCCA GGAGATCTAT	720
AGCAGGCTCA CTGAACAAGA GAAGAAGAGC TATCTGCATG CATGGTATAG GAT	773

## (2) INFORMATION FOR SEQ ID NO:570:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1394RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GATCTGACG ATTACCGGT ATGATTATAT CCCAGCAACA TGGGCACAG CGGCACACAC 60  
 AGACATGATA CTGGTCGGTG ATTGCTGGC AATGTCCAG CTGGGTCATG TGTCCACGGT 120  
 GGACCTGGAT CTGCAGGAGT TCCAATACCA CGTCCGGTCG GTGTGTACAG CACCAGGCTC 180  
 GTCTTTTATA ATTGCAGATA TGCCATATGG TAGCTTTGAG CGAANCATTG AGCAGGGAGT 240  
 AGAGACGGCG ATCTGCTTA TGAAGACATC CAGCAGGGTG GGTGCTGTTA AGCTGAGGT 300  
 TGGGCGGGAA GAAAACGACT ACTGTCTTGA GCTTGCCGCA GAGCTCTOCA GGGCGGGGAT 360  
 CCCAGTAATG GGCCATGTCT GGCTGACCCC GCAGGCGCATG CATGCATTGG GGGGTACAA 420  
 GGTTCACGGC GCAAAGGACT TGGGCCAGGC GCTGGCGGGG TACCACCGGG CTAAAGATCT 480  
 GCAGGCTGCA GGCTGTTTTT CCATGTCAT CGAATGCATT CCAACTAAAC TAGCCGGTAT 540  
 CATAACCGAG AAATCAGTA TACCTACTAT TGGCATTTGG GGGGGCCCC AGACAAGGG 600  
 GCAGGTGCTC GTACAGTGG ATCTGCTGG CATGTTGCCA NGGAAGGCC CAAAATTTTG 660  
 TGCNGAATTC CCGGACTTC CNNGGGAGC CCATANGTTC CTTGTGCCCC CTATGTTGAA 720  
 AANGTGCCA NGGCTCTTC CCNAAAGTNG GGGCA 755

## (2) INFORMATION FOR SEQ ID NO:571:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1394UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```

GATCGAACTC CATGAAGGAG CGTAATGGCC TGTGGAGCT GCACCGCACT GGGTGGGTAC      60
ATAGCGGGAT GTAGGAATGC GGGGATAACG ATTCCGAAAA GCTGACTGGG CTGCGCCTCT      120
AGCTTCAGCT CAAGCTGGCG CAGCAGCGTT GCTATAGGCT GTTGTGGCGA CAAGGTGAC      180
ACTTCAGTTG CAGTAGGAGC AGGTAGCATA CGACTAGTTA TATCGAACTG GTGCCGTAA      240
TGAGGATGAG GGTCAATTTC TGGCTCCGAG CGCTGGCTAG CACCACAATT ATCAACCAAGT      300
CCATACCTCC ATGCAATTCT GAGATCTTGG CTACGTGCGA CCGGTTTTGC ACCCCCTCCG      360
GCTAAGTTTT GCACCGTGAC CTTGATTCC TCTTGGGAAA TGGAGATTT CTTTACCTCT      420
TTACGTGTGC CCTGGAATAT CCCCAGCAGC TCTTGCAT ACTGAGTGT GAGCGTGATG      480
ACCACCACAT GGTATTCC TCCCGCTGT GCGCCGCGAC TTTCGGGCG GTTATGTGCT      540
GCTCCCTGG CTGCAAGAG CTTTCCAAGT ACCGATGCAA AGTCTGTACC CCTTGTCTCT      600
TCCACCAGAA GCATCTGGCC CATTTGCAAG CCATATGCC CTAGGAGCCG ATCCATATCT      660
GCACAACCCG TGGATGTTGT GGGATGCGAA GTAACCGCG ACGGACGCAA GCCCAGATGC      720
GACTGCCTGC CNOCTCACTG TTGGATGCCA ACCTCTCCAC GCTCTINGAA ANC      773

```

## (2) INFORMATION FOR SEQ ID NO:572:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 746 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1396RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

GATCAATCAT TCTAGAGCTG GAGCAAAGGA TACCTATAGG CTTGCOCTGCT CATTGGCCCC 60  
 TTTCAATTATT ACATACCCAT CGTTCCACAG CGTGTCACAT TCTGCCATTG GAGAGCAGGA 120  
 CACCCAAGTT TTCAAACAGA ACAGCOCTGT TCTCTTGGTA AAAGTTGGAC CTTCTAACGG 180  
 TGTCCTCATC GAAGCOGTG TCGCCACTGA GGACCTTGAG GCGGTGGAG GTGGCTTTGA 240  
 TGTAGTCGTT GAGCATAGGA ACCGGGTGCT CGCAAGCTT ATTGAAAAT TGGTACTTGT 300  
 TGGCTGTGGA GCTGANCTGC AGGGGAGAGC AGTTGGGTCT TCTTTTGGAG GGTGGCCAGC 360  
 TCGGGCTCGA GCTGGCTGGT GACTGTGTGT AATTCTGTGA GCAGCAGCAT CCOCTGTTGG 420  
 GCAAGGGAGT TTTGGGCGGA CGCGGTTCG GGATCCTTAA CCGGACACG TGGCACGGCG 480  
 ATGTCGAAGA CCAGTTCCGC GTAGGTGGAG GTCTTGTCGA OCTGGATGGT GTAGTTGATG 540  
 CGCACGGGGG GGATGGGCTT GATGTGGGCG TTGACACCTG GGCAGCTCG GTGAGCTTGA 600  
 GGTACTTGCG AGGCTCTGCG GCGGGCCGCA GGAACCTAAC GATCATGGCG TCACCTTGA 660  
 TGACAACTTG TCGTCGTTCT GCGTGCTCTT GCGGTGGCCG CTNGGTCTG CGACNAAGAA 720  
 CTCTTGAACA GGATTTCTTG TNAACC 746

## (2) INFORMATION FOR SEQ ID NO:573:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 772 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1396UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

GATCGGTTAC TTAGAGGGAG TGCAAGACCT GGCTGACTT ATCTTAGGGT TATTAGCTAT	60
GACGGGTGTG TTCGGATTTC TGTCGAAGGG TTTAGATGCC ATCAACTCCC TGAATTCCCA	120
CTACTTTCCG TTGTGGGTGG ATGAACAGAA GGCCATGACT TTCGTTGAGC GTATTAGATA	180
CTACAATTGG ACGTTTGAGG GGATCTGTGT GGTCTGCTC GGGCTGATGT ATGCCGTGTA	240
CGTGGGGGGG ACCAAACTAA ACGAGCGGG CTCGGACCGT CTGTTGGAAC AGCTGAACAA	300
GTCTTCTCG GAGGAGCTGC AGTTTCGGCG CGTGGGTTT TGTCCCGGG ACAAGGGAAG	360
GCTGCCATAC ATCAGCGATC GGAATGGCAC ATGGTGCAAC GCATTGCTA CGGGGCGCAC	420
GTGTGTGGAC CATATTGTGG TGAAGGCTCA CTACCCGGCG CGCTTCAACC CTGTGGGGCT	480
GCTGGTGGAG AAGCTGCTGG GGATGTCTT CCGGCAGGTG GTGGACCGCA CGGCGATGAG	540
TTTGTGCAGG TGACGGTGAC CCCCAACGGG AAGTGGACGA AGGACGAGAA CAGCGGGGTT	600
CAGCGACCG AGGACGGGCT GAACGGGTT CCGTTTCATCG CGTCGATGT CCACAAGAAC	660
GGGATGAACG ACTCGCGCG CAAGAACTAC TTCTCTCTCT TGACTCACNC GTCCGANGGC	720
GAAACTCTCC CATGGAANTA CTCTTCATGT CCGANAACAA CCACTGAACA AC	772

## (2) INFORMATION FOR SEQ ID NO:574:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1397RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GATCCCATTA TTCTACAGCA AATATTACAC GCGCGGCGGA CCCTGACAA TGCAGAATTC	60
GATGCATACA CAAACATAT TACTACAAAG CTTCACAAAG GTGTCTCTCC CACAGACGCA	120
TTTCTAGGCG CACTCAAGGT TTACATCTCT AATTGCAGTT TGAAACGTTT ACGCTTGCCAG	180
AAAGCACACG TTATACTTCT TGATAAAATT GCGATATTCA TCAATACAAA TGTGGTCCAT	240
GTGTCTGTGG AATCGATACA TACGATACTG AAAAGTTTAG CTGAATATTT TATTGATGCC	300
AAGGAATATA AGCGACTCAA CAACGTGCTC AATATTTTCAT TCAACGCATA TGTGATGTAT	360
AAGCATGAAA GCCTTATAAG ACTTGACAGCA GATCTCGAAT TATTTCTCTT TATGTCCGTC	420
AAACAGGACT GGTCATGTT TACCAAGTTC GAGAAGTTTA TTTCTGTGCG TTCAGGAGAC	480
ATCTCAGTAT CGCTCTTTGA ACAGTGTTC AATGTTTATG TTATGTTGCG GGATCCCTCA	540
TTGGCCCGCC TATGGGATGT CTGCTTGAAC AAGTCGTTGA AGTGTTCAC GAAATTGGGA	600
CTAACTAGTT ACACAGACTT TAAGGCATCG TCCGAGCCAA TGCTAGTGTT GGTATACAGT	660
GGATTTGTTT CTGATATTTT TACAATACCT TATAATGGCT GGGCTCGCT ATCGAAAATG	720
TTATTCATGG CATTAAATGG GGTCTATAAA TTG	753

## (2) INFORMATION FOR SEQ ID NO:575:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 767 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1397UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GATCTGAAAT ATTGCTCACC CCCACCGTGA CCTATGTAGA TGAACGTGCT GGAGTTCTGT 60  
 ATCATTTCTGA CGAATTCATC CTCTTCTGGC TTTGAGCCAG TTAATATCCG TGTGAACCC 120  
 AAGTCGCAAC AAAGTCTGGT AAAATGTTCT TTAAAGGCA GTTCAGTCTT GGTCAGTCC 180  
 CCATGCGGGT TTAAACAAT GGAAAGTCTG CTGTCTAGGT TAATCTTTGG AGAGATCTCT 240  
 CCTCTGAATT TAGTTAGTAG CTCGTGAAGG AAATTTATGG ATGGTAACGG GCTCAGAGAA 300  
 GCATCGGAAA ATATACTGAG AGATTCCCAT GGAACCAAC TGCAATCGGA GCTTATTACC 360  
 AGAAACGTGT GTCTAACCT TGGGCGCTCT GGTGCGTTGG CATGATAGTC GTGAATTAGT 420  
 TCCTCAAGTT GAATATGTAT GAGATGAACG TCAATCTCAT CATAGGCATT TTCTTCGCCA 480  
 TGGAAAAGCA ATATGTCAAA GATGAAGTAT ATCAAGTCTT CCATGAATTC CACCTTCTTT 540  
 TCGTGAGGAA GGGCATCCCA ATCCACCTTT AAAAATAACT CTAATATGAA ATCGTCCACC 600  
 TGTTAGAACA TAGACGGGTT TCCATACTGT CTTCTTGTG GAAGATTTGT TGTAAACCT 660  
 TTGAAATCCT AATTGGAATA NTGCAAAATG GTTTTATCCA ACTGTTTTTG GTTGAAGAAA 720  
 CCGCNGAATC CCATATCCAG ATCTCATGGG GGGCNCNAT CTACATC 767

## (2) INFORMATION FOR SEQ ID NO:576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1398UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GATCGCTCTT CTTTGAAAGA ATATGTAGGC ACCCTCTCCT ATCTTGOGOC GGAATTGGTT	60
CGCTGCAAAG ATATGAAGAC GATGACACCT GCAGAAGCAG AAAGAATCCC AGAGTACGGT	120
GCAGCAGTCG ACATATGGGC TCTTGGTGTC CTCTGCTACT TCATGATGAG TGGCTATATG	180
COGTTGATT GCGAAGACGA TGGCGAACT AGTGACTGCA TCTTGAAGG TGACTATTAC	240
GTTGACGAGG AAGCTGTGTC CAAOGCCAAT GAGAGCTATA ACAGCTGCTG GAACTTCATG	300
CAGCGCTGCT TTACGATGGA TGATAATATC CGGCGGOGG CACAOGAAT CATGGGCCAC	360
GCATTCATGC GGAATACIT CCAATGGCT GGGGCAATG ACTTGGCATC TATCCCGCTA	420
CTGAGAGAT CAAGATCTC GAACTCCCTG CACCCTTAG CGCGGCATC ACGGCAACG	480
TTTATCTGCT CTGGGCTGCC GGTATTAAAC GAGCGGCTG TGCCAGTGT TGGCTCGGT	540
GAGCGCAATT TGGATAAGTT GCGGGATACT TTGCGGAAGA CCTTCCCTC ACTTGGCTTG	600
AACCTATGCG CTTGTGCT CAAGCGAATA CTCTAATCC TAATAAGAAG AACTCTACTT	660
TTGTTCTTGA GCCAGCTCCT CCCACGGGGA GTCTAATGAA TGGGTGTTT ACGTCACACC	720
GGAAAGTAAT CCAACCTCAA TACGOCAGTC CTTTGGGCA GAAGCTCCGG CCAA	774

## (2) INFORMATION FOR SEQ ID NO:577:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1399RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

```

GATCATTACT CGCAGAACT GAGATGTTAG GGGGACCAA CTCCTTTCTT TGATGAGATA      60
CGGGAGGATG CCTCGGAGA ACCAGAACA TGCAGCAAA GGCAAGAAGA ATGCCAACGA      120
GAAAAGCAGC CATCGCTGCA TATGCAGTCC CACCCCATAG TAGTTCCTTG CGCCATATGC      180
CTGGGGGCAG AGTGTATCTA AGCTTGTTGA AATACCCCTCN AATATTGCGA AAGTGATATT      240
GGTGGTCATG GAAGCCAGGG AAACCGCTGC CAACTCATTC TTTOCCAGGT GACCCACAAC      300
TAATGCACAT ACAACCGGAA ACATCTGCTC AAGCAGAAAT GTAAATATGA GCGGCAAGGA      360
GTAACACAGA AGCACCAGAC TCTCGGACTT CACGGTGGCT GGTTCGTCTG CGAGATCTCT      420
GGACCTCGG AACGGGCTGG AGGGGCCCCC CTTCCTGCCA ATGGAGTAGT AAGACAGCTT      480
TCGGGGCGGT AGAACACGCA CTCTTGCCCT GTCCGACGGC AGTTGCTGCT TAACCCGATG      540
CATGAAGTGA GTGTAGTGCA CCATGTCTGG CCGGGGCCCC TCACATCGA CGGCACGAT      600
GTCTCGGGC CTGCGGTAA CAGTCGAGTA CCGCGGTTG TGCTCTCCA ATATCCAGTC      660
TACATTCACT GCAGAGGACG GCGCGCTCA CTCGCAAGCG TCGACGGCAG CGAGACTGTC      720
CGGACAGCT CTCCTCGTC AAGCAGCCC TCCTCC      756

```

## (2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1399UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

GATCTTGTAC	GACGGCCGCG	GAAGAATCGG	TGCCATCGTT	TCCAACAGAC	AGTTCCAGTT	60
TGAOGGCCCC	CCACCACAGG	CTGGCTCCAT	CTACGCCAAG	GGTTGGGCCC	TAACCGAGGA	120
GGGCAACTTG	GCCCTAGGTG	ACAGCGACGT	CTTCTACCAN	TGTCTGTCCG	GCAACTTCTA	180
CAACCTATAT	GACCAGAACA	TGGCACCACA	ATGCTCTCCA	ATTAAAGCTCC	AGGCAATCAA	240
ATTGGTGCAC	AACTGCTGAA	CAGCCACAAA	GGTATATAGT	GCATATATTG	TATTAGTTAA	300
ACTAGGAATT	TTTGTGTGCA	GCTAGACTGC	CCTACGTGGA	TTTCTCGTTG	CGGATCCTGG	360
GCTGCCGCTG	GCGCTGACGC	ACAAGAGCAA	CTGCACAAC	ACTGGCGTAC	CGCATGCGTC	420
CTTGTGCATT	TTTGCCGGGG	TGGACGTGCG	TGACGTCAGC	GTGGCAOGTG	ATCATAATAT	480
GTCCCGGGCC	AGGCCCCCTAT	TGTGGCGGAC	AGGAATGCAT	GCGGAGGTGC	AAAATGGTGC	540
AAAATGGTGC	CGATGCAAC	TCTAGGCCCG	AGCTGAAACA	AGATTACCTG	GCGAGCCTAA	600
ATTTGCAGCG	GCTGCGTGGC	AGCCACATG	TGTATTGTGC	TTTACAGTT	CTTGCTGCGG	660
CTGTCCAATA	CAGCCGATCG	CGACTTTGCT	GCGCACGGGC	CACTAGGCCT	GCGGACAAA	720
AACTGCAGGC	GCGCGGGCGT	GAATGGCGCC	GGACGATGTG	CTGCGGCGGA	ATTCC	775

(2) INFORMATION FOR SEQ ID NO:579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1400RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GATCCTGTCA AATATGGCCA ATACCAAGCA GCGCGTGTT GTAGAGCATG TGGTTGAACT	60
CAAACCCCTCA AGCAGCCGGG TTTTGGACTG TGCACAGGAG ATATTGTCTC CATTTCACA	120
GTCCAAGAAC AAGCCCAGGC CGGGGGACTG GAATTGTCCC TCTGTGGTT TTTCTAACTT	180
CCAACGGCGC ATTGCATGCT TCGGTGCTC CTTCOCAGCC ACTAGTGCAG TGAOOGTCAG	240
CAAGCTGTAC AAGCCACAGC AGCAACGCA TTATCAGAAC CCACACCACG TOCCATCGAA	300
ACAACAGGTG CAGCACCCGC AGATTACGA CCAAGACACA CAGCAGCAIT CTCAACATTT	360
CAACATCCAG CAGATGCCGC AGCAACTCCA AATGCAACAG CAAGCGCACG GTACCGTICA	420
AGGGGGCAGT AGCATGCAGC AGTACAAGCA CAGGCTCAG CACGGCTTAC AGGCGTATCT	480
TGGCTGCTAC CAACAGCAGC AGGCGAAGTC ACAGCAGCAG TACCAGATGA ATCAGCAACA	540
GGTGCAGATG ATCGCTGGCG ACGCCAGAGA CGGTATAACC GGTACAACAA AATGGTGCAG	600
GGCAACGGGC AGAACGGTAA TTCTGTACG GAAATGGCTC CCTGGGCAGT AGCAACGTGC	660
CCTTCAGAGC TGGCGACTGG AAGTGCTTGA ACTGTCTTA CCATAATTTT GCCAAGAATA	720
TTGTTGTGCT GGGTTGTGGT AATCCAAAGA CGGCCAT	757

## (2) INFORMATION FOR SEQ ID NO:580:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1400UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GATCGGCGGG TACTTCAGGT CATTCCTCTC CACCACCACC ACCAGCTGCC CGGGCCCCGG 60  
 CTCATACAGC TGGTACGCCA CGCGAACATG TCGCTCCGCC TGCGGCACAT CCGCCTCGTA 120  
 GAACTGATCC GCAGCCACCA GCGCGTCCG CCACTCCCCG CCGCGGCTT GCGTCAGGT 180  
 CCCCCTAGC TGCGCGACCG GTGTGAGCTG CACCATCTCA GGGGGCATCA GCCAGCTCAG 240  
 CGTCGATGGC ACCACCAGTG CCGCCGAGTA CCGCTCCCG AGCTTCCCC TGAACTCGAC 300  
 CTGCGGCTCG GCCCCCGGA GAAGCGAATG CCGGTCCATA GGGCCGAGGC AGTCAGTTG 360  
 GTGTCTGGGA AGACGCTCAG ATTGCCATTG TTTGAACTGT CCACAGTTAG AACTTGCACT 420  
 ATGCTACCTC CGCGGCGCCT GCGCGACCCC ATAGTCACAT ACTATCATCC TCACACAACT 480  
 CAGTACTTGC TCGAGTCCC AACTCAAGCT AACGAGTACC AGACTTGGTT TTGGCTGTTG 540  
 CTGTATGCAT TCCAATGGTT TGTATAATCG AAAAATTGTT CAGTTGCTCA GCACATCTCA 600  
 TACAAGCAGG AACAAGAGCG AGTCGCGAGC CAAAGACCTC TTAGGCATTA GTATCGGTAG 660  
 CTAGGATGTC GCCAGAACAG TTGCGACAAG TACACGCACT TGCAGGGCGA ATTGGAGGAG 720  
 CTGGTGGTGA CAGACAGAAG CTGGAGAGC AGCTGCAGGA GAACAAGATC GTGAA 775

## (2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1401RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GATCTGTGTG TTGGCAATAC CCTGTCTTAC GTTGAAAAGA AGTGTCTCTG AGGTGTCCAT	60
CAACAAAAAT ATTACCACTT ACAACACCCA CCCGAACCTT ATTGGCCAAA ACATCCAACA	120
ATGTGTGCTT ACCTGCACCT GAATAACCCA TCAGAGCAGT CAAAGTCCCA GCCTTTACCC	180
AACCATCCAC GTTGGTTAGG ATCCTCCTGG TTTCATTCTT AATCTGTATA TCATAGCAGA	240
CATCTGCCA GTGGAAAATG CTATCAGAAC CAATCTCTG AATAAGTTTG CGGCAITGGT	300
CACTTCTAT AGTACTAGAT TCCTTTCTG GTGCATTACC AAATCTATG TGCAGTTGA	360
TGGCCTTTT ATTTTGCTT TTTATTTCT TCAAAGTTGA CCTTAGGAAT ACAGCCATTT	420
CACCTTTTG CATCCACTT TTATTATACT CAATTAAGAT CAGATAAACA CCTAAGAAGA	480
AAAATGCATA AGCAAGAACG ATCCCCAAT TCATCCACTT GTTTTGGTG TTGTAACCAT	540
AAGCAAATC TATGTAACGG GTCCATTTA CAAAGCTCTG ACCAGGAAT GCTCCCAACG	600
ACAAGCAGAC TTTATTCGAA ATAGGGAATC CTCATAGAA ACTACCATG GGTACCATTC	660
GAGAACATTC GAATATGCGT CGTCAAATT CATTCGCAAC CATGGCTTCC ATGATGCGTG	720
CGA	723

(2) INFORMATION FOR SEQ ID NO:582:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1401UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GATCTGCTGA GATTAAAGCCT TCGTGTCTG ATTTGTTTTT TATTTGAAG TCTGCAGGAG 60  
 CAGGCTTTGA AATAGAGTTC TTATGTTATT TAACGTCCG GTAACGAGTA TACAAGCATA 120  
 TGTATTATCG TATGCTAGTT ATATGCTTTG AAGAGGTGGT CTGCAGCTGG CGGTCTATTT 180  
 TATTTTATTT TTTCATTTC CTAAGACTTT ACATTTTTTT TTTAAATTAT TTTTTTTGCG 240  
 CTAAGACTGT GAACAGCGAT TTTAGAAAA AGCGAAAAG TTCAGGAGGC CTCAGCTACA 300  
 TGATATCCCA GGCTTTGTAT TTGTGAGACT GCACTCCCGG GCTAGGTTGT GACCAAGAGT 360  
 TGACGTGCGG CGCGGTGCGG ATTGCAGGCG TTCACAGTGT GGTAAATTTA ACAATTTATA 420  
 GAGAATAGAG ATGCCCGAGC TTAATCAACT GTGGGGCGCG CCAAATTGGA TTTTTTGGAG 480  
 TTTGTGATT TTCACAGCAG ACGAGAAAGC AGGACAGGCG GCGCGGCGCA GGCAGTCCCC 540  
 CCTGCAGGCG TGAGCGGACA CAGAGAGAAA ATACAGGAAG ATGAATACTG ATAATCTACA 600  
 GATTTCATTG ATATCTCATT GATCCGCTGA TTATCAATGA AAGTACCCAA TGATCCATGA 660  
 AGCCAGTAGA TGTAGTATA TTTTATTAAA TATATGCACC TTGTTATCC AATCTCTGTT 720

## (2) INFORMATION FOR SEQ ID NO:583:

## (i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1402RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GATCAGGAGC CCATCAAGGC GCCTAAAAAT CGCATCCCCG CTGTGGTTT TCCCGACTAC	60
GCGCTGTTG CTTGAAATAC AATTACTGCT GTAGTTCCTC CTGTGATGCT GGTGAAATG	120
TTGGGGGCG AAAGGGTCTG CCTGCTGAAA GGAGCTGAAA GGTGGTGACG TGGTTCCGGG	180
ACTACTAGCG TCTGCAACCG TCTTTGAGCC CAAAACACG AGGCGGATTA CATTCOCGTC	240
AGCGGGCCCG AGGGTAGAAG ACCTCCCTG ATGGGAGTTC ATGCTCTTAC TGCGGGTGTG	300
GTAATAGTAC TCACCACCAC TGCTCGACGA AAGCGGAGCA GGGGGTAGCG CTGCCATCTG	360
TTGTTCCTC CTGCGAGGTG CTTCTAAGTG TGCCAAACG AGCTGTGCTT GTTGCTCTG	420
GTGCGGTCC ACCTTGGCCA AGAGTCCGG ATCATCATGC AACATCTCCA GCACCTCCAA	480
TTTGGCCCCT AAGCCAGTG ACTGGCTTC CAGGTGCTCC ATTCTCGAT GCTTGATCAT	540
GACCTGCAGA TGGAGCTGCT CCAGAATCTC GCGCTTCGCT ATCTGTATT TTATCCGCTC	600
CGTCTCTCG CTCTCAGCC CCAGCGGCC CTCTCCGCA CGCAGCCCGC TGTATTGCTC	660
GTCGCCAGG GAAAGCTGT GCGGCGACTT CGGTGTGCGC ACCTGGTAAT ATGCCGGCC	719

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: PAG1402UP

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

20

GATCAAGTTA TGGTTGATCA AAGCGTCAAT ACCCTTTTCT CTAAGCATGT GCCAGGTTTC 60

CTTCGCGGGG CGTAGGTATG GTTTCGGTA CAACGCAATG AAGCAGTAGG CATAGTGGTT 120

GAAGTACTCT GCCATCCATT CAAAGACACC AACAAACGGCA TOCAAGATTA ACCACAAGCA 180

25

CTGCATCCAC CCACTGTGGG ATATCCCGGA AATAATCCCA TTGOGAAGCA GCTGAATAAT 240

CTGCCGCACT AGTTGAATCA GAGACACAAT CAGCGAGCCA AAGCAAATGG ACCCAAAGGA 300

30

AGTGGTCAAC GCTCTCTTTA ATGAGCCAAA AGCTGCCAA CGTGGCATGC CTGGGTCCGA 360

CTTCGAAAAA TAGTACCAGC AGCCGTAGAT GCGCGGATG GTGCAATGAA TCACATTCTT 420

35

GATGACCTCA GAAATGTAGA ATCCACAGAA GAAAACGAGT ACCAAAATAC CAATTAACTT 480

TCACGTGAG CAAGAGCCAC CAGATACATC GCAGCCACCA TTCTGGCTCT TGGGGTCATA 540

40

CTTTATGTAG GTGCAACCA AACTACAGA GAATATGACA GAGAAOCAG CCGACACAAT 600

GGTACCTAAT AATGACACAA GCCACGTCTG TGGATGTTTC TTCATACTG ACATGACCGT 660

45

ACCAAGACA GCGACACTAA ATGGAATCTT TGAGGCATT AACCAGTAGC ACACCGCCGT 720

CAGAAT 726

50

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1403RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GATCCGTTCC TTGAGAAGCA CCTAAGCCT GAACTCCTGG CAGAAGCGAT CAAGGGAACC	60
TCTTGGGAGG GTAAAGTTAG TATTAACITG GTAGACGGAT TCGAOCCTC GTATTACTTC	120
GTCAGCACGT TCGTGCCGGA ACACGCAAAG TACCATGCAG AAAAGTTGGG TCTAGTTTGA	180
GATTTGACGT TCGGCTGTT AATTGGTATA TACTTACATA TTTAGTCATA TGACGGCTTC	240
AAGTACTCTG ATTCTGCATT ATAAGTGCAG CCGAATGCCA GCTCCGGCA GTAATGCCAA	300
CGCAAACCTGA ATTTGCCGGT AGTTCAACCT TGGCCGGTTG CAGCACCGGT ATGCTCCGAG	360
CAGACTCAAA CGTCGCTATT TGGCGGSTAT CTACAGCCTC GTGGGGATCT CCTTGCCCAA	420
GACAGCCACA GATATCACTC TCCAGCCCCC AGGAGTAGAG TTCACCTTTG TGGTTTAGAG	480
CTAGGTTGTG GTAGTCTCC GCAGATACAG CAATAAACTT CTGGCCTTGT TCCAAATTCA	540
TCTTCATGAA TGAGTCCTCG ACGATATCAC CATTATTCAC CTTCAGGGTG TATGTGCTAT	600
TCTCGGTACA TAAACCACT GTCATGCAAG ATGCTCAAT CTTGTTTTAA CCGTCCATCA	660
AATGGCAAAT CAACGGTTTT TGAAACGCCA TGAGTGTATA TCCACAGTTT GCGCCCATTG	720
TTAGTAATGT A	731

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1403UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GATCTCAATA TCAACCAACT TGTGACGTGG CTTAAACAC CATATGGGA GGACATTATG	60
TCCATCACCG TGTACAAGGA CAATGTTTTT GCCACGCACA AGCAGGGCAT TACGGGGTTC	120
CACCAAGGGA ACGTGAACIT CTGGAATGCT CACCAGGGAC TGTCTTTGAG TAGOGAAATA	180
TTGGGCAAGA GCTGTACCAG TAATCGTATA GATCGGATGG TTAAGGGGG AAATGATGGG	240
TCATTAGGT TGTGAATAT TAACGAATGG CTGAAGGTA CAGCGTCCC GGGTGGATCA	300
GCCCCGACCG AAGAACAATC GCTTCCCTCT GCGAGCGGC GAAATCTTG GACCGAGTAT	360
CAACAAATCC AGTTAGATAA CGATCACATG ATTGCAACAC TGCGGGAATT CATTAGTTAC	420
CAGACTGTTT CCAACTCC AGAGCCCCAA AATATCATCG ATTGCGGTAG GTGTGGAAC	480
TTCTTGCAA ATCTCTTAC TAAGCTGGT GCTAACCATT GTGGGCTTAT ACGTGTAGT	540
ACAGGCAGCA ACCCGGTGGT TCTCGGCAG TTCAAGGCA ATGCAGCGC GCGCAACGC	600
ATACTATGGT ATGGCCACTA CGATGTGATA TCGCGGACC ACGTGCAG TGGGACAACG	660
ACCTTTCAG CTCACTTGG AAAATGGTA TCTTAAGGA AGAGCGTGT TGATAAC	717

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1404RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GATCTGCAAC GTTACTGATT ATCCTGTAAAG CCTCTTTTG GGTAAAACA TCCTGTGAGT	60
TAACAGTGGT GTTGAAGATA GAAATAAAG CAGTGTATGA TGATGCTGGA ACAACCTGG	120
ACATAACCAC CACAAGATCT AGAAGTGTGG CACTCATTTT TGGCTGGGOC TTCACAGGTT	180
GGCTAGAAGC CTCCTTATOC ATGGCATCTT TTAGTAATGC GCATACGTTA TCAAACGTGT	240
TAGACAGGTT TTCCGCAGAA GTAATTTTCA AGTATGCCTC GATGGTTTC AAAATATAGC	300
TCCGAGGGTT GGGTGCAGTC TGGTGTAGA CATTGAAAAG AACGGCCAAC ATATTGGGGC	360
ATTCTGCGGA GAGGTATCTT ATGTTTTTCT CCGCTCTGT CGCGGGAAT TGCTGTCCCA	420
TAATAATGTC GTCTTATAC GCACCATCTC TGTATAGAAG ATTACTTGTG ACCAAGACCT	480
TCAATCCATT GCATATGACA GTACGCAGTT CAATTCTGGA ATAAAGTAGG GACGCTAACT	540
CTGCAGCAAA CTCATCGGTG AATACATCGT TTAGATCTTT TGAAGAAGC CAGAACTGAG	600
GGAAGGTAGA CCACAATTGG TCAACAACAG TCTGAAGTAA TGTGCACTGG ATAGACTCCT	660
TATCCAGTTT CTCAATGGTG GACTCGAAAT GACGAATGGT AGGAATAAAT	710

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1404UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

10

GATCTTCAGC AAGATCAGCA CCACTTGACG CACTACAAGA AGTACCGGCA CTGGCGGTGG	60
CAGGCCAAGC GCAGGCTGGC CGGCTGGGAG TCAGGAAAAG TGGAGCAGG TCGTACAGGA	120
15 GCGCGAAAAC GCGGAGCGC TGGGGAAGCT GGGGACGCG CTGAOGGTGA CGGCGCTGAC	180
GGCAAGATG AGCTACTACC GGCAGCTCCA GGGGAAGCGT AGCTGGTTC TCAGTTCTGT	240
20 GTGCAACTA ACGAGCTCCA CCGGGGCGC AGAATGCGAC TTCACTGAGC AGTTCATCAC	300
CTTACTCGTG AACACCTACC ACGAGATGTG TCTGGATGCA ACCGTCACAC CGTTGACAA	360
25 GACTAACCG CCATCTGCTT TTCTCAACAA GGTAGGCGT GCTGGGTGG AGGTTCTGA	420
GCAGCAGAGC ATGCCATCG GACGTCGGG CGATAAATGG TTGTGACCT GCACGGGAA	480
30 GCGGCTTCTA CAGGAAATAA AGCGGGAGC CGAGGACGTT CCACAGGGGT CCGTGGGCTC	540
GGTGGCTGT TCATGAACC ACGGCACCT ACAGGCGAT CTAAGCTCG CTTTTCAGA	600
GGAGGGGAT TTCTTCTACT GGGATCGGA CTTCCAACTG TTCAAGGCA TCACGGCAA	660
40 ACTTCTAACC GACACTGGAG ACATCTGGG CAAAATACC CCATGTCTTT GGATC	715

(2) INFORMATION FOR SEQ ID NO:589:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1405RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

10 GATCTTTCAT ACITTOGGGT TCGTGCTATA TAACTAAGAT TGGACAGAAC TGCAAGGGCC 60  
 ACAGAGGAAG AGCTGCTGCA TTGCACATTA GGCAGGAACA GCGAATGTCT ACAAATGCAC 120  
 15 ACTACACACT ACCGCTCTCA GCGATCCCA ATCTCAGATG CGCACAGCAA GGGACCCAGT 180  
 TCTTTGCCCA TGCCGCTGTA CTGCGAGGG GCGGCAGATG GCTGCTAAC CATTAATGCG 240  
 20 AGCGCTGTGG GCTCGCTGT GGGCCCCCAG CCGGTGATAC CTCACTCAT GCACCAGGTG 300  
 GCGGTGACA AGCAGCTCA TATCATGCCA GCTCGTACG CGCTGCGACA GAGCTCGCCC 360  
 25 CAGGTACCGG CGATTATGGG CGAGTTAGCG ATGCTGAAGA AGTCGATATT CCAGTCGCTG 420  
 AACGCGAGT TGACGACGGA GGAATACAAC AGCATCTACC AACATTGAG TCAACTGCTG 480  
 30 GCGTCCCTCC CACGCGCGGT CGAGCATCT GCAGGCGAGC CCCAGCTGGG ACTGCGGTGG 540  
 ATATCTCAA TTATGCGGG AACAGAGCCC CAGGAAGTCC AAGTACCTT CATCATAGCA 600  
 35 TCCTCGAGT CACAGCAGGG CCAGCGTAC ATCTGCGGC CGTTAAGCTC GACAATGTCT 660  
 ACGCACCGC TTTCACGGG CATGTGGTA GCCAAACCGA ACTACTCGT GAGCACCAAG 720  
 40 AAGAATGTT 729

(2) INFORMATION FOR SEQ ID NO:590:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1405UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

10

GATCCAAATA ACACCAAGGT TTTCATCGGC GGGTTGTCCT CGCTCGTGAC TGAGGATGAG 60

CTACGGGCTT ACTTCCAGCC ATTCCGACAG ATAGTCTACG TGAAATGCC GGTGGGCAAA 120

15

GGATGCGGCT TTGTCCAGTA CGTGATCGC AGTTGGCAG AGAAGCGAT CGCCAAGATG 180

CAAGGATTTC CAATTGGTAA TTCCAGGGTG CGGCTCTCAT GGGGCAGGAG CGCAAAGCAA 240

20

ACAGCCGCTA TGCAGCAGGC GTTTCGCATA GCACTACAGC AGCAGCAGCA GCAGCAGCAG 300

CAGCAGCAGC AAGCCCGGCC GCAGCATTCC CAGCAACATC AGTATCAGCA TCAACAGCAT 360

25

CAACAGCAGC CTCAACATGT CATTTCTGCA CAGCCGTTCG TGCAGCAGCA ATTGCAACTA 420

CAATTTCCCT ATCAGCATCA ACCTGCCATG CCGCAGGCT ACGGTTACAC ATTGGACTCG 480

30

TTGAGGGGCA CCGGTTGGAA ACATGTTCCA ATGCAGGGTT TTCTTTCCGG TAATATGGGC 540

TTCCAACCTT CTACGGCAAT TGATAGCTCT CCAGCAACGA CCTTGCTTCC CAACCTTTCT 600

35

TGTTTGGACT ACTCTGGGTT TCCACCTTCC ACGTCAGCGT TCACTTTTCA CCCAGGAAT 660

CTTTAGGCAC AGCTTTCACA ACATGCCCTA GATTCTCAAC AATGGCAGCG TGTC 715

40

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1406RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

5  
 GATCTCCTTC CAGTGACGCT GATGCACAAC TGCGGACCTC AGCCCGCGTG CCTCACGTGA 60  
 10  
 CCACAGTGGG CATTTTCTCA GTTAGCGCTC GTTTAGCTTA GCTATACGAG GGATGGCACC 120  
 ACTTAGGGCC TGCTGCGGAA CCAGATACGA TGAAGCCGCG CAAATTGGAT AGAATGCTGC 180  
 15  
 CTCGCTGAGC CGCCGTCATA GGGAAACGAC CAAAGGTTCC GTCTGCCGCA TCGTATGTAT 240  
 GIGTCTGTGT ACGAGGACCG AAAAGTTGAC TTTTAACGAA GTAGATTTTT TTATTAGATA 300  
 20  
 TTTAAGCAGG TATGCGTTAA CGAGCAGCTT GCAAGGCGTA TACCAAGGCT CTGTGCGCTT 360  
 ATCATTAGCA GGGCGACATG TCAGAATCCT TGCTACAGAC AGTGGTGGCG TACGTGGAGT 420  
 25  
 TGGTGCTGCA CCACTTCATG GGGTTGTCGT GGACGCAGCA GCTGTCCATA GTAATAGTGG 480  
 CACCATTCAT ATACTCGCTG GTGTGGCAGA CGTTATATTC ATTCAGGAAG GATAGAGTAC 540  
 30  
 CGCTAGTGCC GTTCATGGTA CCCTGGGTGG GTTCGCGGCT CCGGTATGGG AGGGCTCCGT 600  
 ACGAGTTTTT TGGCAAGTGC AGCAGAAGTA TGGCGATGTG TTTGCGTTCA TGCTGCTGGG 660  
 35  
 GCGTGIGATG ACGGTGTATC TGGGGACGAA GGGCCACGA 699

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1406UP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

5	GATCTTCAIT AGAAGCGGOG GATTAGTCAA AAAGTGCGGG AATGTTCCAT CCACTAGGOC	60
	ATCTGCCTTC ACCCAOGGAT TGCAAATGCA GACAAGGITT ATTAGAATTA TACCGATTGC	120
10	CCAAACGTGG CCTGCAGCAG TAGGAGCTCG GAGCTCAOGA COGAGCGATC CCGCTCGGG	180
	TGCCATGTAG TAAGACGAGC CTACGCAGAC ATTGGGGGCG AGCTCCGGCA CCGGTGTGGC	240
15	CAGCCCGAAA TCGCATACAT GTACGTGTGA CCATTGTGCC AGAAGAATGT TCTCGGCTT	300
	TAGGTGCAA TGATAGAGCG CGAGTCGGTG GCAGTAGAAA ATAACCTGGC ACAGCTGCAG	360
20	GAAGACCTTC TTAATCAGTA GGCCATCCTT AGCAAAGACT TGCTCGTTGA CAATGGCTGA	420
	GAAAAGGTGG CACGTGATGT AATCCATAAC AATAAATGTT GOCAGGCTTG ACTCCATCAC	480
25	CTGATGTATG GTAACCACAT GTTCGTGGGT GTGCACAGTC AGGTGCATCA GCAGCTCCTT	540
	ATAATGTGGC GCGTGGGCGA GCTGCTCTTG GGATAATGTC CGGATCGATT CCAGGTCCAC	600
30	AGATGGTAGA TACAGCCGGT TCTGGAAAGA TTGAAGAAGT GGTACAGCTG CGTGGCGAAA	660
	ATGTGCGACC GGCTGACGC CTCGTCTGGG CTGCCGCTGT GCTGCTTCA	709

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1407RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

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5 GATCAACCAG ATAACTATCT TAAAGAACAA CCGAAAATG CGCAAAGCAC ACCACGGGTC 60  
 CTTCGGTGAT AGACTGATAG AGATACAGAA AGTAACTTCT GTGTCAAGCG AACCGGAGCT 120  
 CGGGTTTTTA CACCTTCGCA ACAGCTGCCC CCATGOCATA GCACTCTTTG AGTTCTCTTA 180  
 10 GTTGCTTTCC ACTAAACACC GTCGATGT TTCACAGAAC AGGTTTAATA TCGGCAACCA 240  
 AAGAGGAGGT TACACTCAGA GAATCACAGT GTCGAAACAC CGGCTATTCA ATGAGGCATT 300  
 15 CCCCCAAGTC GGTTCCTTTG GTTTGGATTG CCATTGGCTA GTAATCCACC AAATCCTCCG 360  
 CTGCTCACCC ATGGGATCGC TAGATGCCCA GGATGAGACT GTTCAGGTTA GGCAGGTGTT 420  
 20 GTATGCGCGG CCAGAGGGAA AOCOAATGAC TTTGCATAGA ACAAAACCGC CATCACCCAT 480  
 GTCTTGCGCT GTATAGAGAC TAAGGTATCT GACGATCCT TAGCGACTCT CTCACCGCT 540  
 25 CGACGAGGCC ATTGAAGCTC TTACGAAGTG CACAAACCTA CTCGAAGTCT GTTCCAGAC 600  
 TTCTTTCTGT TTGCTTCAA CTGCTTTCG ATGAAGTACC CCCCAGGCTA TTTTCTTAC 660  
 30 CCGCCTGGTG TTGCTTATA TACCGGTTG TATTTTGTGA TAAAAA 707

(2) INFORMATION FOR SEQ ID NO:594:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 571 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1407UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

55 GATCGTCGAA TTGGGTATA GGGCGAAAG ACTAATCGAA CCATCTAGTA GCTGGTTCCT 60

GCOGAAGTTT COCTCAGGAT AGCAGAAGCT CGTATCAGTT TTATGAGGTA AAGCGAATGA 120  
 5 TTAGAGGTAC CCGGGTIGAA ATGACCTTGA CCTATTCTCA AACTTTAAAT ATGTAAGAAG 180  
 TCCTTGTTC TTAATTGAAC GTGGACATAT GAATGAAGAG CTTTITAGTGG GCCATTTTTG 240  
 10 GTAAGCAGAA CTGGCGATGC GGGATGAACC GAACGTGGAG TTAAGGTGCC AGAATACACG 300  
 CTCATCAGAC ACCACAAAAG GTGTTAGTTC ATCTAGACAG CCGGACGGTG GYCATGGAAG 360  
 15 TCGAATCCG CTAAGGAGTG TGTAACAACT CACCGGCCGA ATGAACTACC CCTGAAAATG 420  
 GATGGCGCTC AAGCGTGTTA CCTATACTCC ACCGTCAGGG CAAATATGAC GCCCTGACGA 480  
 20 GTAGGCAGGC GTGGAGGTCA GTGACAAGCC TTAGGCTGTA AAGCTGGGTC GAACGGCCTC 540  
 TAGTGCAGAT CTTGGTGGTA GTAGCAAATA T 571

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1408RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GATCCCGCTT ACCAAGCAAT TACAGGAGAC AGAAAAGAAG GATAATAATT TACCACAGAA 60  
 CTCCAAGCCT GACAGAGCAG CGATTACAT TCTGAGTCAC ATGACAGCAG ACTCTCTTTG 120  
 CTTTGGAGCT TCAATAAGCA CCAATATGAA TATGAATAGT TTTAGATGCT TTGTATAATT 180  
 55 ACCACTATTA ACITTATCTT GATTAAATATT TATTATTTTG TTATTTTATT ATTTTATTAT 240

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TTTATTATTT TATTATTTTA TTATTTTATT ATTATTTAT TTTATTATTT ATTTTATTAT 300  
5 TTATTTTATT ATTTATTTTA TTATTTTATT TATTATTTAT TTATTTATTA TTTATTTATT 360  
TGTTTGTGTTG TTTATTATTT TTTTATTTAT TACCTTTTTA TTTTATGTTA TTTTATTTTA 420  
10 TTTTATTTT ACTTAGTATA TAATATTATA TTATATCATA GTATAGTTAT ATTATGGTGA 480  
CTTTATTCAT TATATAGATT GTATTTTGIG AACATAATAT ATATGCTATT TCTATTTCTA 540  
15 TTTTATTTTA TTTTATTTTA TTTTATTTTA TTTTATTTTA TTTTATTTTA TTTTATTTTA 600  
TTTATTTTAA TTTTATTTTA TTTTATTTTA TTTTATTTTA TTTTATTTTA TTTTACT 658

20 (2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1408UP  
35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

40 GATCCGCCCTT CCATCGAAGA GGGTACTGTT TGATTATGGT GATTTCCTGG TGTGGGTTG 60  
ACATTCAAGT GCATAGTTGG AGGTTACCGA TAACTTAGAT TTTCCTATAA ACGGTTACCC 120  
45 TACGTCCTCG CGGTGGGCGG ATATACTGAT TAACAGTTGG AGAGCCTTGG CGGGATACTG 180  
TGAATGCCCTT CTCCTCAACA TTATTTGAAT ATGCCAAAGT TATTTAAATT AAGTAACACA 240  
50 CTGTGCTTA TATATTCAAT TGTTCGAAGC GGGCCATCCA ACATGGGAT TCTCATCTAG 300  
TTTGAGAACT TCGTCTATT CTATTCCTGT GTACGGCAAC GGTATTAGGA GAGACTTGA 360  
55



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GTTTTGGAA CTTCAAAGTC AATACTTCAT CATCGTAAGT AGCAGTTACT TGGCCTAAAC 420  
 CAGTGCCAC CTTTGTAGGG AGCCTGATTG TTGCGCGAAA CTCGGGTTT GTGGGTTC 480  
 CAGTAGTCCA CGGGTCTGTA TTCTCATCCG TATTAATGGC TGSCACGACA ATAGAAAGAA 540  
 CTGCATCAIT CATGCTCGA TGCAGGGCAA TATCTATGTG GTCTTGAGAC ATTACGCCAG 600  
 GAACTCTGAT GTGGATCTCA TAGGGCTCCG AACGCTCCAA AATTAATAAT GAAGGAAGAA 660  
 CGTCAGAATT TGCGCGGAG AGCTTGATT CTGAAGTACG TGCCACACTC TCAGCTTTGT 720  
 GT 722

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1409RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GATCCTGGCT ATCTACCTGC TGCTGGGCGC GCTGCAAGCC ATACTAGGGG GCACATTCAG 60  
 CGGATTAATG TATGTGAAT ATGCGCGAGT AGAAAACGCA CGTKCATGTG ACAACAAGGC 120  
 CACCGGACTA ACCAATTTAC AGAACCGCGG CTATTTACAG GGCTGCCCTG ATCGGATGA 180  
 GTACTTGAT TCGCTTGCA TCGCAGTGG TACAGGCCCT GTACTGCTA TGCGCAGCAT 240  
 TTGTGGCACA ATCCAAGCTG ATATAGGATA CAGACATCCA GCAAGACGCT GGATGGATCG 300  
 GTGTATCCC TCTGCTGCAT CAATACGCTA TCGCGGCGG GCAGCTTATT GTCAAGTGAT 360

TCGCTATCTT GTGGAGCACC CAGACATATG TTGCTGAGCC TCCCTCAGCT ATATAAGCGT 420  
 5 CGAAGAAGGG CCGGAGTGA ATACATGTCT CTGGCGCTGT GTGCCTCGTG CAGTCCCTCG 480  
 CGATGTCTGC AACTCTCATA AACCGTTCCT TGGCAACTAT CGGTACAGAG CTTGCCCTTTT 540  
 10 TGGTTCATT CCGGGTCATT ACGGGGCAGC AGTCAGAGCA GATTGAATCT AATCTTCCAA 600  
 ACCCTAACGA AGCCCTCCGT GCGCTCCCG CAAATAACGC AGGGCCTGIG GAGTATGTGG 660  
 15 AGGCACITTTA TCGGTTTCAG GCGCAACAGC CTGGTTGACC TAGACTTCAA 710

## (2) INFORMATION FOR SEQ ID NO:598:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1409UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GATCGGGGAC CAGAAAACCA CACAACTGGT CCTTGAGGCG GCGGTGGGCG TATACGCTGC 60  
 40 TACTGTCTCT TCTTGTOGTA GCTGTGGCCT ACGGCTCTGC GTGCGTAACC GCTGGCATGT 120  
 GGTCATCAC CAGAAAATAT GATGTCTCAA CCGAAGTTGC AATATGTGCC TGTTCCCTGG 180  
 45 TGGTTCCTGG CTACGGTGTG GGACAGCTGG TTTGGGGGCC TCTGTACAGC CTGTACGGCC 240  
 GCGGATAAC GTACTTCACA TCTCTATTCC TTTACGTGGT ATTTAATATT CCATGTGGGG 300  
 50 TGGCTCCCAA CATCCAGAGC CTTTGGGTTT GCAGGTTTAT TTGGGGGTC CTGTCTGTGT 360  
 CTGGACTATG CCTAGTCGGC GGCTCTCTCG CCGATATGTT TCCAGCCGAC CTGCGTGGGT 420  
 55

TGACCATCGC GTTCTTTGCA TTTGCACCAT ATGGAGGTCC GGTATTTTGG CCACTTATAA 480  
 ACGGATTCAT CGCTGTCCGC ACAGAGAGGC TTGACCTTAT CTTTGTGGTC AACATGGCGT 540  
 TAGCOGGAGC TGTTTGGCTG TTAGTOGCAC TGGTGCCCGA AACATATGCG CCAATTATTT 600  
 TGAAACGGCG CGCAGAGAAG CTGAGGAAAC TAACAGGCAA CCAGAATATA ATGACAGAAC 660  
 AGGAAGCACA GGGACTCTCC CTGTCCGCAT GGTGCAGACT TGTCTACTGA GACCG 715

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1410RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GATCAATTGG TCACATTTGG CGTATGCAAT TTCTACCATC TCCTCTTTGG TAGCCTTTAA 60  
 TTCCACTCCT GGIGTAACAT CACTAATGCC AATAGAAAAG CCTCTATTTC CCAGATAGCG 120  
 CGCACAAAGC TTTGCCATCC TATTCATAGC CTGCGTTGCT TCTGTGGGCC CGAAATCTCT 180  
 CAGAATAGTA TAGAATACGG AATGTTTCTT ACCATCACCA AGCACAGACT TATCCATGAC 240  
 ACCAGACAGA ATATTAGAGC CTCTGATAAC TACATAACCA TCATTAGCAG ACATCTCATT 300  
 TGGATAGGCC TTATTTCTAG GCGCAATATA AACCTTATTC TTTCATCCA AATTAAATAAT 360  
 AACGGGAGAT TTCTGTGTGG GTTTTATCAA TAGAGAGAAG AGCTGTTTTC CAGTCCATAA 420  
 GTAGTGTGGT CGCATAATTG CAGGCGGGCG TATGTCAAAC TGCAGGTTGC CGTCAGACAT 480

CATAGAAAGC ATTGACAA AAGTTGCGCG GTGGAAGAAG GAGTCTTTGT GAGAAATCAA 540  
 5 ATATGATCCA GTGATGAAAT CCTGGGTAGC TGCAATGATC GGTTCACGG ATTTCGGAGT 600  
 CAATAAATTG TTTTIGACAC CCATAAGGTT GATTGCTTCC GGGCGAGCCT CTTCGGTTTG 660  
 10 AGGAACATGC AAGTTCATTT CGTCACCATC AAAATCGGCG TTGTAGGGG 709

## (2) INFORMATION FOR SEQ ID NO:600:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1410UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

35 GATCTGAGCC CTAGCATCTT CGGTGGAAG CGGGAAGTCT ATTTTCTTAT CCAAAGACC 60  
 GGAAAGCAGA AGCGCTGGAT CAAGGACATC GACTCTATTC GTAGCAGCCA AGACTTTTAC 120  
 40 CCTATCGTCA GAACCAAGC CATCTAGTTG GTTTAGCAAC TCAAGCATGG TTCTCTGCAC 180  
 CTCTCTATCA CCGGACTTCT CCGAGTCAA ACGCTTAGTT CCAATAGCAT CCAACTCATC 240  
 45 GATGAAGATA ATGGTAGGTG CCTTTTCTTT CGCCAAGGCA AAGGCGTGGC GGACCAGCTT 300  
 CGCACTTCA CCTATGAACA TCTGGACCAA CTGGGAGCG GCCAGCTTCA AAAAAGTGGC 360  
 50 ATTGGTCTGA GCGGCACAGG CTCTTGCCAG AAGGCTCTTG CCGGTACCG GTGGACCATA 420  
 CATCAGAGCA CCTTTCGGTG CCTAATACC CATATCCTTG AACTTGTCTG CCTGCTTCAT 480  
 55 GGGTAACAG ATTGCTTGA CTAGTTCTC GATCTGCTTG TCTAGCCAC CAACGTGGGA 540

GTATGTTTCC GTAGGCTTGT CATCCACTTC CATAGCTTTC ACTCTAGAGT CAAACTCOGA 600  
 5 AGGAAGCGTA TCCAAGATCA GGTACGAGTC CTTGTTTACA CCCACCAGGT OGTTCGGCTT 660  
 CAACTGCTTA AGGGTCCACT AGCCCAACCA TGGGAGAAA AACGGTTTGT CGGACGAAG 720  
 10 TTTCACA 727

## (2) INFORMATION FOR SEQ ID NO:601:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1411RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GATCAAATGC OCTTCCCTTT CAACAATTTC ACGTACTTTT TCACTCTCTT TTCAAAGTTC 60  
 35 TTTTCATCTT TCCATCACTG TACTTGTTCG CTATOGGTCT CTGGCCAATA TTAGCTTTA 120  
 GATGGAATTT ACCACCCACT TAGAAGTCCA TTCCCAAACA ACTCGACTCG TCGAAGAAG 180  
 40 CTTAGATGGC ACTAGCACC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCTGTTC 240  
 AAGGAACATA GACAGGGACT AGCAACCAAG GTACTTTCTT CAAATTACAA CTGGACGCC 300  
 45 GAAGGCGCCA GATTTCAAAT TTGAGCTTTT GCGCTTCAC TCGCGTTAC TAAGGCAATC 360  
 CCGGTGGTT TCTTTTCTC CGCTTATGA TATGCTTAAG TTCAGCGGT AATCCTACCT 420  
 50 GATTGAGGT CAACTTTGG GAATACTATT CGCTGGAAG GCTTGTGTG TGTACGTC 480  
 TTCAAGGCGC AGCTCCACTC CACGATCTGG TCGAAACCTA ATACGCAGTG TAGAACTAG 540  
 55

CTCAGACCGC AGTCCGGCGA AGTTCGGGCC ATGGCCAGCA TTTTCAAGTT AACCTTGICT 600  
 5 TACGACCGAG TATCACTCAT TACCAACCC GAGGGTTTGA GAAGGAAATG ACGCTCAAAC 660  
 AGGCATGCCC CTGGAATACC AGAGGACGCA ATGTGCGTTC AAAGATTGGA TGATTCAAGA 720

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1411UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GATCGTCAGA TACCTTAGTC TCTATACAGC GCAAGACATG GGTGATGGCG GGTITGTTCT 60  
 35 ATGCAAAGTC ATTGGGTTTC CCTCTGGCGG CGCATACAAC AACTGCCTAA OCTGAACAGT 120  
 CTCATCCTGG GCATCTAGCG ATCCCATGGG TGAGCAGCGG AGGATTTCGT GGATTACTAG 180  
 40 CCAATGGCAA TCCAAACCAA AGAAACCGAC TTGGGGGAAT GCTCATTTGA ATAGCCCGTG 240  
 TTTGACACT GTGATTCTCT GAGTGTAAAC TCCTCTTTGG TTGCCGATAT TAAACCTGTT 300  
 45 CTGTGAAACA TCGGAGCGGT GTTAGTGA AAGCAACTAG AGGAACTCAA AGAGTGCTAT 360  
 GGCATGGGGG CAGCTGTTGC GAAGGTGTAA AAACCCGAGC TCCGGTTGCG TTGACACAGA 420  
 50 AGTTACTTTC TGTATCTCTA TCAGTCTATC ACCGAAGGAC CGTGGTGTGC TTGCGCATT 480  
 TTGGGTTGT TCTTTAAGAT AGTTATCTGG TTGATCCTGC CAGTAGTCAT ATGCTTGICT 540  
 55 CAAAGATTAA GCCATGCATG TCTAAGTATA AGCAATTAT ACAGTGAAC TCCGAATGGC 600

TCATTAAATC AGTTATCGTT TATTTGATAG TTCTTTTACT ACATGGATAT CTGTGGTAAT 660

5 TCTAGAGCTA ATACATGCTT AAAATCTCAC CTTTGGGAAG AGATGTATTA TAGAATA 717

(2) INFORMATION FOR SEQ ID NO:603:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1412RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

30 GATCTGGAAC CAGGATGACT GTCTGGCAGT TAACTCGGCG GACCAGATTC GCTTCCTACA 60  
 CAACTTCTGC TCCGGTGGCC ACGGTATTTT CATCGGGTCT GTTGGCCACA AGAAGGGCGA 120  
 CTCAGTCACC AACTTCCTCG CACAGGACAA CCAGGTCTGC GAGTCGGACA ACGGTCTAAG 180  
 AATCAAGACT TTCGTGGGCG CCATTGGCAA GGTGACAAAC ATCAAGTTCA TCAACAACAA 240  
 GGTCAAGAAC ATCCGCAAGT TCGCTATCGT CATCCAGGCG GACTACAAGG ACGGCACCAC 300  
 CACCGGCACC CCAACCGGCG GCTGCCCAAT CACCAACCTA GAGGTCAGAG GCAACACCGG 360  
 TAACACCGTC GGCAAGGGCA GCAAGCTCAA GATTCTCGTC AAGAATGCGT CTAAGTGGAC 420  
 CTTGCGCGAC AACAACATTT TGGGCAAGAC CTTCCAGGC TGCTCTGGCG CACCTAACGG 480  
 CATCAAGTGC TAAGCGCCTT TTTTTTTTTT GGCTGGCGCT CGAAACTATT ACTATGAACA 540  
 TTGGCGTCCA CCGCCACTAC AAAAGCATCG GGTCTATCCC ATTATAACAT TAAATCTCA 600  
 GTTGATATTA TATTTTACAT TCGAATGTCC TTAGGGCTTT TTTATATTAT ATAAACTTTA 660

55

GATTAAAAAA ACGAGGTACA AGCAGATCAA CGAAGCTTTT CGGCCAGCCA

710

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1412UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GATCGAACGA GATAAACAGA GGTATTGGTT GTTATCACAA ACATATAATC CTGGGGATAC	60
AACGCTGTCA AACTCTGGGC CTTCTGCTTT GTGTCTAGAT TCCTTTTGCA GGCTTGAGAA	120
TAACTGTAC AATTTTTTGA TGTGGTTAGT AAGAGACCA TCAACGATAT CATGGCACAA	180
AGTTCGGTTT CTTTCCCTG CAAGCGGAA TGCGCCTTCA TTACTTCCG AATCTTCTCC	240
ATGAGTCGAT GGTCTGGCG TTGAAGCTTG TAGTGTCAA GGTCTATTG TTGGAGAAGG	300
TTCTATCTCT ATTTTTTGTC CCCAGAAAGA ATCATTGAC ATCCAATATC TTGTAACTTC	360
CCTGGGATGT AATCTTTGAA TAGCGGGTT TCGGTACAAG CTGCTAAGT CCAGATTATT	420
AATTAACGAT TCTTCTGGTC CGTGAAGGTG ACGTATAAGG TGGACGCTAT TGGGTTTCTT	480
TTCCAACATA GGTGTTCAT CAAATGAGAG GTAAAATGGT TCCTGCTGGG AACGGACGA	540
AGGCTCCTTT ACTTTAAGTC TTAACAAGG GTCAACATAT TCTTTTGA TGGTTCTAGA	600
AGTGGTTACA AAATCCATAT TCGGCTTAG ATCTGACTCC TGAACGCTT TGTCTAGTTT	660
CTCATCCCC AGTGGTAAAT CTGAACGAGG GACAAAGTAC ATGCAACTGT CCTCATCATT	720



GTAAGTCA

728

5

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: PAG1413RP

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GATCTGCTGG GAGTGACTCA GGAAGCTTTG TCAGTACCTG GAATGAAAAA ACAGTCTCTG 60

30

ACAGAGCGGG GAAGCTGGGC CTGATGGTGG TTACAGCGGA CCAGTTCAAA GAATATGAAC 120

AATTGAAGAC TGTACGCCCC AAGGATCAAC TTGCTCAGCA GGCGAAGGAG CTAGATATGG 180

35

TGCTAATTGA TGCTGCTGAA CTATACGAAT TAAGAAGCAA AGTTTCCGAT GGACTGTCTG 240

GOGATTTGAA CTCTGACTTT GTCTTGAGCA AGGAGATCAT TCTTGAGAAT GCTCATAGTT 300

40

ATGGTTTAAC GGTTCCTTCAA ACGGAAGAGT ATCTTCAATT ACAGAGTAGT TTGGAGAGAG 360

AACAGGTAAC GTCTACAAAC ATTGCGGAGA AAGCAACTAC AATTGGCTAC GTTGCACTTC 420

45

CAAGAACCGA GTACGATGAA CTTGTAGCTT CGCAAGCTTC TACGAAAGAA CAGAAATTTG 480

AGGTATACGC GCGGAAAAAT GGCAAGGTCA TAGTGATAA ATCTGACTAT CACGATTTGA 540

50

AGATCAAAGC TATCCAGTG ATTTCACCAT TGCTCAAAT GAGCAAAGAG CAGATGGTTG 600

AAAAGGCCAA GGAAGTTGGA ATGGTAGCTT TGCTCAATTG CGAGTATGAG AAGTTAAAGA 660

55

GCCCTATTTT CGATAACGCT TTGAATGCAA CAGCGAAGGG ACCGTGGAAA GGTGTGTTCTC 720

CTAAAGGAGA GT

732

5 (2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PAG1413UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GATCCAGTTT TAGGTCCACT TCAAACCTGGA TTTTCGGGTA CTCCCCGCAC ACCACCGTCA	60
AGTCATCGGC ATAGATGGAC TCAAGCACTT CCAGCTCTTG CTTTGTCTCC TCCTGATAGT	120
CCATACCTAT CCGCTCGACC AACTATGAGC CCACCGGCAG CTTAGGGCTA GACCGTTACA	180
GCTGCAGGTG ACCGTCCGGG GGACGATGGC CTATCGCTGG CGAAATTTT CCGCTATACC	240
ACCACTTATG TTACCCGGTC TATAGTGCTG CTCTCGACC TCACTGATGG TGCTGTCCCG	300
CGGGGACTGC TGCTCGTGC GGCCAAATCC CCACCGCTCT GAACGCTCGT TCCATCTGGC	360
TCACGGGTTG ACCGAACGGG AATTGCGCGC GCCGAGAAAT CTTGGCGAAC CATGCTGCAC	420
GTAGCCTTAC TGCCAAAATT AAGCCGTCAA ATGGCTGGCT ATCCTTCCAC GCACGCCCAT	480
AGTCACCTGA AGCTGGCTGG AACAGTGGTC ACCAGCTTT CTGACGCATA CCAGGAACAG	540
GTGGCCGAGC CCGAGGCCAA CCGTGGGTGA TTATGTCAGC GACTTTTGGT GGATTACGTA	600
AATCTGGGTG CATGCTGGC ACGACAGGC GCATGCGACC CCAAGACAAA CGTGCCACAC	660
CCATTCAATA TTAGAGGACT TTGCTGCACA CCCTAATCAT CCGTTGGGTT GTGAGATACG	720

C

721

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1414RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GATCCGTAAT CGAGTTTAGC TTCCGTGTG CATCATCGAC AGGTGAAAT GCTCGCTTGT	60
CGCCCGTCTG AAAACGAGTC AGATGTGCAG AGAGGCTGAA GTCCAACATT TTAACCACCG	120
CTGAAGACCG GGAATAGTAG GGCAACGTAG TTCCGCGAAC TTCAGTTTGT TTTTCTTTTA	180
ATTTAATGGA CTACACCAA AAAAGCTCAA CAACAGTCCC AATTAGTTCT GCTAGAAGAT	240
GCAACACGT TAGTGATCAG TAAGTATGTG TACTCGTGTA CTGTCCTGC ACTGCAAAGT	300
TCGCGTCACA ACTAGCTGTG AACCATGGTT TGAAAAAAAA TAATGATAAT GATTCCGCC	360
AGGATCGAAC TGGGGACGTT CTGCGTGTTA AGCAGATGCC ATAACCGACT AGACCACGGA	420
ACCACCTATA AGCCCTTAAT TATACTCAGA TACTAGTGAC CATTTTCTAG TCACATGATG	480
CTAGTTTCCT GAATAAAGA TGCACGTGAT TACCAAATCT GTATTTACTA GGTAAAATGC	540
CTTGGTGAAT AAGTACGTAG ATATTATATA TGTATACATA TGCATTTTAG ATGCAATAAA	600
AGCTCTATTA TGTATGCGCG CGGAGCTTTA AGCCAGTGTG TTTTCCGATT GTTTTGTGGA	660
TGCAATGGTC TTTGCATAAA AGCCTGACTT TCATCTTTTT CGTGCCTTGA TGTAACTTC	720

CAACTCTGA

729

## (2) INFORMATION FOR SEQ ID NO:608:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1414UP

## (x) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GATCTGGCCC	CGCGGGGGCA	CCGCGGCCAG	GGGCCAAAAA	GGAGAGGGCC	CGCGGTGGCG	60
GCCGCCACTG	CGCGGTTTC	ACAAGACATA	TATGTGGTA	TATAAGACCG	CGGTTGCGC	120
GTGGCTGCG	TGCAGAACCC	GCGTGGCG	CGCGGCAGA	GATTTCTAAT	ACTCTGGTT	180
TTCTTTTTC	AGCGCTGGT	ATATAAGTTC	GGCTGTGTC	GCGGGCGTC	GGCGCGTTC	240
GCCAGGGAGA	TAGGGGAGCA	TTCCGCAGCA	GCGTCTGTA	GCGGACCAG	TACGACAGG	300
ACGCAGGACA	CAAAGCAGC	GACGGCGAGT	GCGCGGATC	AGCAGCGCAC	AGCGAGCCAG	360
GGGTATAAGA	GCGCGGTAC	GAGCGGCTG	GTAGGTATAG	GCCAGATGG	AGGTGGGTGC	420
TAACGGGATT	TTTCTGCACC	AGAAGACTC	TGCGGAGACG	ATCAAGCTGG	AGATGTGCGC	480
TGTCGGCGGT	TGCGGGAGCG	CAGGCAGCGG	CATCGGATG	GGCAGCGCGG	ACGACGAGCT	540
GACGAAGTGC	ATCAGCGACC	TGAACATCTT	CGATCTGCTG	CACAACAACC	CGCGTGGAG	600
TTGCGACGAC	AACAAGGAGG	GTGGCGGGCG	GCGGGCTGC			639

## (2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1415RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GATCGTGGTT CTGTTATCGA AACGTTGGTT GCTAGAACAT TCGGCCAGGT TGAAAGTAGC	60
CAGAGCATGA TACGAATTCT GGGATTATCG GCTACATTAC CTAACTTCTT CGACGTGCGA	120
GACTTTTTTG GGGTTAACAG ACATGTGGGA ATGTTTTAAT TTGATCAATC GTTCGGTCCA	180
AAACCCCTTAG AACAGCAGCT GCTTGGTTGC AGAGGCAAGG CGGGCAGCAA ACAAGGAAGG	240
GAAAATATTG ATAAGGTTTC ATATGAAAAG CTTTATGAAC ATGTCTTAAA TGGCTCCCGAG	300
GTCATGGTTT TTGTGCACTC AAGGAAGGAT ACTGTGCGCA CTGCGCGGAA TTACATTTCT	360
TTTGCCCAAG CCAACCAACA GTCGATGTT TTCTAAGTA GCGATCAAAG CGTTACCAAG	420
TTTCCCGAG ACATCTCCAA ACATAAGGAT AGAGATATGA AGGAGCTCTT CCAACATGGG	480
TTTGGTATAC ATCATGCTGG TATGTCTCGA TCTGATAGAA ATCTAACAGA AAAGATGTTT	540
AAAGAGGGAG CTATTAATGT GCTTATCTGT ACAGCGACGC TGGCCTGGGG TGTGAACCTA	600
CCGGCTGATG TTGTCTTGAT AAAGGGAAGT CAGATATMTG ACTCTAAAAA AGGTGGTTTTT	660
ATAGATTTCG GGATCTGAT GTGATACA	688

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1415UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

20	GATCATCAGG AGTTCGTAC CTTGGAAACC AATTGGAAC CACAATTCCT TCTGAGCCTT	60
	TGGAAATTTG TCACACCAA CTTGAAACC GTCTTGTAA CTTTCATTAT GCGGAATGC	120
25	TACAAGTGTC AACTTATCAG GGTGATTG GTCTTAAAA TGTACCTTAT CCAGAACAGG	180
	AAGCATOGAG GCTTCACGTA TAACTTATC TTTCGGCGCT CCTTGAATGT TATGCACGG	240
30	GCACACTGAG CACAACGCAG CATAGCCCAT CCGAOTAGC TTCTCCAACG TCAGCATCTC	300
	GCCACTATAC TCATAGGGAA AGCCATCATC CCCGAATAAT TCGGGGTCTA AGCGTTGTAG	360
35	CGTAATTCOA GGCAAAGCAG TCACCGGGTT GTCTCATAC CATGTTCCCT GCTTAATGCA	420
	CTGCATGGCT TTAATCATAG TCATAACTGT OCTGAGGTAC CCAGATTGCG TTGCAATATC	480
40	GATATAGGCC TGTAAGAATAC GTAGCGCCTG GTCGAGAACT GAGATCGTAT CTTGGTAATA	540
	ATCTGCAATT GCTAAGTCAG CTCTACTTAG GTAAGCTTGT AAAAGCAAAA AGGCTTTGAC	600
45	ATGGGGGTCC CATATGGTA ACTCTGTTC TCTGTAAAA GTACTTTCAA CGGAATATCT	660
	AAGAGTTTCT GACATTTCAA CATTATGAT AGTCTGCCC CCC	703

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1416RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GATCATCATT ATTTCCTGCG TTCGTGCCGA CGATTGGAAG GCGGGGGTGG GTTTCCTTGAA	60
GGATTTTCAGG CGTATGAATG TTGCTCTCAC CAGAGCAAAG GCCAGTCTCT GGATCCTGGG	120
TCACCATAAA TCTTTATACA AGAACAAGCT ATGGATGCAT TTGATTTCAG ATGCGAAAGG	180
GCGTGACTGC CTCCAAATGG CATGTCCGGG CTTCTTGAT CCACGGAACA GAGCCGCCCA	240
GGATGCTCTT CATAGGTTCA AAAATCACCA TAATTATATC GAGAAOCAG ATGATTATGG	300
GCCTGAACCG GTGATGACTA AATCAAGAGG ACGCAATAGA TCATCCAGAA AACGCAAACA	360
TATGGAAGAT AATCCAGATG ATAACCTACGA TCCCGTTGCT GAATTCAAGA AGGAAAATCA	420
AAGAGAAAGC AACACAGGCA CCGGTGGTTA CCGTGCGGAT ACATCTAACC ACAGATTGGC	480
ACCTGCTAGG AACGATAGCA AGAAGGCCAA GACGTGCTCC AATGCCGCCG GTATTTCCGA	540
GGCTACTTCA GAGGATGGTG ATCGAGGTCA GAAAGGACAT GGAACCTAGA AGAAGTCTTC	600
CATATTCCGG AATTTTATGC CCCAGTTGA TGACCGGACC CCTGCTGCC ATGTGTACGA	660
CCCTAAGGAA CGCAAGCCCA AGAATGCTGC ATCCGCTTAA GCGGCTGGCC TTGGGAAC	718

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1416UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GATCTTGCCC GGCAAGACCA GGAAGTCGTT GTACGTCAAC CCGCCCCCGG TCTTGGAGTC	60
CATCAACTGC TCCACGGGAC AGCCCGTCTT TCTCGGGGTA CGTGGCCAGG TGCTCCAGTG	120
CCGTGGCTGC GTCTCTGTAA GTCAITGCGC TTTGTTCCGC GTGCTATGAA GAGAAGGAGT	180
CAACACTAAA CCCAAGCTCT CAAGTTGACC CATCCATCAA GTAAGTATCC CGAACAGACG	240
CCGTAAACC CAGCTGGGAT TTGGCGCATC TAGAAAACCT ATTATATCTG CAGCTCATCG	300
CTGCAAACTT TTCACGTAAA AGAAACGATG ATCCAGCGGG GCCCAAAAAG CAATGGGCGT	360
GCGCCGCACG ATGCGAGCCC TACCGCGGGC CAGCACCAGG TAGGAGCTGT CAGGGGCGTA	420
GAAAGCGCGC ACGCTAGACG GGCTCTCTGG GGGCGCGCGC AGGCGTCCGA CCGGCGCGTC	480
GCAGCAGCAG GCGTGCCAGG CGGAACAAAA GACCGACCAG CCAGCGCAGC AGTCTGTAGA	540
CGGCGCGGAG CAGGCGAACG GCCAGGAATA CAGTCCAGAG CACGGCGGAG AGCAGCAGGA	600
AGTTGAACAC GCGTCCATG CCCAGCGCGG CACAAACGGG AACAGCGCCA GCGCGCGCTC	660
GCAGAGCGGC TGCAGGAATG CGACGACGGA CAGGAACGGC AGGATAGGAC TA	712

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1417RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GATCCCCCTTG GCGTCGTGCT TGACCAGGTA GCGGCGCTGT AGCCCGAAGA AGCCGGACAT	60
CGGGTCTGAC GCGGTCTGTA GCGGACGGC CATCATGGC GCGCTACTGG AGATCAAGCG	120
COGGTACAGG GGCCAGTCTT TTTCGATTTC GACGCGGGC GCGTAGCGG TGCCAGCAC	180
GAACGGATGT GTGCGTAGTG AGTCCAGAAG CAGCGGTACG CTCTCTGGG GATGCTGCAG	240
GTCGCGTCC ATGCACACCA GGTACTGCG CTTCGCTCG TAGAAGCCT TGAGCACCGC	300
ACTGACAGC CCGGCTGCT CCGTGGCAC GATGATCCG ACGTTGTAG CCTGCTTGGC	360
CAGGCGCTCC ACCTCTTCCA CAGACCGTC CTGGGAGTTG TGTGACAA AGATCAGCTC	420
AGTCTTCTTG GAGTCCGGT TACCGAGGC GGCAACAGC CGGTGGCAA GGGCTTGAT	480
GTGGGCTT TCGTGGTAGG CCGGACGAC CACAGAGTCT CGATGCTCAT GCGCTGTA	540
TGTCCTTAA TGTAGTAGT AGCGAACGTC GGTAGCTGTT TCGCAATAA GTGAGGCTG	600
CGCGCTAAT GTCGTGCTT TATCGTGTCT TTTTGGTTCG TGTCAGGGG TTACCGGCC	660
ACCAGGCTAG ACAGCGAGC CCGCGGTGAG CAGCCACGA CCAAGAAGG CTGTA	715

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

# EP 0 866 129 A2

(A) ORGANISM: PAG1417UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

5			
10	GATCTGCGTA GGTAGTAGAT GAATTGAGGG TATAGGGAAA AGTTTGGTGC CAAGCGAAG	60	
	GAGCGGGGGT CGCCCTTGTT GTAGTCGGCG TACTTCTGGC AAAGCTTGAT CAAAGTTCTA	120	
15	TGATCCACC GGATGACGTC AGCGCCATCA TCGGAATCTG CCTTATCGAC TGCAACACGC	180	
	GCCATTAGTA CAGCAGCGGC CTCCTGGTCA AAGGAAGCAG CGATTGCGCG GTTACCGAAT	240	
20	GGCAACATCT GGTTAGCAAC TGTAGTCACT CTGACACGGT TGGTACCAGA TGCATGCTGG	300	
	TATGCAGTAA TGAATTGGGT GTATGCCAAT TTGCTCTGT CCCCCATGAG GCTGGCAGTT	360	
25	GCAGCGGTAT TTGCAATCTC GAAAAAGATA GCGTAAGAGT GGTGAGGGCT CAAGGACGCC	420	
	ATTTTCCATG TAGAAGTGCC CCAATACCG ATTTCTGAAT CGCTCACGTT CTGTGCATCA	480	
30	ACGTTAACCG GCGAAGCATG GCCAATCAGT CCTGCAGCT TTAGATCTGC ACTGGTTTTA	540	
	ATGCACATGG AAGCATTGAA CGCCATGGTT AGGTACCCCT CTCATCTTTA GAAAACAGTC	600	
35	TGATGAAAGA TTGCTTGAAG ATGGCGCTCG AGAATGCGTC AGTCAACAAC AAAACACCAC	660	
	CAGTGGAGTC GGTCAACTTC TTCATCTCAG ACATACAACC TGGTGTAGC ATCCA	715	

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1418RP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

5	GATCCGCGAG ATTCATCGTG GACCCGCCAC AGGCAATTAC TATAACAACA TCCTGGGGTG	60
	TTAAAGGACC TAACTCAGC TCAAGTATTT CAGGATGATA TCCTAGATGA AGAGCTGGC	120
10	CACACGCTGG TTCGGTTACA ATATTGCTCT CTTCGCCAAA ATTTAAACAT GTCTGTA	180
	CAGCGAGCTG GTCAAGCACA ACAGATTTTG TCCTGTATTT TTGGGGTAA CTCAGAGTAA	240
15	GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGGATTC ATCGAAACGT	300
	TCCTGCCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACCC CTCTGTTTCC ACTGCTACAA	360
20	CAGGGATAGA GTCTGCCAAA CCATGTTTCT CCAGCCCAT TACAATCCCA TTATATAACC	420
	CCCCGCCACC TACGCTGCAG ACGATACCTT TCACGCTCTC CAATTGCACG CCTTGGAGAT	480
25	GCAGTGCTTC TACTACTTCA TCTACCATTG TTGCATGCC TTCCAGATG AGTGGTTGT	540
	CGAATGGATG TGCATATATC GGAGCGACTT TTCTAAATT CACATTCCCC ATCAACTCGG	600
30	AACGTAAGTA GTCATCGCTC TCTTTCAATA CACTTCCCAT TGATATCACA TCTGCCCCCG	660
	TTGACCGTAT CGCTCTACC ATCCGCGCTC GAGTAGTTTC AGGCACTACC ACTGTGCAAG	720
35	GTATCCTA	728

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1418UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

5 GATCATCTGC GTGCGATACT GGCAAAAAT GAGAGACAGC ATGATGAAAA TATAGTTAAT 60  
 10 AAGATATTGC ATGATATAAG CACAGGCGGG TTTCGTCGAA GAGGAAAGGG TGCACTTGAT 120  
 CTGGAATGA GTGAAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA 180  
 15 CTTTGTAAAC AAAAGATATT GGAAAATGGT GATACTAGCA AGCTCGTATC TAACCCCAAG 240  
 TCATACGCTT TTTTTCAGAC GATGGTGGAC GATGTTACTG AAGCATCATT TGGAAATACA 300  
 20 TTTGATGCCA ATATAGATGA AAAACAGAT CCATCTGCTG CAGGTGGGAA AATTGTCATA 360  
 TCAGACAAT TTGTAAAGGA AACCCTGTCA TTCTGTGGA GCAAGAGTGG CGACTCAGAA 420  
 25 ATCCCTGCAG AACTAAATC TATTTTCATCC AGCACAGTTG AACGTGAAGA AATTCAAGAC 480  
 CTTCATACA TTGAAGCAAA ATAGTAACAT TAAACATTTG AAAGGAATCT AGAACTTCCT 540  
 30 GCTCAGATGG CTGAACTCAG CAGTGGAGAT GAAGGTGATT ACGGCTTTTC TTTAGATAGA 600  
 TCGCTCTGC GGCAAAAAGT TTAATAATGG AACTAACGTC GACGATAAGT TTAAAAGTGG 660  
 35 CACCAAGGCA GTGCGAATCT TAAAGGCAAT AAGACAATTG GCGGTCAAAA GCC 713

## (2) INFORMATION FOR SEQ ID NO:617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1419RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

5	GATCTGGGGA GTCTCATOGA AACGTATTGG ATGAGGCTTG GTGGTGGCAG GCGGCTCCTC	60
	GCTCGATTGG CGAGCTGGTG ATGACTTCGC ACTTCTCCGG GCCGGAAAAT TCGTGTGAGA	120
10	CAGTCGGCGT TGGCGTTGAA GCTGCCGCTG TTGCTGCACA CGTGGTGGCG CCTTAGCTG	180
	AATACGTAAC GCTGGCGCGG TGTCOCGGGC ATCCAGGTAT TCTTCGAGGC TTCTTCTTTC	240
15	GGCGATGTCT GAGATATCTG GAGCACCGCG AGCATTCTGA TACAGTGGC CCGAAGATGT	300
	TTGCTTCGGG GTGAAGTCTC CCTCAAACCC GTAGAAGTCA TCGGGGTATT CTCCATCCGG	360
20	CATTGTCAAT GTAGTAGTGG TCTCCACATA GGTACGGCA TTGATGTGCT TCACCGTCTG	420
	GCGAGTCAAG GTCCGTGTAC GGCCTGGAG GTCTTCGTT TCCGTGTCT TCACCGTTAT	480
25	CGTATTGACA GCTGCGACAG CAGGAGGGCC AAAGCCGTTG TTGCTCGCTA GCGAATGCG	540
	GCGTCGTTGC GAGCTCATAC TGTAAGTCCG CGGAGGGCCA CCGAGGTAGC TGGGCGAGC	600
30	AGCTCCTAGC GACCGCGTCC GCGGTACCC AGTCAGTGAC TGAGTCCGCC CCATCCCAAC	660
	CCTGGTCTT CGGAGTGACG CAACCGAGCG CGCCGCAGAC GACAAGCCGC TGCTGTGTGA	720
35	ATA	723

(2) INFORMATION FOR SEQ ID NO:618:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 721 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1419UP

55

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

5	GATCGGTCCG CGCCTGGTA CCCATAGGGG CGAGGTGGC GCGGCCCCG CAGGTCACTG	60
	CGCCCCAACC GCACCTGCAC CTGAACCGAG CCTGCAGCCC ACGAAGGAAC GCCACGCTAC	120
10	ATGTGCCCCG GCAGAGCACC GGCCTGTGCT TCGGGGCTG AAGTGA CTGT GGCACGCTCC	180
	GCAGGACATA TCTTTTAAAT GAGCTGTGTC ATGCGCACAT TCTCACCGTC GCGCTACCGT	240
15	AGCGTGGCCC TCTGTCAACG TGTGAGCTGC TGCCAAAACA AACAAATCGG GACGGGCCCC	300
	CATGCAGTAA TTACCTCCTC CGAAGGCAA CGCCTGGTT TGTTTTACGT TGGCCAGAGA	360
20	TTTTCTCTTT GGGGTGGATT AGCTACGCG TCATCCCGT GGCAGAGGTG CCTGCOCTGA	420
	CAGTTCCTCG AATATTAGAT GCTGGTATGC GGGCAAGCCT AGCGCAACCG ATTGTAGTTT	480
25	ATTGTTTCGT CACACCCGCG TAGAGGGCCG AGCTACAGGA TCGCCGATGT GCGGTGACCG	540
	ACAGCGTCAA CGTTACGATC TCAACGGTCG CTCGTGGGG CCGTCTGTG GTAGGCGTTG	600
30	AGATACGCTT AGGATGAAAG CACGAAAATT AAGTTGTGCG TAAAAACACA AAGTCAACTG	660
	GGGTTCGGA ATGGGTAGA GTGCCATGCT AATGGCGGAC GGAGAGTGT CATGGTGGGA	720
35	G	721

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1420RP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

5	GATCAATTCA AGGTTGCTTT CCCAGACATC TACGCTGTTT TCCAAAAGAT CGCTCAGCAG	60
	CACCCCGACT ACGAAGTGAC TGTCACGGGT CACTCACTGG GTGGCGGTTA TGCTTACTTG	120
10	ATGGGCTTGG AGCTCCAGCT ACTTGGCCAC AAGCCACATG TGATCACTA CGCCGGCCTG	180
	CGTATGGGTA ACGCTGACCT CAACAAATGG TACGACAAGG TGTTCGACAA CGTCAAGAAG	240
15	GTGAGGACT TGAAAAACGG CGGAAACCCA AGAAACGCTT ACATCCGTGT GGTTCAGAGC	300
	CGTGACATTG TTCCTATGGT TCCAACGGC CCTATCTACA CGCACGGGGG TATCCTATTT	360
20	ACCATCACTG ACGTGGACAG CGAAGTACCT CTACAATCGG GCGTCAGACT TGATGGCTGT	420
	AACACCAAGC TAAAGGAGTT GGTCGGCGAC ATCCTCTTCA GCGGGAAGTT GCTAAGCTTG	480
25	GTGGCTCTCC TGAACCACAA CAAATTTTTC AGAAGAATGG CTTTGGCATG CACTGATAAT	540
	TCCTTGAAGC TATAATTCCG AGGAAGTAAT GAATTTTAAG TACGGAACGT GCAGTCGCTG	600
30	CAGTCTTCTG CCTCTTCCTT ATGCCCTATA TAGTTAATTT GATGTTCTGT TCTATTTTTT	660
	TACATTTTCC AAACACTGGG AATGCCACCT TGTAGATGTT GTTCCCAAGA TGGATATTTA	720
35	G	721

(2) INFORMATION FOR SEQ ID NO:620:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 626 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
50	(ii) MOLECULE TYPE: DNA (genomic)
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1420UP

55

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

5	GATCCGTCGC GAGGCGGCGCA CCAAGCGCAA GTGCATGGTG GTTGTCGCCG GCGTGGAGGT	60
	CTTCGAGATT GACATGAAGA AGCTGGOGAA GACCTTCGCG TCCAAGTTCG CGACGGGTTG	120
10	CTCTGTGTCC AAGAAGCTCG AGAAGAAAGA GGAGGTCTGT GTTCAAGGCG ACATCGCGGA	180
	CGAGGTGAG GCGTACATCC ACGCGCTGCT AGAGGAGAAG GGGATGAAGG GTGTCAAGGT	240
15	CGAGCAGATA GACGCTGCCA AGAAGAAGAA GAAGACGCGG ACGACGACGA CGCGCGCGCC	300
	GTCGTGAAGA GCGGGTCCGG ACATGTGTAT CAGATTCGTA TGTAGTGATT AATGATTGCC	360
20	GCGATTTCOA GTGTCTTACC AGTCCAAGAG GACAGGTGTC TGGCATGCTT GCACATTGCT	420
	GGCGTCTCGG TGGGGACCAT GAGCCTGGAG ATGGATCTAA TTGAATGGGC GCTTAACCTG	480
25	CGTGCTGCGG GAGGCGGGGT ATTTGGCAGT GGCAGCGAGG AATTGGACAG AGTGCTAAAA	540
	CTGCACTACC GAGTGACATA CCATGCGTTT GACCGGGGCA CCAAGCGGTC GGTGTGGGAA	600
30	GTCTGCTGGC GGAGGCGGAG AAGATC	626

(2) INFORMATION FOR SEQ ID NO:621:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 582 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1421RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

55	GATCCCTCAG TTCCCATCT TGCTTCACA GCCAGGATGG ACCATCCGTA ACTGGGAGTT	60
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5 ATGOGGTTTC ATTTGTCITT TTAGTACAGT ATTATCTCTC TGGTTTTACA TCCTACTTGT 120  
 TTTATCGTTA CTTGGGTATG TATGGCATCT TAAATTTTAT CGACTCTAGT ATTTTATGA 180  
 CTGTGTAAAC TAATGAAAAA TAATGAATCG AAGTCTCGTT TACCTAGAGC TGATTATGCC 240  
 10 ACATGCGTAC TATOGGCGTG CCACCGCAAT TATGTATCTA TCCTACAGAT AATCCTTTCT 300  
 ATTAGCAGTT CTCACGAAAC GTCTCAGTTG CCACTCGAAG TCAGCATCCT TGTTCCTCAA 360  
 15 GGTGCCAGT GTCAGCTCGT AGAGCTTCAT TCGAACCGT GGTCCCACT CCGCCAATTC 420  
 AACTCATCT CTCGTCTGA CGTATACGTG CTGCGGCACA CTAATGAAAT CGCGCGGTT 480  
 20 CGCAAATGTG ATGACCTAG GGCTGTCITT CTTGACTCG GGGGGAACA TGTGCTTCAG 540  
 TATTTTACG ACCCGTGC CCAATGGAGT ATTGAAATTA TC 582

25 (2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1421UP

(vii) SEQUENCE DESCRIPTION: SEQ ID NO:622:

45 GATCATCATA CCGTGTCCAA CATCGCCAC GGAACCAACA GTCACTTGAA GTGGAACGCA 60  
 GGTAACATAC GCGATGGCCT CCAAGACGAC TTGGCCAGCT TCAAGGAGC AGTGTGCAC 120  
 50 TGTCTACGT TCCGAGCGG CCACTCCGC GACTACCGC ACCAGTGTG CATGTTCCG 180  
 AACGGTTCTG CTGGCAGTGC CAAGTCCGG TCGTGGTTCG GTGGGCGAC TCACTCGGC 240  
 55

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	GATGGACTAC TOGAGCGGG GCGCGAGGCC GGGCGGAGG CCGGTGCGA GGCCAGCTCG	300
5	TGTTTCCGCG GCGACAGCCG CACCGAGGAT TCGGGCCGGT CGTGGTTTGG GCGCGAGCCC	360
	CGCGACACCC GCGACACTCG CTCGGACCGC TGTGGTTTGG GCGCGAGCGC ACCGGAGGCC	420
10	CGCAOOGACG GCACCTGGCT CAACGGAGAG CCGGACCGCT CGTGGTTCCG TCGCGAGAAA	480
	CACGCCACCC TCGACGAGTC CGACCGTGTC TTCCGGAATG GCGGCCGTCT CCGGTGCGAC	540
15	ACCACGGCGT AGGCGCCGAC GCGCGCGCA AGGTGACGA CATCAAGCAG GCAGGTGCAG	600
	ACCTGGGCGG CTCGCGCGAG GCGAAGGTG ACGACTTCAA GCAGGCCGCG GCTGACCTCG	660
20	GTCGCTCTGC CCAGGACCGC CTCAGCGCG GGTGTGCGA CGCCAAGCAG ACGCTCTCAG	720
	GCGCGGCTC CACCGTCTCC GCGCGCGCG CCTCCGCTGC TGGCGCTCT CCGGACGCCG	780
25	CCTCGTCCGC CGCGACAAG ACCCAGTCCC TCTTCAACTG GGGCTACAAC AAGGCCGAAA	840
	AGTGAAGGC CATCGCCATC GCGAGTAGC ACAAGGCCAA CAAGGACTAC CAGCAGGCCC	900
30	TCGACGCCTA CAACCGCTCC AAGCGCTGC TCGCGACCG CGACCGCAC CTTCGCACCG	960
	GCCTCGAGAG CGCCAGGCC CAGCTCGTG ACTGTGCGA CAAGCTCGAC GGCATCTCCG	1020
35	CGGAGTTTGA CCACTACGCC CGCGAGAACA TCTCGACAT CTNCCGGGN CTGGACCAAG	1080
	AGGACCGCGA TTCCGCGCT TCGGCGCTCT TTAGCTGGTT CGCTTCAAG GCGCGCTGT	1140
40	CGAAATCGAC CT	1152

(2) INFORMATION FOR SEQ ID NO:623:

- |    |                                   |
|----|-----------------------------------|
| 45 | (i) SEQUENCE CHARACTERISTICS:     |
|    | (A) LENGTH: 713 base pairs        |
|    | (B) TYPE: nucleic acid            |
|    | (C) STRANDEDNESS: single          |
| 50 | (D) TOPOLOGY: linear              |
|    | (ii) MOLECULE TYPE: DNA (genomic) |
| 55 | (vi) ORIGINAL SOURCE:             |

(A) ORGANISM: PAG1422RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

10 GATCCGTGTC CTGGGGCTGG TCGAGAACAT GAGCGGCTTT GTGTGCCCAT CGTGGGAAAA 60  
 CGAGTGGACC ATCTTCAAGC CAACAACAGG TGGTGGTGGC GCCTTGTGGC AGGAGCTGGG 120  
 15 GATAAAGTTC CTTGGAGCGG TCGCGATTGA TCCGCGAATT GGAAGATGCT GCGACTCTGG 180  
 CGAAAGCTTT TTGGACGGCT ATCCGGACAG TCCAGGCTCG ACGGCCATCA TGCATGTGGT 240  
 20 AGAGGCTCTC CGTGACGGCG TCGGCGACGT ATAACGGGCC TAGCAGTTCC TGCCAGTGAC 300  
 AGACTGATAC CAGTTTATAC ATACATACAT ATTTGTAAAA AAGACGCTTA GTGTTACGTG 360  
 25 GATGCGAGCG CCGGTTTCAG GTAGATAGTT TCGGCTGTC CCAGCGGCAA TGCAAGTAAT 420  
 CTGTCTTTAA AAGACGGGGT CTCCAACGCT TGTCGATAAT TCTCAAGGAT GATATGACAG 480  
 30 ACAAGTTTGG ACATGACACA GCAAACGACG GAGAGTTCTC GGTGGGAGCC GAAATCCGTG 540  
 GCCAGGACCG GCAGAACCCG GACCAGATCG GAAAGCAGCT CTGGGTGTG GTGTGTGTCA 600  
 35 AGTGCTATCT GGAGGTACTT CTCAAATACC CCCAGGCGGT GAGTCCAAGT TTCCATCTGT 660  
 TGTGCGGGGA AAGTCTCCAA TAATTGACGC AGTGTCTGCA AGTTAGCAGC TGA 713

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(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 642 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1422UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

5	GATCTCTAG GCGCCAAGTC GACGACTACA GCGGGGCTTT TTGGGCCAAA GACGGAACAG	60
	AAGCCCGCAG GCGGCTTTT CGGACAGAGT AGTGCGGCTC CCAATGGCAC TGGCGGGGT	120
10	GGTCTCTCG CTAGCACGGG CAACAGGGC AGCACCCAAT TGGTGGGCT GTTCGGCAAC	180
	AGTCTGCGG GCGGTGGTGG GAGTCTTTT GCGCGGCT CGGCGGGAA CAACAACGA	240
15	TCCACCTCGT TGGGAAATCT CTTTGGGAAA CCTAATGACA CGCACCGG AGCTGGTGA	300
	GGTCTTTTCA GCAATCGGC GAACACAGCC ACCACAAATA CGTTTCTTC CACTAACAGT	360
20	CTTTTAGCA ATAATCAGG AAATGGTGG CAGAATAATG GGGGCTCTT TGGTGGGAA	420
	CCTACCGGG GGTCTTTGG AACACGACC GTCAGGCAC AGTCTCGCT TTTTGGAGCT	480
25	TCCTCTCAC AGAATAATCA GCAGCAGCAG CAGCAAACAC AGCAACTGTC CCTTCTGGT	540
	TCCAATCCAT ATGGCTGAA TCTGACTGGT GTTCTGTGA CTACCATGCC GGAATCTATA	600
30	ACGGCAGCAA TTACGTCTAA GAAGAAGAG AAGCTACCG CT	642

(2) INFORMATION FOR SEQ ID NO:625:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 719 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1423RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

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15  
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GATCGAACAC AAATTCATCT ACGAACACAA ACTTGGAGCG GTTCGTGTTG GTTATATTGG 60  
ACAGGAACAT TGACCTACCT TCAATGTTTG CGCATTCGTG GATCTACCAA TGTTTAGTAT 120  
TTGACGTATT CAATCTCTCC AGAAATACGA TTTCAGTACC GAATACTGAT GAAAAGGGAC 180  
AACCACATA TAAGAAGATG GATATTGAGC CTAAAGACTT CTTTGGGACG ACAAATGCGC 240  
ACTTGCCGTT CCCAGACGCA GTGGAGAATG TCGAAATGC ATTGGCAGAC TATAAGGCCG 300  
AGGCGGAAGC GATAACCAGG AAGACAGGCG TTGACAATAT AGGCGATTTA GATCCTAACT 360  
CTCAAAATGA TACTTTGCAA ATTACAGGAGG CAGTGAACAA GTTCCCGGAA CTGACTGCTA 420  
GGAAGAATAT CATTGATACA CATATGAATG TTCTGGCTGC GTTGTGTAAA GAGCTAGAAA 480  
ATAAAGGGTT GGATTGCTC TTTGAAATGG AGCAACAAAG TGACTCTGCT AAGGTGAGGC 540  
AAGCATTCAT GGACGTTTTG AAAGATGGCA AGACCAATAA CCTCAAGGAC AAGTTAAGGA 600  
CATACATAAT CATCTATTG ACTAGTTCGG AGAAGCTTCC CGATCAATTC GTCCAACATG 660  
TTGAGAGTTA CTTCCAAGAT AATAATTTGG AAAAGCCAGC GTTGAAGTAC TCTATAAGT 719

(2) INFORMATION FOR SEQ ID NO:626:

35  
40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 719 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1423UP

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

55

GATCATCTCG TTGAACTGCA TGCTCATGTC GTCOGATGAG TACACATGAT TGAAGTCAAA 60

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CAAAATGTTTG CCGACTTGA CCTTGCCGOC ACGCAAAGTC GCAAACAATC CGTCGCTGGA 120

5 CCGAAAGTCT GGGATGCCTG CAGCCACAGA GATCCCCGCA CCGTGACCA CCACGATGTC 180

CGGACTGTGC TGGAGCGCAT ACGAATGAA GTGGGGTCC CGGGCGCTCA CCAGCTCCGG 240

10 GTCACTGACG TAATGCGCTA GCTGAAATAC CGAGTTCGTC GCAGGCTGT AGTCAGCCG 300

CGGCTTCCTC CGCACCGGAG CCGGGCGCTT GCGCAGGOC GGTAACAGCT CCTTCGGTGT 360

15 GACCTCCTCG GACACGCTCG GCGGCTGTC GCAGGCTCT GTCTGCTTCT TTTTGACGCT 420

CGACGGGGC GTGATCGCA GCTTCACCTT CATCGGOGAC CGGTACCGCT TCACACCGAT 480

20 ACCACCACTA GCTCCGTC TCCGCACTG TCACAAACC TCTGCGCTT GCTGCACTG 540

TGGTTGCCCC GCTGCGTGGC GTGTAGCGA CATGAAATGA GTGACGGCGG GCCCAATTTT 600

25 GCGGGGCTC GCTTTCGACC AATCCGAAA ACTTATCCCC CGTAAAACAA AGGCAGGACT 660

TCCGGTGTGG CGATAGCGC TTTGTGCGA TGGGCTCTG GTCCCGTTAC GCCTACATT 719

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1424RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GATCTCATCT GTATTTGGAA GGAACGCAC CAGACGGGG TGACTGCAG AAGCTGCCAG 60

AGGAGAGAGA AAACATAGAA AATATATTTA TATTATCTAT ATTCAGTTTA CATAAGAATG 120

TGTCATAATT TTATTGTTTT TAGATTTTGA CTTCGAGTG CCTGCATAT GACTATCCTT 180  
 5 TTATTCTAGA TTCAGTGCTA GCTAGTCGCA AGGAAATCGA TATCGTAAAT CCCATTTAGA 240  
 ACAAGATACA AATTAGCGAA TTTCOCGGAA AAACCGTCT TATAATACAG CATCATTGCC 300  
 10 GAATCCATAC CAGTCCTTCA ATTAAACTTC CGAATCAAAA AAGGCCCGGC GCGTCTCAA 360  
 GAATCTTTTC GCCAGTACTC GAATGGTGAC TATCAGCAAG CGACTCTTCA CTACCCGAAA 420  
 15 CGACCAGTAT ATTTGTGTGC AGCAAATGAT TTAAGGCTCT CGAGACACCT CTTATTGGOG 480  
 TCCTATGTGT TCTGTGCAGC CCTGGCCCC GATAAGAAT GCAGGTGOC TAATAGTAAT 540  
 20 TACTAACCGT TTTTAAATC GCGTCTTGG TTGAGACCTG TGAAACGATA ATCCCATTTA 600  
 TACCAGATGA ACTCGCCGCA CTATAGTGTG CGTAATTCAG CACTGTGGAT TCCGAGTTAG 660  
 25 GGTCCGCGAA GTAGCAAATT TGTTATCCT CCATAATAAG GATATCCAAT GCCAGTATAA 720  
 TAGT 724

## (2) INFORMATION FOR SEQ ID NO:628:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1424UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GATCATCGTA TGCACTCAGT TGTATTCTAG CATAGCCCGT GCGATTGCGG TGATTTCGAA 60  
 55 CGATGATGAC AGGCAAATCA CCATGAGGAG CCGAGGATTC TCCGCTAAAT TCAGCTGCAT 120

TTGCAACAAA GATGGOGTGT TTCTATGOGA GCUUCTTCAC ACGGGGTAA AACATGTTGG 180  
 5 AAATGCTGCT CGCTCTGCCT TGGCTGGGT GTGCCCTCAG CCAGACGGTC TGTTTGCTTC 240  
 TAATGTGGGG GAGAGTCGTT CTA CTCAAGT GTTCAGCGTG CTGAATAACT TGCTATCCT 300  
 10 TACAGCTGCT GACCTGAGGC AATGCACGTT TCCAAGTCCA ATAGTCTACG GGCCCGAAGG 360  
 TTGTGCGGAA TGCACAGTGA TGGTAATCT ATTACTACAG CCCACTGCAA GCGTACAGAC 420  
 15 AACCTACAAT GACGGGCGGT TGTACAATAA AATCAATTCC GCTTGCTCGA CCGTTAACC 480  
 AAAGCTATAC CGTACCTTGT GTCCCTCCCT GTTCCATTA GCGTTGCAT GTGCTTTTTT 540  
 20 ACTGTGATTA CAGAGCCTTT CTGTAGAATG GTTACGTGAA TTAAATACTA GAGAGCTATA 600  
 AAGCTCTCTT GTTCTGTAA TGTCTGTTTC AGAAGATAAA AGGTAACACC AGAAAACGAG 660  
 25 GTACGACCCA ACGCTATTG GACTACGAAC TGGACAAAAA CTAAGAGTCG TAAGTAAGAA 720

## (2) INFORMATION FOR SEQ ID NO:629:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

40

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: PAG1425RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

50 GATCAGCTCC CACTTGGTTG CAACAGTATT GCTGAGACTA TCATTCTTGT AGAGCGATTC 60  
 TTGTGAAGCA GTTGGCCCGG TGTATGAAAC CGCGTGTTTA CCAAGTGGAG GCCTTTGTTT 120  
 55 AGAAATTTTA GTTCCTTCTC GAACGTATTC GTGGTCTCG AGAATAAAGT TTTGTGCTC 180



GACATAGTCA GGGTCAAAAA CATTCACAGG TGTCATCA TATGGGGGOC GGCTGCCGGA 240  
 5 GGTGTGTTGA TCAGCCTTTC TGTTGGCTTC CGAGTCTCCA ACCITCGAGA TAGCTTTTGA 300  
 TAAGTTGTAG AAGTCGTCCA AAATATCGTC TTCGCCGAGA GGAGCAACGC TOGAGCCCTT 360  
 10 GAACAGTGAT CCACTAGAAC TTCTTGCACT AGCCTCGCCG TCAGCATTAT TGCTATTGTG 420  
 TGTACTGCTC GAGTTGGCA GATTAGATAT ATCAAACTGT TTCGATTGTG TGGAACTTT 480  
 15 ATATTCATCA TATGCTCCAA AAGAATCTCT GCTTTGGGGA GAGCCTCGCG CTGCATGAGG 540  
 AGGAGGAGCC ATAAAAGATG AATCCCTGCC AGGAGAGTTG TGTAACCGOC CAAATGGTGA 600  
 20 TGCAGCGTAG TTGTCATAAA TTGAACCAG ATCTGCAAGC GACTTGTACA GGTCCCTGGG 660  
 GTTGTATCCT GCCTTGGGGT CGCCAACTTC TTAAATGGAC CGAAGAAGC 710

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1425UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GATCATAAC GCGCTGGGCA TACAGTTGGC CAGCAACAGC ACCCGCGACA GCTTCCAACG 60  
 50 GCTAGAGACG GACACCGCAG GCCTTGTGTC CCAAGACCTT TCCCGCTGGG CCGACAGCAC 120  
 CAATGCATAC ATAAACGGCA CAGAGGCTTC CGTAAATGCC GGCCTCCTCG GCTGGGTTAC 180  
 55 CACAGCCACT ACAGCCCTCA ATACCACCGT CGCCGCCCTG CTGGCGGACA TCGATTCCAC 240

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CGTCGACCGC GCGTTGCGAG ACACGCCACT TCACCGCCCC ATGGTGACCG TTGTCTCCTG 300

5 TGTAATCGGG AACAAAGTTGC GCGCCATCGA GGCAGGCGTC ACCTGGACCC ACGACCACGT 360

ACGCATCGGC CTGCCGCGCA TCCATACCGC CCGCCTTCGC GACGCTGTGG CAGAACCAGA 420

10 CCTTCCAACC CATCCCGCCT ACACAGCGGT GCTCCAGTCC CTCAGTGACC GCTTACGTCA 480

TTCCGTTGAC CGTGTGCTAC ATCAGTGCTG TCGCGGGTTC CGCATTGAAC TCTACGTATC 540

15 GCTTGCGCTG CTGCGCCTCT GGATTTCTGA GACACCTCTC GGCTTGGCAA TGCTGCTATT 600

CAAGTCGCAC TCGCGTCGCA GGAACCTGGG CCGCAGAATG CTTTGAAGCT AATTCTTACA 660

20 TAATCTTAAT TCGCCATTCT GCTGCTCGAA CACGAAGTCC GCGTTAGCGG G 711

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1426RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GATCTTCTCT CCGCTCGAGC TCACTGGCGG CATGCAAGAC GCCATGAAGT GCTGCTGCCG 60

45 CTCCTGATCG CCTCGTGA CTGCTAGCGG CGACTGGCCC TCCAGAAACC GCGCCATCTT 120

GTTCGCATCC TGCAGCAGCA CCACCACATG CGGAACCAAC GGCTGCGCTG CTGCTTTGCG 180

TAGCTGAAAC GAAAGAAGAC GCGCTATAGG CCGCTGCGCT AGCATATACA CCCACGGGAC 240

55 ACCCATAAAC GCGCTTCTAA CCTCAACCG AGTCACTGAG AACTGGCGTA GTGCGCATCA 300

# EP 0 866 129 A2

TCGAAGCTCGC GATTTTTCAT TCTAGTGAAT AATCCTTACA CCGCCAACAC AAAGGCAGCT 360  
 5 TCACCACCAT TCTGGCTCAA CTAGGAGGCG TGTOGGGCGA ACCAGGAACG CGTTACTCGG 420  
 TAAGGGGGCA TCTAGTCAAG TGGGCACTTG CAGGCGACTT CTTTTTGTGT GTTATTCAGG 480  
 10 GTGTAGGATG CTTGTTATAG GGTGACAGG AGGTATTGCA TGCGGCAAGT CGACGGTGTC 540  
 GCGGAGACTG CACGAGCGAT ACGGATCCC GGTGATCGAT GCGGATGCGA TTGCGCCGGA 600  
 15 GATTATGCGG CCGGGGGAGC GGGCGTACCA CCGGTGGTGS AACGGTTTGA GCAACGGGTG 660  
 CCGCAACTGG TGCAGGCGAA CCGGGAGCTG AACCGCGCGG CGCTGGGGGC GTGGATCTTC 720  
 20 CA 722

## (2) INFORMATION FOR SEQ ID NO:632:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1426UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

45 GATCTGCTOC AGCGCCTGCT TGAACCAATC TCCAGAAGAG TGTCCGCTC GTCAAGAACC 60  
 TTGAAGTCAA CCTCGGTAAA GTACTTTTGA CCGCAAGCCT CGAGCATGTC GATCAACCGG 120  
 50 CCGGGCGTGG CAACCACGAT ATTGGGCTC CTGCGCTCTA GGGATCTGAA AGTTTCAGTC 180  
 CCGGAGGAGC CGCCCATCAT GACAACGCA TTGAAACGGC GAAGCTTCCT GTTGGCGTTG 240  
 55 CGCATCTCGT TGATCTCGTT GAAGATCTGC GGGGCAAGT CCTTGGTTGG TGCAATCACA 300

ACAGCCTTGA CATTTTCCGA AGGAGGCCCC TCCAAGAGCC GCTGGAACAG CGGCATCAGA 360  
 AACGCAAGTG TCTTACCTGT TCCAGTTTTC GCGCGTGCCA CCACATCGTG CTCGGTCTGC 420  
 AGGATCGGCT TCAGCGTCTT CTGCTGCACC GGTGTTAGTT TATCGAAGCC GCGTGACTGC 480  
 AGCATCTCGT ACAGCTCGTT GCTGAGCAGC CCTCCTCCA CCAAGGTCCG CGGTGTGCTT 540  
 TCGACCCCCG CAGCTTGGTC GGCCACAGCC ACCACCTGGG TGTGCGGCC GAGGCTGAAT 600  
 CCTCGCGCG CCGCGCGCTC TGTACGGCCG CGTCTGCOCT GTGGCTTCGG CCACATGCCG 660  
 CCGCGGGGAC CAGGCTCACC ATCCTCCCTG TCGCTGCCCG GCT 703

## (2) INFORMATION FOR SEQ ID NO:633:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1427RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GATCTTTCTA TCGGGGAAAG AGTCCATCGA ATACAAGGTG CTTCTAGAAG GCGCCTATGG 60  
 AAACACCATT CCGCGGCTTG CTGCTCCTGA CCGCGCTAC GTGGGCGCCA GCGCAGGTCT 120  
 TGGCGTAGCA GCGGTCTACC CACACTTCGT CTCCTGTGTTG GACAAGGAAA GCCAGTTCAC 180  
 CCATTCATT CACTGGATTA TAAATGACCT TTCATATCTG CATTGGTTTTT CGCATGAGCT 240  
 GAGGTACCTG GCGGACCGGA ACTGCGACAT CAAAATTATT TACACGAGGA GCAATGAGTC 300  
 GGCTAAAGAA CTGACCCAG ATGTTGCCGA TTCCGCTCTT GCGAAGTTCG TGGATTGCT 360

GGATATCTGC AGGCTCCTCC TGGGCCCAAG TCTCAAAGAG ATCGTGAAG AGCAGATCCT 420  
 5 GCTCTCGTCT AACCAGGCAC AGGACGTCAC GTTTATTAGC AGCGGOCCTT CGAOCCTTAA 480  
 TGACCATTTT CGCTATGCTG TGAAATCTAG CATCACGGGC AACTCCAGT GTGATGTGGA 540  
 10 OCTAGAGGAG GAAAGCTACA CCGGTAGAT AGATACCATC TTATTAGTGA ATTGTACTTA 600  
 TTTATCTCTC TTCTGTATC TTAAGCAAAT CCGGCCATGT CTCAACCAGC TTCTGCATGC 660  
 15 TTGCGGATT GAGCCCTGCC TCGACCACTT CCAGAGGTAC CTGGTTTTC G 711

## (2) INFORMATION FOR SEQ ID NO:634:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1427UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GATCATCTTG TCCATGCCCT TGGGGCCCAG CGACGTTCTG ATCGCATCCG CGACTGCTCT 60  
 40 GGCAGCAATA ATGTTGCCCT TTCTCACTTC CTGGGGCTTC TCGGGTTTTT TGAACGTCCG 120  
 ATTGCTGGCA CTGACCTTGG GTGGCATCTT AATATACTTC CTGATTCGGC GCCCCAGAAG 180  
 45 CCTTACTTGC TGCTAGAGAA GTTAAGGTTG TTTGTTTATG CTGACAACGC CTAAGTTACC 240  
 GTCAAACGAT CAGATTTTTG CCACTGGAAT TTCCCTTGTG ACAAACGGAT ACTTGATCCT 300  
 50 TTGATCTCCA AGAGCTGTTT CATCGGGATG GCGTCTGAG TAGTCCCGGG TTGAAGGGAA 360  
 AATCGGGCT CGACAACCTG GGAAATGTCT ACGGAGGACG CGCGTTAAC AGGGATCCGG 420  
 55

GTGACGGCAG AGCTCAAAAA AAAATGCGCG TTTTCCAGCT GGTATGAGGC GTTCAAGGGC 480  
 5 CAACTCCGC GGGCCGAGGT GATTCCGCCG CTGCCCGAGG AGTTGTGAG CTACGTGGAT 540  
 CAGCGCGGGA TCAGGCTGGC GCGCAAGAA GGCTCGAAGT ATTTCTACCG CCAGGAATGG 600  
 10 AGOCTACGAC GGACGGAGAG TACAGCGACT GGGAAGGCGG CGACAGCGCG AGTGAGCGGT 660  
 CGTTGTGCC GCTGGACCGG TGGCGGACTT CCGGAAGTG CACGCGCGGG TGAAGCAG 718

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1428RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GATCATACAC GCATTGCAGG TATACATTAT AGTGCTCATA ATTATCGGAT TGCAAATAGA 60  
 40 ATGGGGCCCT TACCGTAGTA CTGTCTTGGT AATGCAGCGA CGCTCAGGCT TAAGAAGCTT 120  
 TTGTCTTCC GTGTATTACT AACAAAATAA TTTCTCGAG CACAGGGAGT AGAGATGAAT 180  
 45 TACATAATCC ATATGGACAC CTGTCACCT TCCAGCGACA TTAACATTTC CTTATGAATG 240  
 CCCAATAATG GTGCCTAAAT GATGTGCTTG GTGTAATGCG CATTATAAAA TGTATGTGGA 300  
 50 TTATATATTG TTGTAGCAT CTAGTAGAAC CATGCTAGCG AGGTCTTTGG CCATACCCCTT 360  
 CTGAAGAGAG ACATAGCAAC AGTGTCTTGT GCAGACAGTC TGCCGTGAA TGTGCTTG 420  
 55 AAGTAACCAT GAGTACCAAG ACTCTCCTTA ATGAAGCCAG AGCGTCCAGA TTTCGTGAAT 480

AGTGGGATCG ACTTGAACCA CTCGACATCT TCTGGCCTAA AGAACATATA GGGCACTGTG 540  
 5 ACGACGGCT TGTGGAACCT GAATGGATGG CCAGTTAATA TGATTCTCTT GGCCAATATC 600  
 CGTGTGTGGT CTGGGTTTCT GAAAGTGGCG TGGCCACGA ACGTCAGGCG CTTTGGATCA 660  
 10 GAGGGGTTTT CTTTGAAGTA GATGGCCGGT GACTGGGTCA GGTCCAAGGG AAGCATGCAT 720  
 GTC 723

15 (2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: PAG1428UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

35 GATCAAACCA GAGTGGAAG CGCACACGG GCACTGGCG GAGCCCTTAC CGTAGTTTCT 60  
 TGGGTGGGAG AACCAAAGT TTTGTGAGC CATCTTGCT GCAATGGGT AGTACTCTGT 120  
 40 CTGACCGCTT GGAAGCGCTC CGGCCCTGCT GAGCTGCCA CAGCTGGC GTCTGCGCG 180  
 TTCTCATTGC CGCACCGTA TTCTGCTGC ACGACAGCT CTAGACCACA CTTGGCCCA 240  
 45 TTCTGTGCAC ATACGATTAT GCTTTGCTC TTGSTATAT CCTTAGATT GCTAGACTTC 300  
 GACACTATGG TTATCACCAC TGTGAAGTC TGCTTCGGT GGCACCCAA GTCTGGGAC 360  
 50 TGTAGTTGGA AAGCGAGTT CGGGCAAAT CAAGCATCTC ATAATGTGTG GTTCAACCG 420  
 TTGAATGTGT GGTGCAACA GTCAATTGTA ATTCTTTTT TTGATGAGA GATGGATGC 480  
 55

GATGAGCTAG TTGAAAAATT TTAGTATGGC AAAACTGGCA TGCATATCTG AGATGGGCCA 540  
 5 TCAATTGCGG CAGCTTAGTG TTAGACGACC AATCCAGAGG TGGTAATTGG GCTATGGCAG 600  
 GTCACCTGCA CAGGTGCTCG GTAAAAAAGG GCCACAAAAC GTTCAAGTGG AAGCATGCCA 660  
 10 GCAAGGGGCG GTTGAAACGG CTGCACAAGG GCAAAGTGGG ACAGGAGACC GCTGCTGGGG 720  
 TGAAGG 726

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1429RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GATCAAAGTT TAGCATGTAA ATGTGCAACA AACTATTTAT TACCTCTGCA CTGCCCATGT 60  
 40 CGCTTGAAAC CGCGAGGAT CCAAACCACT GCTTTCATAA TGGAAITGCA AAATTGAGTG 120  
 CAGTAATIGA TAAGTATCTT GAGAAAAGCC CTCGCGACTT TACCTAGAT GATTGCTTAA 180  
 45 TATGTTCAAA AGCCTCCGAG TTAATAAAAA GGCTTGCTAC ATCCAAGGTG CATATAGATG 240  
 TGATAGATGA GACTAACAGC ACCATTCATA AAAAGCGGAA GCGCAATTTT CGAATCACAT 300  
 50 CACCCAGAGC AGTATACACA TCATTITGA ATGTGCTATT AAGAAAGTTG GATAGCGTTG 360  
 TCGACCAAGG AAAGGTAGAA ACGTCCAAT CCTTTGATCA GATACITGAG AATTTCTTAA 420  
 55 TTAAGTIGAA AGAAGTGCAC TTTACTCTAT CTGGGGTTGC TCTGATGTAT AGCACTATTG 480



ACTACTGGAA CCCCCACATG ATCCCAGGCT ACGGCAAAGT TAOGACTGTA GAGCATTTCC 540  
 5 TGGTGCAGTA TATCTTACAT CGATATGAGG TATTATATGT GCGCGGCGAT GAAAGCCTAC 600  
 TAGATAGTCT GGTGGTGCC ACTATTGGGA AGCTATTTGA ATGCATGCAG TCACAGCATG 660  
 10 ACCACCAGAG CCTGGTAGCG AATAGCCAGG CTGATACCGC ACGAAGAGAT AT 712

## (2) INFORMATION FOR SEQ ID NO:638:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1429UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GATCAACCGA TAGCGGAAGG CGGACGAGCC TCGGAAATAG TACTAGGCAG TGGTGGCTT 60  
 TTGTTTTITAG CTGTGTTTCA AGATGTCAGC GAGAACAAGC AGGGAGGCAG GCGCCTCCAG 120  
 40 GGTGATGGGA GGTCCGAGTA GTATGGATGG AAAGTCCGGG ACAGGAACAG GGTATTTGGA 180  
 ACAGCTGAAC TCGCCAAGCA TTCAGAAGCT CATGCACTCG GACGCTTCCA CGACAGCACT 240  
 45 ATTGGAGAGG TTGAAGATGT CCTAGTGAC TTGGGTGGAG TTCACGAAGT TCATAAGAAA 300  
 GAAATACTTG CTAGAAGAGG GCCATGCGCA GGAGATGGGC AAGGCTTATA AGAACTTCTT 360  
 50 TCCGAGGGC GGTGAGTGCA GCTTGCAGAA TAGCATACAT AAGGTTTTGG AGTATGACGG 420  
 AAAACTTGCG CAGGTGAAAC TTTCATATGT TGCTGGGTTG CAGAAGATGT ACGATGAGTT 480  
 55 AACGTGGCTT CTTGCATCCA TGAATAAAT GCGCAAATCC CTCAGGAGA GCAGTCGGCG 540

GTTGAAAAA GAAGTCGCAG ATGCTATACA TAGCGCCGAA AAGGCAAAGG CAAGATATAT 600  
 5 GTCCITGTGC ATGGATTGGG AGAAGCTCAA GCTTGTAGAT CCTGCAAAGA CGAAGTTGAC 660  
 ATTGCGGGGC TCAAAGACCA CTCGAGAGCA GGAAGAGGAC TTATTAGAAA GATTGATA 718

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1430RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GATCGCAGAG AGACACAATG TCCTGTGGC CACTTTGTCT ATGCTTTATC ATTTATTGAT 60  
 TCTTGTGCAG GGGAAACTG AAGGCCCAAC AGGGAATTGT CAACCATGTT TAAACTTTTC 120  
 CATGTGCATG GAGCTCGTGA TGTAGCAATA TATTCTCATA GCTAGAGATC TCACTATATA 180  
 TTAGCTTGGC ACATTATATG CATATCGAGC TTGGTTTTTG TACACCTTTG TGTGAGGTAG 240  
 CAGGGGCGGC ACATAACTAG TTATAAAAAC GATGCCGCGG GAGAACGAGA TCTACTATCT 300  
 CTCTGAGTAG GCACAGTTTC CAACGTATTA GTCTTAATG AGCAAGCGAA TCATTCAACT 360  
 CATACTTCTC TCTGCCTTTG CGCGAGCTAA TTACGTGGAG CCTTCAAAT CAAATCCATA 420  
 CATTGCTTGC TCAGAGGCAA GCCATTGCC AAAGGAATGG CCATGCTGCT CGCAATATGG 480  
 ACAATGCGGG AGTGGGCGGC TATGCATTAG TGGCTGCAAC CCAAAATTCT CGCATAGCCC 540  
 TGAGAGCTGC GTGCCAGTGC CGCGCTACT ACCGCAATTG GAGATAGTGG CCAGCGATGA 600

TAAAGGAGTA TACCTAGAGA TGTCGGGTCA GCGTGCCCTTG GTCACAAAGT TCCAGCGCAA 660  
 5 GAGCTCGGCG CAGTTGTTGG AGGTACATCA CGAGGAACAG CAGTATGGTG TGTCGGCATT 720  
 AGAGCAGGAC 730

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1430UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GATCGATTTG GTTACCTTGT TGCCAACCC ACGTACTTCA AGAGATTCCG ACCCAGAGTT 60  
 GTAGACAGCG TACCTATTCC GAGCGACAAA AGTCGCAAAG CTTCCCTTAT CCTCAACTAT 120  
 ATTTGTGGCA TCAACAGCAC CGCTAGCCTG TTTTGGGAAG AGGCAAAGAG CATACTATC 180  
 GCCATCCCTG CTACTTGAGT TCACGAGGAG AGAGTGTTGC GAGGGATTAT AAGAGATGGA 240  
 CTTGAACAG TTATATGGCT TTCCAAAGTT TTTTAGAGAA ACAAAATGGCA GAGAGGACAC 300  
 CTTCTTTTCA TAGTCAAACA TTGGACCTG CTTCTCTTTG TTGACAAAGT AAAGCTGGTT 360  
 CTGGTTCACA GCCACAGGTG GTCTCTCAG GTCCAGTTTA AAGACCATGA TACCGAGTC 420  
 ATGCGCGCGG CCAAAGAGGT TCACATTAGG GTGCGCCCTA ATGACCAGA ATCTGTCTG 480  
 TTCTCTTTTG AACTGTTTTA CAGGAGTGGC CTGTCTAGA TCCAGACCC TAATGGTAGA 540  
 ATCTCGCCG ACAGAGATAA TTAGGTTTGT AAATGGGIGA AATATTACAC TGTCACGTT 600

GTTCGTATGA CCTGCACTT GTCGACCTCC CACGCTTTGG TGGAGCTCAT ACGCCACAAC 660

5 TTGACCTGTC TGCTTCAGA ACCGGAGACA ATCAAGGGCA GAATGGGATG GAACGAAGG 719

(2) INFORMATION FOR SEQ ID NO:641:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 730 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1431RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

30 GATCATGTTA TACAGACCTT CAAAGTTGAT ACCAAAACCC TCAATGGACT CGCTGACCAT 60

ACTTGGTACT TCCTGTTTAG AGGCCCTGGG GCACACTTAC TGCCCTCTACA AGAAAAAACT 120

35 GTTGCCCTCTG AATTGGATCA CCCTTTTTCG GACACTAACC ATTGCAATA CAATGCTATA 180

TTGCCCTCTAT CAATGGTCTA TTGACCTTGT TGAATCCAAG CTCGAAATCC AGCAATGTGT 240

40 AGAGATACTG CAGCATTTTG GTGAGAAATG GGTTTTGGCC AAGGAGTGTG CGGTGCTCTT 300

TCAAAATATT GGAAATGCGA TACTAGATAT AAGTCTCTCC CGAGGACAGG TAGAAAACGT 360

45 TGATAAATTG ACTAGGGAGC TATTTGGAGC TAGCAATGAA TACCAAGATA TATTGGACGA 420

AAATAACGTA GATATATCCT GGATTGACCT GGCTATCTAA TTTCTGAAAC CATTGAGAAC 480

50 CTGTTTAAAC TATTTGGCAG TAATTCATAA TGTATTGGTT GTTCATAGC TGAATTGCTA 540

TTGCCGCTAT GGAGTTGCTT ATGCAATACA CGGGTTAGTG GGTGATTGTC GTGTTCTTAT 600

55 ACCCAAACCTA ACCGAATCCG GTCTTAATCG ACTCCGGTAG ACTTTGTCAT CCAGTAAGAC 660

ATGTCCTTACA CGCCCGAATTA ATGGTTGTAA TCTTTAATCG ATGAATGAGA AATGGTATAT 720

GTATGTGACT 730

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1431UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GATCTCTGT ACCATCATGA AAGTCTTTTT ATCACGGGAA AACCGTTTC TCAGGCACAT 60

CTGACGCACT GCTTGTGCA CATCAAAGT CAAGTTCGA TCCCTGTGA GCGCTTCCAA 120

CTCCAGAAC TCCTTCGCA GATTTTTTAC TGGGCGGGC ACAACTTCTG CCTGCCCTCTG 180

GGGCACATAT TTCTTTAACA CCTCCTTCGG AATCTTAAAG TCCTTCACAT TATAGCGACT 240

TACGAGACCT TCGAATAAGA AGAGGCACCT TATATATAAG TTGACATAT CCAGTTTCAT 300

CTCGCACCCC CGCAGGATCA GGTCCCGGTA GTCCAAGTGC GCCTTCTTC TTGAATTCGT 360

AGAGCTGGC CCCGAGGATG AGCCTGCTG ATCAGAGGTG CCTGTCTTCA GCGAGAGCTG 420

TGGCATACTC GGCTGTGTGG CAAGCTCCAC CTTCACCTGC TTGGCAAAGT TCACATTTAG 480

GCCCTGGGCA AACGGGTCCA GTGAGCGAA GATATGGTTC ACCAGCTCGA GTGGCATGGC 540

CATCTTGTTC ACGTCCAGTG ACAAGTTCCC TTGGCCTAGC TGGTGCACTA GGGCCGGCT 600

CTGTGTGAGT TGTGCTGCC ACACAGAGTC CAATTCCACT CGCATCATGC GCATCGGGTG 660

CTTCAACGCA CGCTCACTGA TCTCCCTCG CTCAGGCATC TGTGGAGCCT CTTCTGGCT 720

5 TC 722

(2) INFORMATION FOR SEQ ID NO:643:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 724 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1432RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

30 GATCCAGGAC TCCCGTGCCTT GGTGCGCTC AAGGAGACT TAGAAATGAG GTGTGGGOC 60  
 GCATTCTGGG CTGCAGATAG AAACGAAGAC AAGATGCCAC CGTTACCCAA TTCTCAGOC 120  
 35 CCAGAGAAA AATTCCCGTA CCGGTGCTC CCAGTACCAT CCTGGTCAA GGTGTGATA 180  
 TCCGAAATT TATCTCAGT GTCTCTCTG TATCTGCAT CCGAGCGGT GCTTTGGOC 240  
 40 GCGGCGGG GCTCGCGCC CGGCGCAGAC CGCACATGG AGTGCGGCG GCTCATCTCA 300  
 ATTGGCATGC TGAGCGACGA CGAATTGCTG TCGGCGCGC TATGCCAGT GCGGCGTCC 360  
 45 CGGCCACCC ACCCCAGGG GAGCGACGAG TTTGTCTGT TCGGTAAAC CACCGTGGC 420  
 GACATGAGC ACGATTCTG TCTGACAC CGGCTCTCA CATCCGAGC CTCCCGGOC 480  
 50 GCCACCTGA CATCACCGC CTCGCGCCC GTCCGCGCT CCGATTCCG CGTCGCTACC 540  
 CGTCTTTGG CACTGCTGC GCGGCGCTC CGCGGCGCT CCGCGTATG CTTCTTGAA 600  
 55 AGTGCGGCG GCTCTCTG AGCGACCGG ACGCTTCG CTCTCTGCC ATCTTGCTA 660

GCCCTCTGCTT GAGAAGAGCA TCTACCTCTC CTCCTGTGTT ATTCCGCGGC CTCTTTTGGGA 720

5 AACA 724

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 615 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1432UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GATCCCGGTC GCGCGCTCCT CCTCGAACAT GTCTGTACC CCGCGCAGCG GCTGGAACAT 60

CCCGCCACC CCACCGTACT GCGCCGGGAA GAACTGTGTG TCACACAGCT GTTCGTGGCG 120

CGCTGGTCC GCGGGCGCA TATTCTCTC CTCCTGGTAA GCTCTCTCT GCGAGACTC 180

CGCCAACTTC TGTGTGTGT ACTCCGCGC CGCGCGCGC CTTCAGGCG CACTGGGTGC 240

GCCAGCTGC GTGTGCGCG CGTGCTGAA GTACAGCGAG ATTGCGGTTT CCACGTGCG 300

ACCTGCCATA TCAGGAACT GCGCGCCAG CTCGCGTGC GCCACCGC AGATGCTTTG 360

GAATAGCCG AGCTGCTTGT CTGAATCAT GCTCTACTT TCTGGCGCTG CCGTGTGTG 420

TGGCACACTC AGGAGTTTGT CTGAGTTGT CGCTGGCTCC AGCTTTTAT ACCGGGCGT 480

GCCACACATG CGCGCGCCC AAACGCTTAT ACATATACAT GCTACTTAGT CCGCGCTTG 540

GTACCCCGC CGTCTCGAA GCGGTGTGC GTGCGCTGGA AGTGCACCG CTGATCGCG 600

CGCGCTGGG CGCG 615

## (2) INFORMATION FOR SEQ ID NO:645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1433RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GATOGATGCG GACCACCGTG CGGAGGAGGC CGCAGGTGGA TATGCAGTTT GCGGCGCTGA	60
GCGGCGCGAT TTGAGAGCT CGCGCGTCCG CTGGGTGCC CGCTTCGCGC AGCCACGGAA	120
CCAGCTGACG CGAGGTGTCT CCCCCGGGC TGGCGTTTG CCGACAGTG CTGCGCGCT	180
GGTAGTTCTG TAGCCACGC GCGCGTTAA TCTCGGCAT TAGTAGCGC AGCATCTGCA	240
CGAGCAGCG CGACTCGCGC ATCTTCTGTA TTTTGAGCAG CTGCGCTCG ACCTTCTCGT	300
CTGGGTGCC CATGTCCCG CCCAGCCGT ACTGTTCTG CAGTCCAGC TCTGTCACT	360
ACCGTGCTAT TTGCGCTCG TTCAGCACTT CGTCATTCTC AGCCACCGGT ATTCCAGGA	420
GCTTGCAAT TTGCGCGCT TTCTGTAGGA GAACGTGGTA GCGCGGATG ACCTTACGTG	480
CTTTGGATGG TTTGATTGCC GCGTATGTT TGACGGCGCT CTTGCCGTA ATGCTTCTTC	540
GCTTCTGGC CAGCATGTAT GAAAGTTAAA CGCAGTTAC TACTGGTACT AGATATGCCC	600
TGGGAATGCC ACCCGATGAC CTGCTGGTGT ACCTTGCTTT TGTATCACG ATGCTTCGAG	660
CTGAATCGTT GAAGAATTTC GAGTGAAA	688

## (2) INFORMATION FOR SEQ ID NO:646:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1433UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GATCAOOGAA GAAGGCAAGG TCAAGAAGGT TACATTIGAT ATOGAGCOGT ACAAGCCCAT	60
CAACACTAAG CTATACAAGT GTGACAATAA GTTCOOGACG GAGGTGCTCT CGGAGCTGCT	120
GGAGGCTGAC GAGAAGTTCG GGTTCATTGT GATGGATGGT CAGGGGTGTC TTTTCGGTAT	180
GTGTTCGGGT AACACCCGGA CTGTCTTACA AAAGTTCACT GTGGACTTGC CGAAGAAGCA	240
CGGTAGAGGT GGTCAATCCG CGGTGGGTTT CGCCCGTTTG AGAGAGGAGA AGAGACACAA	300
CTATGTGGGC AAGGTGGCTG AGGTGGCAGT GCAGAACTTC ATCACAAAGC ACAAAGTTAA	360
TGTTAAGGGG CTAATTTTGG CTGGTTCTGC GGACTTCAAG ACGGACTTGG CCAAGTCTGA	420
ACTGTTTGAC CTGAGGTTGG CAGCCAAGAT TGTGAAGATT GTAGATGTAT CGTACGGTAG	480
TGAAAATGGT TTCAACCAGG CTATTGAGCT GTCCCGCGAG GCGCTGGCCA ACGTTAAGTT	540
CATTCAGGAG AAGAAGTTGC TCACCGAGTA CTTTGATGAA ATTTCCGAGG ATTGGGGCAA	600
ATTCTGCTAC GGTTGTGACG ATACTCTGAA AGCGCTAGAT TGGGTGGGT GGAGAAATTG	660
ATTGTGTTTG AAAATCTAGA GATTGTTCG GTACGTGTTT AAGACTTCTG AA	712

## (2) INFORMATION FOR SEQ ID NO:647:

## (i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

- (A) LENGTH: 716 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1434RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GATCAGATGC TTCTGTGGTC CTAGAGAAGA CTGCTATTCT TAACCCCTTCG TCAACGAATA	60
TAGCCGAGGA CGAGTTTGTC GATGCCATAG CGGAACCTCC ATCGGCGTCC GTGGATAGTA	120
CGCCTTATGT GACCGCGGCG CGCGATTATT CCTCGGAAGA CACCGGGGAA CGTTCTGAAC	180
CTACAATAAC GGAATACAAA ACTGCAATTG AATCACCATC CACCTTTGGC GACGATAACG	240
AGAGTGTATT TCTGTAACT TCTCGGACC TGCATCCATC GGTGTCTCT GCGAGTCAA	300
CATTAACAAC GGAAGAGCTT CAAGCCGTG CGACAGCCA CCAATATAAG ACCGAGGTGC	360
AGATTGTAAA ACAAGACGAA GATGAAGTAG AGGATGTTCT AGAATTGGAC TCGCACCAG	420
CATCTCTGTA TGATGGTGAT GTTTTGAAG AGGCAGAGAA AAATGATAGT AGCAATGTTA	480
TTCCTGATGA TTCCATAGAT ATCGATGAAT ACCTCGATGA AACTTTGGTT AAAAATTCA	540
CATTGGAAAA CGCTCTTCT TTAGATGAAA TCTTCGACGA TGATAATGTA GTTTTGGAG	600
AAGAGAAGCT GCTTGTGGAT CCAGACCTAG AATCCCGGA ATTAACTGGA ATGGAACAAG	660
ATATGGAATC TGAATATCTG CCGCTGATTG AAAATGGTAC GGAGGCTGTT CTACAA	716

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1434UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GATCAGGTTT TCCGGTACGT GAGAACGTAT CTAAGGCACA AAGGGCTTTG GGCGACTGTG	60
CGGACGCTTG AGTTGCGAGA TACAGGACAA AGCTGTTACG GCGGCAACTG GTGCAGCAGG	120
AGCAGCCGAG GAGCGATTCT GCGCGAAGCG ACGGTGAATT CGAGCCAGCT GGTAGCAGGA	180
GTGCCGGATC GTCTATTTAG TTGCGACGGG CGTCGGAACA GGATGCACGT AAACGTTGCG	240
GTAACACGCG ACGCTGACGC GACGGCTGCT ACGCGATAG CACGGGAGCG CAAACGAAGG	300
CAGCCGCTGT CGCCAGAGAT GTCTTCACCA CTGCGCGGTA GCAAGCTGCA GCGGCGAAG	360
CAGACACTTG AGGCCGGTCC GGGTCGCGCC AGTGGGACAC ACACGGTGGA CGAGCTGGCC	420
GCGCAGCTGG AGCGGGCTG CGAGCAGGCG TCGGAGCGGA AGCGCGGTA CTCGTATGCG	480
GTGCTGATCG GCGTTGCGAT CCTACAGTCG CAGGAGGGCA AGCTGACCTG TCGCAGATAT	540
ACCGGTGGAT CTCGTCTTC TTCCCTTACT ACGGCTGTG TGACCGGGG TGGCAGAACA	600
GCATCCGGCA CAACTGTGCG CTGAACGAAG CGTTGTCAA GGGCGGCAA TCGCTCGATG	660
GCAAGGGCCA CTTCTGGGAG ATCAAGGCAC TGTGAAGGCG CTTCTCGCG ATGGG	715

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1435UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

GATCCGATGC TACCCGTCGC CCTGCCAACC CGTTGCGCTA GCGTTGACGC CTAGGTCTGA	60
AACTGAACAA CAGGTGGCAT TGTTGGGGGG CCAGCAGGOC CTGGGGGAC CATGCCGCCA	120
TGGGGGGGGA ATAATACCAC CAGTTGTGAA GCCCAGGTGT CTGTAATCTG CACCGAACAT	180
CTTTATCTAC CAAGGAGGAG CTTGAAAAT TATATATCTA CCGCTCCCC TAATATATTT	240
GACCAATTCG CTCTCCGGA ACCGAATGAT CGAAGAGGCC ATCAGGGCAG CGGACAGCAC	300
AGGAAGTGAG GAGTGATCTC GCAGGTACGA TGGAAACACA GTCTATACAG TCTATTGGT	360
CGAACCAAAG CGTACGGAGC ATCSOGAGCA CGAGCGGAAC CGCAGACGAG TCGCTAATCT	420
TTGAACGGAG CGTTGAGGAT CGTTTGGCCC CGTGAAGGAC GCGAAGGGTT GCAGCCTGTG	480
TGGTGTCTCC CAGGCAGGCT CTCTGCAOCC CGCGTATCG GCGACTGGGG GCGGTCT	538

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1436RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

5	GATCAACCTC GGAAACGTAT TTAAAAGCTT GTACTCGACA TCATTAAGTC TTCTCCTCGT	60
	TTCTTTTGGT AAAGTATWAG CATCCAGTAA AGTAACAACG AAATGCAATG CTGAAAGATC	120
10	GTATACCCTA GACGACCTAA ATGGGGTATT TTGATCATCC ATACTAGCTT GAAGATCAAT	180
	GAAGTCAATA ATAGTGTGTA CAGACTCAGG GGAGAGTTTG GACTTGATGT ATTCTCAAA	240
15	GCCAGTCCAT CCCAOCCTTC TAGCACTAGG AGTAATCTTC AGCGATTCTT TAAACGGAAT	300
	ACTTCTGATA AAATCCTCCA GCTTTTTTTC CTGTAAGG ATCTGTACAA AATTAGCAAG	360
20	CGGGGTGGTA TCCTTGTTAA TTATGATTCT TCCAACCTCA ATGACCTTGT GGTGGGGAT	420
	TTTCTTGATA AGCTCACCAA ATAACATCGG AGATTTTTCA AATACTTGGG OCATTAGAGT	480
25	GACCAATAGT TCGTTAATAA TCGCCTTATT TTCAACCATA AGACTGAAAT GCTTCGTTC	540
	TGAGATCAAA GTCAAGGCCA AATATTCGGG AACAAATATG TAATCATCGA AGAAACAATC	600
30	ATGGAATAAT TGGACATAG GACTGGAGOC AAACCTCTCT CTTGATAAGA ACAGTCAAT	660
	ATCGAGCTTC GATACCGATG TGAGATATAA CAAGGAGTTC TTTGAGTTTG GGAGTACTTT	720
35	AGAGACTT	728

(2) INFORMATION FOR SEQ ID NO:651:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1436UP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

5	GATCCAGAAG ATTATCCGAC AATATTAGTG ATATCAAGGC ACAGATCGCT GCCAACACTA	60
	GAGGTATTCA ATTGCTTAAC CAACTGGTTG ACGTTTTCGG TCTAGGGACT GTTACAAGGT	120
10	ACATGGACGC AATTCAGGAA AATGCAGCTC TTACTGTAAA GAATGTCTTG CGAAAGATTA	180
	CCAAGCATTT TGGCAAAACC GTCTATTGGG COGAGGATTA TATGGATGAT GGCTCTGTTA	240
15	TAAAACTTAG GGTGGAGCTA AATGCTAAGG AAGATAAGTA TATTTTTGAT TTTACGGGGA	300
	CTTCTCCACA GGTCCACGGT AACCTCAATG CACCTGTTC TATTACCAAC TCTGCCATCT	360
20	TATACTGCTT ACGTTGTTTT GTAGACGAAG AGATTCCGCT CAACCAGGGC TGCTTAAAGC	420
	CCATTACTGT TATTATTCCA GAGAGCTCTA TCCTATGGCC GACCAAGGGT GTGGGGTAG	480
25	TGGGAGGTAA TGTATGAAG TCTCAGCGTG TAACTGACGT AATTCTCAA ACTTTTAAAG	540
	TCATGGGGGA CTCCAAGGA GACTGCAATA ACTTTACTTT TGGGACAGGT GGGAACGACG	600
30	CTTCTACCGG TGAATATACT CAGGGTTTTG GATATTATGA AACCATATGT GGGGGGCATG	660
	GTGCAGGTGG AGATCATGGC GTGGTCCGGG GTGGCATGGA ACACATCTTG TTC	713

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1437RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

EP 0 866 129 A2

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GATCGCGCGC GAGCTATCGC TTCCGCCGGT CAAGCTGCAC TGTAGTATGC TCGCGGAGGA 60  
CGCCATCAAG GCCGCCATCA AGGACTACCG CAGCAAGCGC AAGGCGACCG AGCTGGGCTG 120  
AGCGCAGGCC GCCGCAGCCT GTGGCGGGCC GGCCGGCGCC AGCCGCAGAG GGAAGTCCGC 180  
GGGCGGGCGA GAGCGGCCCG TTTTCTATGT AGCGACTCKA GCATCTAATA GACATGGTAA 240  
TAGCTTCTCG TTTTCTACGT TTGCACACAG TATACAAAAT TTTCACGCAG CTCATCGCCA 300  
CTTCCACTTG CTGAAGCGCA GGTACGGCAC CAAGACCTCG GCTATGTCTT CCACTCTCTT 360  
TGACGACATC TTCAAGATCC AGGAAGTGA CCAGGGACCG TACAATAAGG TATCGCGCAT 420  
TGAGGCCATC TCCAGTCCG AGGACACGTG CAAGCTGACG CTGGATGTGA ACACAGAGCT 480  
CTTCCCGCTG CAACCACAAC AGCAGCTAAC GGTGATGCTG GCGACGACAC TCAACCTCGA 540  
CGGAACGGAG GACAGCCACG GGTCTTGGCG GCCTCCGGCC CCTGGGG 587

(2) INFORMATION FOR SEQ ID NO:653:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1437UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

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GATCCGGCGG GACCGCTACA ATATTCCCAT ATGTATTAYA GGCAACTTTA TACCCATCTC 60  
CTAAGTGCAG TAGTACTGT TTGTACGTCT AGCGTCTCGC TCGCGGTGAG CCGGTGTGTG 120  
CGGTCCACCA GCGCGCGGAC CGCGCGGCCG GGCCCGACGT GCAGCGCGGC CGTCCGCCCC 180

GCCTGCACCG CCGTGCAGCA GGCTGCGACG AACTCGACCA CGTTGTGTCT CGAGCGCACG 240

AACTTCTCCA CGGCCACGTC 260

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1438RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GATCTCTTTT TAACGGCTGT TACCAATAAC GATACGGCAG CTACATCTGG AGAATAGTCT 60

GCATCCCATG CCTCCAAGTT CCTGTGAACA TACTCTGGG GATOGACCTC GAAGCTCTCC 120

AAGGTCTCTT CGCTAGGACA AAGAAGCGG AAGATAACAT GTTCCAAAAT GGTTCATATA 180

TGTGGGTCAA CTATGGGCA AGTAGACTTT TGGACCACTG TTGTTCATAT GAACTCCAAT 240

ATGTAATATA GCGACTCCTT GCTTAACCAC AATTGGGCTG CACCCACCTT TTCAATCTGC 300

TGGAAATGCA ACTGCAATAG TTGGGGCAGA AACTGCTCCA CATAAGCAT TTTAAATTC 360

GTGTACTCAA ACTTTTGTCT GAGAGATTCT GAGGCATAAC GTTGAATAA TCGATACATG 420

TTAGCATATG CCACTTTTTT GGCTCTGACC CATGGATGG CCGGCTATC ATGACCGGC 480

AGCGCCATCA CATGCTCGG CAGCTGGCTT TGTATCACAG AAACATGGAA GTTGGCCAC 540

GGAATGAAGT TTTCGACCG TTGGAGAGTG AACGGCAGT CATTATATGT CACAACTTG 600

TAGATCTTCA GCACAAGCTT CAACATATTC CCCAGATCT CGTTGTGCTT TCCTGCTGT 660



ACAAAAGCGC GTTTGGGTAG TGCAGCAAGT CTGGGAAATA TCTCATGATC AGCATCTCCA 720

GCTCTCTGA 728

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 774 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1438UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GATCGGCAAA CCTAATGCGT CTGGACGTAA TGTAATCCAA CAGCGACTGT AGAGCTGCGT 60

GCGGTTCCTC GACAGAAATC AGCTCATCTG CCGGCTTCAA GGCGTTTTC A GCGCGCAAAA 120

CAGGTGGAGC CATGCTGAAT TAGAGCTATT TGGTGACCTG TTTGAGTAGT GTGGACTTCC 180

TTTGAATGTG GTGAACTTTG AAGTAGGTTA TTCAACTAGA AAATTTTTC A CCCAGAAGGA 240

TGCCCTCTAT CAGCGGCGGT GTCTGACGAT GATCTCAACC GCGTAAAGGA CGAGAAGTCG 300

TAGGTCGAGT CTAATCTACT ATTGGTACTG ATGAACGGGA CTGGCCAGCT AACGTGAAGG 360

CACTGTCTGC GGGATGAGGC CCCAGGGCCA GCGCACGGGC CCTGCGATGA GCACAGGTTG 420

CCTCGAGAGC ATTGCGATCG GCTGACGGGA AGCCAGGTTT CCACAGGTTT GCGGACTCG 480

CGTCGTCAGG CTGGAAGTGT AGAAGGGTTG TCTTGAGCTC CCGGCACGCC GCAAGCTGCC 540

CAGGTAGCTG GCGGGCGGTG TTCATGGGCG ACAGCGGTGG GCTCGCTGTC ACGTGGCATC 600

GAATATGTCA CGTGATTACA CGCAGCAGGG CATGCGAGAC AATGCGCAAG CAGCAACAGG 660

AGGAGGGTGT GATCGGTGGT GTGCGTTTAA GAGTATGTGA GCTGTGCAGC TGGCTCCCCA 720

5 TCTCTGGGTT TACTCGTACC TGTGCGCTTA TATAGGCATT GCCAAAAGGT TTCC 774

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1439RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

30 GATCCTGTGTG GACGCTCTGC AAAGTCGTGG TCACCCCGAC CAACTTCTCC TCTGTAATAC 60  
CGCTGTACTT CGTTAAGTAG TCCACAATGG GCTCATCTGG CTTGACAAAC TTGTCATAAA 120  
35 CTAAGTTACA ATCAAAATCG ACGACGCTCA CACGGGTCAA CACGTATCCG TTTTTTGAAA 180  
GGCACATCTC ACAGTCGATG GCAAAAGTGT GAGAACCGTC GGTGTGGAAA CTGACAGTGT 240  
40 CCACCCACCC ACTGTACTTC TCCTTATTCT GATACTTTAG CAACAAAGCC TTTTGGTACT 300  
CCTCCGATAA GGCAGGTGTG TTTAGATGGA TGGGGTACTC ATTATGCAAT AAGTCATCAA 360  
45 CGGTCATTAG CAAATCAAGC AAAGTGATTT CCTTTTGTGT CAATTGTTC ACCTTTGCGA 420  
TCTTCTCCTT TTTTGACAAG CCTACATTGA CAAAAGAATT GTATGCAGAA AATAGGGAAT 480  
50 TCTTTGATCC CGGCGCTGAT AACGGCAAGA TACACATTTG CTTCACATC TGTTCATTTT 540  
CACTAATCGA GTTTAGATGT GCGTCTTCCA ATTTCGGAAT ATTTTATGA AACAAATGAAT 600  
55 CCTTCGGTAG ACTGAAGTCC TCGGGTAAAA GGCCTGGAGT GAATAAGAGC ACCACCTTCT 660

TCAAAGAGGC CTATTTTCTA TCGTAATCCA GTTGGGAGAG TTGTTCTGTAT CGTGGGAATAT 720  
GTACTGGA 728

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1440RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GATCTATTCT TCATTCAGCA ATCAACAAGA GCTGGTGAAA CTTGGGCAAG AAGCTGAGCA 60  
AAGCGGTAAA TACAACCTGG CATTCAATGC ATACTGGATT GCAGGAGATA TCAACAAGGC 120  
CAGGGACGTG CTTTGAAGA GCGGACGCA TTCCGAGGCT GTGCTTCTGG CATCCACATA 180  
CACCTCAGAC AATGACGCCA TCAACGCTGC TGTAGAAAAA TGGAAGGAAC AACTGAACTC 240  
AGCTGGAAGA GTATCTATCG CAGAAAGAAT TATACTTTCC GGAGAAGACG ACTTCCCTGC 300  
AGCTCCCCAG ACTTTGGTCG AAATGGATGA CGGATCAGAG TCCGGTCTA AATAAACTAT 360  
AATTTTAAAG ATAACAGCAG GAATAAATTA ATTACCACGA AGGAAATTG TATGTACATT 420  
CTAACTAGAC CCAATGGTAG AATTTCAATTG CGTAAACACG GCAACCTTAT CAATATCTTT 480  
CCGTTTGTC AGTCCGACAA AGTAAAGTTC TTTGGATTCA GATCGGCATG CTTCCGGCTT 540  
AAAACGCCGC ACTTTGGTGA ATACCTTTTC CAGACGCCGT TCTAATAGCT GGTCTTCCTT 600  
GCCAGTGTAT AACTTGCAAA CGAATGAGCC ACOGGGCTC AACAAATGCA TTGCACATAG 660

CAGTGTCTGGG TTCACACAAG TCATCGACA TGTA

694

## (2) INFORMATION FOR SEQ ID NO:658:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1440UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GATCCTACAG AAATAATCCA GTACAAGGTA CCTCTAATCT ACTGTGTTAA CATGGAAAAC	60
ATTTCGCCCTT TAGGCTTTTT CTTTTCACCG AAAAGGTAAC GTGTTCGAAA CATATATCAC	120
GGGTTCGAAA CTGACTAAGG TTGCTCATGC CTAAACCAGA TAGGCAGCAA TGGCAAGGGG	180
CTTGAGGTGG TACCAGAAAA GCTGCCAAGT CCTGCTGGGT GCTTACTCTC GCAAACGGTG	240
TATACTATTA GTGTGGAGT ATTTATTCCT TATTAAATAA CCGAATTGTG GGCTTAGAAG	300
TGGCGATTAT CACTGAGCAG CAGCGGCTGG CAGCGCAGAC TGCTCGGAA GCGAGCAGG	360
TGCGTTTGAG GCAGCGTTTA GAGCTGCAGC CGTGACCATC AAACCTCGC GCGGAGGAC	420
GAGTATGAGG GCTAGCTCGA GGCGCATCAA GAGCTTCTTC GATATGCGGC AGACCTTGCT	480
GAAATACTCG TGGGAGTGCA CGGTGCTCTC CACAATCTTG GTTGAGACAC GTATCAAGGC	540
CACTATGAAG CGATGCACAT AACTCTCGGC GATGGGCCAG CGGATCTGCA CCGGACCGGT	600
TTCCGAAGGA GGCCATTTTA GCGTGAGGCG GAGTAACAAG CAGCCCGCGG TCTGGTAGAC	660
TATGGGCGCA AACATGCATT TGGCGTTGAT GCGTCTAGG TACTCGGTAT AC	712

## (2) INFORMATION FOR SEQ ID NO:659:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1441RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GATCGTTAAT TGTAGCAAGC GACGACCAGA GATGGTCTAC CAAGGCGGTC TACGACAGAG	60
CACGCAAGCA GTCGGTCCOC AGGAGCAAGC CCCCAGGAC AGACCACAAG CACACTTGCC	120
GCGTCTGACC AAGGCCCTCA CTACCCGATC CTTAGAGCCA ATCCTTATCC CGAAGTTACG	180
GATCTATTTT GCGGACTTCC CTTATCTACA TTATCTATC AACTAGAGGC TGTTCACCTT	240
GGAGACCTGC TCGGTTATC AGTACGACCT GGCATGAAAA CTATTCCTTC CTGTGGATT	300
TCAAGGGCGG TCGTAAGGC ACCCGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	360
ACCCCATCTC CGGATAAACC AATTCGGGG TGATAAGCTG TTAAGAAGAA AAGATAACTC	420
CTCCAGGGC TCAGCCGAC GTCTCCACAC TCAGTTACGT TCGGTGAAG AATCCATATC	480
CAGGTCCCG AATATTAACC GGATTCCTT TGATGGTGG CCTGGAAAT CAGGCTTTG	540
AAACGGACTT CCCCATCTCT TAGGATCGAC TAACCCACGT CCAACTGCTG TTGACGTGGA	600
ACCTTTCCCC ACTTCAGTCT TCAAAGTTCT CATTGAATA TTTGCTACTA CCACCAAGAT	660
CTGCACTAGA GCGGTTGGA CCCAGCTTTA CAGCCTAGG CTTGTCCT GA	712

## (2) INFORMATION FOR SEQ ID NO:660:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1441UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GATCCAACCG AACCTTTCCT TCTGGCTAAC CTAGGTAAGT TGTACTCTAG GCGAACCAGG	60
ACTTTTACTT TGAAAAAATT AGAGTGTTC AAGCAGGGC AAGCTCGAAT ATATTAGCAT	120
CGAATAATGG AATAGGACGT TTGGTCTAT TTTGTGGTT TCTAGGACCA TCGTAATGAT	180
TAATAGGGAC GGTCGGGGC ATCAGTATTC AATTGTGAGA GGTGAAATTC TTGGATTAT	240
TGAAGACTAA CTAATGCGAA AGCATTTGCC AAGGACGTT TCATTAAATCA AGAACGAAAG	300
TTAGGGGATC GAAGATGATC AGATACCGTC GTAGTCTTAA CCATAAACTA TGCCGACTAG	360
GGATCGGGTG GTGTTTTCIT ATGACCCACT CGGCACCTTA CGAAAAATCA AAGTCTTTGG	420
GTTCTGGGGG GAGTATGGTC GCAAGGCTGA AACTTAAAGG AATTGACGGA AGGGCACCAC	480
CAGGAGTGA GCTGCGGCT TAATTGACT CAACACGGG AACTCACCA GGTCAGACA	540
CAATAAGGAT TGACAGATTG AGAGCTCTTT CTGATTTTG TGGGTGGTGG TGCATGGCCG	600
TTCTTAGTTG GTGGAGTGAT TTGTCTGCTT AATTGCGATA ACGAACGAGA CCTTAACCTA	660
CTAAATAGTG CTGCTAGCAT TTGCTGGTTG CGCACTTCTT AGAAGGACTA TGGGTTTC	718

## (2) INFORMATION FOR SEQ ID NO:661:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

# EP 0 866 129 A2

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1442RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

GATCAATTGC GTCTTCATCC GATGAGACAT TTTGAAAATT GTTGAATAT TGGGCAACAT	60
CAGGGTATGG TAACACCTCC GGTTCCTAAC TTCTAATGG TAGCCTCGTC GCGGTGTAA	120
CGCATGGATC ATCAATGGAC GGTGCTGGGG GCGATCTAGA CACGCCCGAA TTGGGGCTTG	180
GTGTGAGGTT TTGTCGGGA CTCTCACTT TATCAGGTAT GACTATCACT TGATGATTCA	240
TTAGATTCCG TGTATCCACA ACATGGACGT GGCTTTGGTG TTAGAGATA AATAGTAGGT	300
CATCAAACGA GCGGCTAAC TTGCACACC TAAAGGACC GTTCTGTGCA TGTCTTGAG	360
TTGAAGGTAT CTCGCAAGA GCGGTGTCCA TTTTCTCAT ATGTACACC AGACAGAGGC	420
CGTTTTGGAA TATGTTAGC ATGTGCACT GTTTTTGCT ATAGCTTG TG TAAAGCCGT	480
TATCACCACC AGGCGAATCG TAAATAAGAT CTAGGACTTC GGATCTATCG ACCGGGGCAT	540
ACCTTGGAAC GCACCTTGTG GCGGACCA TTGAACCCA CTCAGGAGCG GCGTCATATT	600
GTAATGAAAA ACAACCGCTT AGTTCATCTG TCTATAGACC GCAAACTTC TGGAACTCC	660
CGAAACCACC ATGCTCTTCC CATGCTGTGA TATTGCGAG CAGTTTAAAG CAAATTTTAA	720
GT	722

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1442UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GATCAAGGCT GGGAAATTGG CGTTGACTGG CTTGGGCTGC GCAGGCTCTC TGTTGCGGCT	60
CTTGCGCGCT CTGTTGCGGC CCTTGCGGCG TCTTTTGTG TCTCTCTGGT CGCGAGACTT	120
AGGAGCAAAG GACTGGGTGC CATCAAATC TAGGAATGC TTGGGCTTCA AGTGCTTGGT	180
CTTGACGTTC TTGACCTTGG TAGGCTCCAT GAAGACCTCC TGCTTCTTAA CGAACAACTC	240
AGCGTGTGCG AACTTCTCGA CCTTTCTGGC GACAGGGGCC TTGTTTCAGGT CGGAGTCTTG	300
CTGCTCCAAG TAGGCTCCA AGGTGACGGC AGCTGCAGTG GCTGCTGCTT CCTCGGCAGC	360
GTCGGCGGCC AACTCGGCTT CGGCAACAGC GGCACCAGCC TCCTCATGGG CCTGCTCCTT	420
CTGTTGTGCG CCCACGGCT GCTTGATCTT CTTGGCAGAG TCAGTCTTGC CGGTTCTCGA	480
GTGGGGGTCA AAGGTCTTTC TGCTGTCTTT GGCTGGCTTG CCTGGCGCAA GAGCGTCTTT	540
GGACTTGTTC TCGGAACGGC CGGCTGCTT GTCTCTGAAC GCAGGCTCGT TGCCGGTTGG	600
CTTTGGTCTG TTGTTCTTGG CACCGGATGG GTGGGCAGAT GGAGGAGGCA CGTCCGCTTT	660
CTTGAAGAG GTGGTCTTCT TCACAAGCTC CTTTGGAGGA GACACAACAA CGGTGGCGTC	720

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1443RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GATCTATGCG	GTCGTGTGCG	CGTGCATCGA	CCAGCACAAG	AGCTTCGAAT	TCGATAGCGG	60
GAGCTTCTTC	TTTCAGTACG	TCGAAGGCAT	CTACTCGTAC	AGGACTGCGA	GCCTTCTTGC	120
GGGCTATCTG	CGGACGCACT	CCGTGCGGAC	GGCCAGCCAG	TACGCCAAGG	TCTTCTCTAGA	180
CCGCGCGCCC	TCGCCACGTC	AGGCGGAGGT	GCTGCTGCTG	GGCATAGTTG	CGGATGCGGA	240
CGCCATGCAG	CGGCTAGTGC	AGGAGTGCAA	AACGAGTGGG	GGCGTGACAT	CTGCGAGCTT	300
CTCGCTTCTC	ACAGAGTGCC	TCGACATATA	CCTGTGCTAT	GTGAACGATA	CGTTTTTGCT	360
GGGGCCCAAG	AGCAACTTCC	CGCTTGAAGA	TCTGTGGTGG	TTTTGCAACT	TGGTGGGTGA	420
CGGATATCTT	CAGGCTTTTC	GTGCTGAGCA	TGATTATGAG	GTGAACAAGA	TGGCGCGGCG	480
GCTCTCTTTA	CTCCAAAAGC	TGTATATTAG	GGATAGAAGG	ACCAATTTC	TCTCGCGGCG	540
CAAGGGGGAC	GACTTCTGGG	TCATTGGGGA	TACCACGGTG	AAAAACTGCG	ACATTACATC	600
TCTCCTTCTT	TACTTTGATG	AGTCTTACAG	AGAACAGTTG	GATTGTGTTCC	TGGGCGAGGG	660
CCGTGCTCGG	CACGAGGTCC	CAGCGGCGAT	CTCGTAGCGT	GGGAAAACGA	TATAAA	716

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1443UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GATCGGGCAT TTACATCTGA CATGTAACCG GGTGGTTCIG TAGGTAGGGT GTTCAATGTA	60
AACTGGTGGC AGTTCGAAGT TGGGGTAGTA CTAAATTGGA ACCCGGTGG CCGTGGTAGA	120
AGATGGGCAT CGTGAAGGIG TTCCACAAA CTATTGGTTT CACCTCGGA TACTTCATCT	180
TCATAACTGC TTCTAACA TACATCTGG TCATAGTCTT CGTAGGCTGG TGGAGGCAGC	240
TTCATGCCGT TCAGCTTTC ATATCCCCAT TTCTTTAGT TTGCTTCAAT GTAGACGAAT	300
CCGTAGGTCC CGAAATTAAC GTGTATCTTG CATGGGACAT TGGACCAAC AATCGGGTAA	360
AGATACTTAA TTTTCCAGCC CTTTATGTGG CCACCAATGC GTTCTCATT TAACTTCTTG	420
CCATTGGCGG TGAAGAAAAC TGTGCGGCTC CGAGTCTGT AGCCAATCC GATGACGTGG	480
CCCTTTTCGC AGCGGGGGAA TAGTGAAGAG AGTTCCTGG GGAGCTTAA CGAGTTGTTT	540
AACCTACGTG CTCCATTAGA GTCATATGCA ACTGAGTGAT GGTGCTGCC GGAAGCCTA	600
AAATAGGGAT ACGCGATGT AGCAAGACCA AAGGAACTA TTTGGTTTTC TGAGAGATGG	660
CTGACCGGGC GGCCAAGCCT GTCACAGAGT CGAAGATCTT GCACTCGAAG T	711

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 736 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1444RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

10 GATCTGGTTT TATAGGTTCA CGAAGGGACT CTGGACGGG ACCCTGCTGA AGTGTGCCAA 60  
 CATGCTGTAC TTCGTGGCCG TGATGCATTT CTACGACGAC TACGAGCAGG CGCCGGTACT 120  
 15 GAAGAACATT GGGTACTCGA TCTTTATTTCT GAGCATTTGG ATGAATCAGG CACTGCATCA 180  
 CGCCGGGGCG CTATTCAGGG GGGACGCGG GGGCGGGTCC TGGTGGTGGC GGTCCGACAC 240  
 20 ATTTGTGCTG CAGCCCGCAC TATATATCAG CCAGTTCTAC CTGCTGCTAC TGAATGTACA 300  
 GAACCCGAGC TTTCATTGCA CGCCGAAGCT TGACATAATT AATCGCACGG TGCTGGTGGC 360  
 25 CTACGTGCCC CTGGCGCTTC AGTGCTTTTG TCGGCAGCTG ACGAGCTAAG TCACTCGGGC 420  
 AGGAGCTGCT CGGTGAGCTC GTGTGCTATG CGTGCGGGT ATTGCTCAGC GGCATGAACA 480  
 30 TCTGTTATCT CTAAATAGCG TTCTCTAGCT TGCTTAATCC TGGTTACCAC ACTGTGAGC 540  
 GGTATATCTG CCTGCAAGGG ATCCAGCTCT GCGAAGGCTG CAGCGGTGCA CGGTGCATA 600  
 35 CGCAGCATAC GCTGCTGCA GGGGATGGAT ATCCAGCAGC TCGCGCACAC TTCCCGCCCC 660  
 TGCTGTTCCC CCAGCTCGTT TGTGCGGCGC TCGCGCCATC TGAGAAGCGC ACGTGTGCA 720  
 40 CTTCGAGGGC ACGCTC 736

(2) INFORMATION FOR SEQ ID NO:666:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 709 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

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## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1444UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

5  
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 40

GATCCAAATA CATCCGGTAT ATATGCTACT TGTGCCAGAA GACATGAAAA GCAAGCATCA 60  
 AGGGAGCTAA TGAGCATTTCT ACAGGAAAAG GCGGAAGAAT ACTACGTTGA TGAAGTCAAA 120  
 GCTATGGCAG AGACTGAACT CTTGAGGAC AAAGAAGATG AAGAAGAACT ATCTGTGGAA 180  
 GAGCAGGTGC AGAAAGAGCT AGAGCAATTG AAGAAAGGCA GTGGTCTGT GGATACCAAA 240  
 AAGAAACCGG TCCTGCAAGA GATTCAGTTG GGATGTGAAT GTATGGTCTT CATCAAGACT 300  
 AGAAGACCAA TCAAGCCGGA ATGCTTTGTC AAACGCCTAG TACAGGAACT TGCATGTCA 360  
 GAAATACTA CCAAGGTTTC GGGTACGTC CAGAGATTGA CACCCATCAC TGATTCTGTC 420  
 AATGCTAGTC TAACAGAATT GGAAAACTC TGCAGAAGGG TGCTTGCTOC TCATTTCAT 480  
 ACTGACAAAG AGATAAAGTA CAAGTTGCGG GTCGAGGTGG TAAAACGTAA CTTCAACACG 540  
 ATAGACAAAA TGGATATCAT TAACTTGTG GCGAAGGAGG TGGTAAAGAG TGGGGATTGG 600  
 GGGCACTCTG TGGACCTAAA GGACTACGAC AAGCTGGTCA TCGTGCACTG CTATAAGAAC 660  
 AATATCGGCA TGTCTGTGGT GGACAAGGAT TACTCTGTGG CTCTTAAAA 709

## (2) INFORMATION FOR SEQ ID NO:667:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1445RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

10 GATCATCTTC CGAACATACT CGAGGGAGTT CGGGTTCGGG AAGTTCTTGT ATCGTTGCAT 60

GTAGTGAAT TGCTCGTAAT CGTCTGTAAA TAGAAAATTG GCGTCAATCA TGTGTGCCCC 120

15 GTTGGACGGG CCGGAAATGA ACATGAACGG TGGCAGCCCC TAGCGCACTT TCTGGCCCCG 180

GCACGCGCGC AGAATGCGAT CGTTGGTGGG CAAAATATCG CTGTACGGGA CCGGCATCTT 240

20 CTCTTCTTGG ATGGGCTCCA ACACCGCCAT CTTCAACAAC TCGCGGCCAT AGCTCATCTC 300

CATCTCCCGC GAGAGGAGAT TGTAGTGGC CTGCGGGGGC CGACTCGTC CCGACTGCTC 360

25 CGAACGCAGC AACGTGACG TGCTATTCAA GCTAGTGTTC GAAAAGTGA CATGCTCGTC 420

ATAAGAGGAA CAGCTGAGCG CCATCTCGGT CACGCTGAGA AGGTACTGTT CTTCCTCGGT 480

30 GTACAAAGAC CCGCCTTGT ATGTCGAGCC TCTGGTGCAT TCCATTGGTG TCGCCATTGC 540

TCTGGGCGAG CCTGATACAC TGCCGTCGA AATACTACCG CACCACGCA CGAACGAAT 600

35 TTCCGCCATT CTTTGGTTC ATAAACCGG ACTACGATA TATTTATCC TGCTCTGGCA 660

TGTCCGATG CCGTCTCCG TGTGACATAG CTGCTTATTC ATCTGGGGG TTCATTT 717

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(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1445UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

5 GATCCTTACT GACGAGGAAG AATCGAGCAA TAAAGTTGAC GCGGCTTCGA GCTCTAATAG 60  
 CGSTAAGAGC ACCGCTAGTA AACGTCCAGC CAAAAC TAGG AAGCCTAAGG CTGACACTGC 120  
 10 GGCTACGAAA AKCGGAACCA CCTCCCGGAT GCCCAAGACT GCTGCTTTGC AGGCGCTGCT 180  
 GAACAAGAAA AGGGGGGCTT CGGCAGAATA GACTACTGGT AAACGTAAGT AATAGTATAA 240  
 15 ACTTGGTTTT TTAATCCCTG GCTATCTCAG ACTGCTAAAG CATGGCCGTT TAGGTGTGGC 300  
 CTCCTCGGTA GATGGTTTGC ACCACGCAAG GTGAAAAAAA GATCACCAC CCTGAAAAAC 360  
 20 GTTTAACTACT TGTCAATCTC TAAAGGCGCT GCAATCAAGG CATATTACCA TTGTGGAGCC 420  
 ATGAATCTTG CCAATGAACC GAAGTTCCAA ATACAAGTTG ATGAAACAGA GGATACAGAG 480  
 25 TGGAACGATA TTTTGAGGCA GCATGGTGTG ATCCGAGAAC GGCCACCTTC ACGACCGCA 540  
 CAGCTGAGG AAGCGCTCGA GGAAGTGCTA CNGAGACCAC ACGAGAATAG ATTAGAGAAC 600  
 30 AAAGACTCTC TGAAGTGGAG GACTGGAAGA TGAAGAAGAT GATGAATTTT TGGAGTTTTA 660  
 CCAACGTAAG AGAATGGCAG AAATGCAGAA GCAACAAAGA AGCGCAAGTA TGGGGAC 717  
 35

## (2) INFORMATION FOR SEQ ID NO:669:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 775 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 45 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: PAG1446RP  
 55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

5	GATCTGCAGG CTGCTACGGA GGAAGTGGTT TCGAGGTTG CTCGCTGAG TAAAGACCCA	60
	AACTTTCTTA GCATTTTTCG GCAGGAGCTA CAGAAGCTTA CTGGTGAGCC CCATATAGGC	120
10	GGCAAGGTGG ATGATATAAC GGTAGTGATG GTGAAGGTAG ACTAGTAGAT TGCACATATG	180
	TAGAATTACT AATATCATTC GAATTTCTGG CTTAAGACAA TGTTCCTAAT CCGCTCTCTC	240
15	TGCTCTTCA ATCTCTGCTC GCTTCTAGT ACGTCATGAA CAACTTGAC GTGGTGCGC	300
	AGGCATATOG GCGGAGTTG AGTCCGCTTT CCGATTTCG TGAGAAAGT AAAGGGCACC	360
20	TTACCCGCTT CGACTTTTGA TGACAGATTG CTGTTGACCT GTGTGCTGGT CCCAGATCCA	420
	ACGATAGGAA TGTGTTCAT GGGGATTTTC TCATTCTTGC GGGATCTTAA AGATTGTTGC	480
25	ATCACAGCTT GGTACATCTT TTCCATTTC TCTTCTGCTC TCCGCTCTC CTCGACTTT	540
	AGCTTTCCTT CGTATCTTC GTTATCTTT TTGGCTCTA GATCTCTGC AATAGTAAAC	600
30	ACGTCTGTGT CGTGTGAGT ATCTTCTTCA CTTTCACTGC TTGACGGGGA ATCACTATCG	660
	TGTTCATCT CATGTTATC TTCTCTGAT AAGTGTATT AACGCTTCT TCTTCTAAGT	720
35	CGCTGGAGTC GGCAGTGTCT CCACTACTAG ACTGTAGCC ACTATCTTCG TCCTC	775

(2) INFORMATION FOR SEQ ID NO:670:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 631 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1446UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

5	GATCAATTAC ACTACTAGCA ATCTACTTTT CAACAATCTG ACTGTCCGGG AGGTTAAACT	60
	CTACCGTGAA CAGCTGATGG TACTCAAAGA GCAGAGGTTT ATAGTGGAGG GCATGCTCGA	120
10	GAACGCCAAG AAACAGCGGC GTTTTGAAGA GGTTAATACG TTAAAGGAAA ATACCAAAGA	180
	GCTAGACAAT CAGATAGCCC AGCTCGAAGA AACCTAGGC GACCAGGGTT TTGTTTAGTA	240
15	TCTAGCATGG AGTTTTTTGC TTAATAATAA TTACTGTGTA GATGCCGCAG ATAGCATGTC	300
	GTAGCATAAT TCGAATTTT CACCAACATG AAAAAGTGTA TGTGTATAAG GCATCCAGTG	360
20	AACTCCTAAC ATGCTGATGA GGTTTAAGT AAAGATATCA CTAGCAATGA ACGTAAGTGC	420
	AGTTTTTGAG CTTTATGTCC TCTGTAGAAC ATAATATTAA CGACAGGGGG ATAGGATGAA	480
25	AGAAGACAGC AGTTATTIGA GCTGAACAGT GAAGCCTGGT CTGGAATTGA TCGGTTCGGG	540
	AATAAAACCA GCAAGCTTGA CTCAAGCATC AAGAGAAACA CAGGTTTAT CAAAAGCTG	600
30	AAACAGGGTA TCACGAAAGA CTCGAAAGAT C	631

(2) INFORMATION FOR SEQ ID NO:671:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1447RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

55	GATCCAGGAT GATGAATTTG ACGAGGAGGG GGGTGCAGAA GAGAATGACG ACTACTCAGC	60
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GTTTAAAAGA TCCTGCATGT CCTCCACGT CCCCCTGTG TAGTAGGCAT AGCGCTCGTG 120  
 5 GTACGGGCGG TCGCCATGG CCGCGCCAT GGGCGGGG CCATGGGCC ACCCGTGGC 180  
 GTACATGTG TACATCGGC GCGCGAGC GTCCGAAAGC AGCGGTAGG CCTGTTAAC 240  
 10 CAGCTTGAAG CCGCGAGG GTTCGTGCTC ACCCAGCCCC TGTGGGCAG CCCCCTCGT 300  
 GTCCGGGTGG TACAGCTTC CGAGCTCGTG GTACCGCTTC TTTAGCTGC GTGCATGAC 360  
 15 GCGGTCTTC ACCAGTCCA GTACCTCGTA GGGCTGGC TCCTTGCCCT GGGGCCACGA 420  
 TAGCCCCCCC TGCCACCGG CGACGGTGT AGCGCACGC ACGTACTCC GACCTGAGC 480  
 20 TGTAAGCGAG ACCGCCAAG TCGCCAGTC CTGAGCAGTG CAGTGGGAG CGACAACATA 540  
 ACACCTAAGC TCCTAGTTAA CGCTTGGG ATGGAGATCT TGTGGTGCA TGCACATATC 600  
 25 CAGGAGCGG CTCGCTCC GCTGACTGC TGGCGTCCA GCTCCAGTT GCGCGCTTA 660  
 GCCATATCG CGAAAAATA AAGTCTGCT CGAGCGGGA TGA 703

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1447UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GATCAGCAG ACGTCCGGC TGGCTGTTG AGATGCACTG GCTCTTGGG GCGAGTGGC 60  
 55 GGCAACGGC CCGCGGGC AGACGGGCC GCGCGGCG CGTGGGGTA CATCGCAC 120

AGGTTCTGCA GCTCAAACCTC CAAGGCCAGC TTGTTTCTGT TCTTCTTGCG CTTCGGCTTG 180  
 5 TACTTGTAGC CCGGGTACTT CTTCGGCTGC TCTGCTKCT CCAGTTCGCG CTGTGCTGC 240  
 CACTCCTTCT TCTCCTCGCG CGTCAGTTTT TTCCACTGGT AGCTGATGAT CTTGCTCACC 300  
 10 TCGCAGTTGT GCGGGATGTC CTGGCCGGAC TECTTCCAGT AGTCTGTCAG CAGCTTCTGC 360  
 TGGTGGGACC GGAACAGGAT GAACGGGTG CCGGGCCGCG GGATGTGCTG CTTCTGCTTG 420  
 15 TAACCAGCGC GCGCGCGCG GCGTGGCGCG CCTGCGCGTC CTGTTCCGCG ATCCTGGTGC 480  
 GCTGCCACTC CTGCGCGCG GGGGGCTGGT GCGAGAAAAA CTTCTGTGCG AGAGGCGCTG 540  
 20 CCGCGCTGCG GCTGGCTGCG CGGCTGCTCC GCGCGCGCTG CGGTTGCGT GCGTTGGTCA 600  
 AAGGCAACAA TTGCCCCGAT CTCCCGCGCG TGCTGGCGCT GGTGTACGAT CCGTGTGATG 660  
 25 GTCAGCTTCT GCTCCAATCA CAGA 684

(2) INFORMATION FOR SEQ ID NO:673:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1448RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

50 GATCCGCTAC GTATACAACG ACATATTGCT ACGTATCGAA TGTGATGTGA CAACATGCAA 60  
 GATTCTCAAC AACAAAGCGCA AGTGGTTTAG TGGTAAATC CATCGTTGCC ATCGATGGGC 120  
 55 CCGCGGTTG ATTCGGGCT TCGCATATT TTTCACAACA TGACACACT GTGTGGCTAT 180

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CGAGACGGAG TCCACTACGA GCATCGTCAT TTTTGTCTAT AATTTCACAAG CATATTGTAA 240  
 5 CTATTGTGTC ATTGATCTAA ATGTGAGTC GATAGAATCC TTCAGCTCCT TGTAGCTAAT 300  
 GATAATGCAG TTCATCTCGT CCGGTGTCAC CAAGATTATC TTTTCAGATA CGCCGGTGTG 360  
 10 GAGTTTGTTC AGGCACCGGA GTACGTGGGT GAGGTCCATC ACGGATTGTC CGTTCTCGTC 420  
 CACCTGGTGG AACACGTAAT CGTAGAACAG AATGATGGGG AACTTGTCCG CCGCCTCAGA 480  
 15 CCAGTGGATG TCCATGCTGG ATTCCATCCT ACCAAAGATG AAATTAGCT TGCACATGAG 540  
 OCTGAAGAGC CTGCCATTCT CTAACCTCCG CGACAAGTGC TGCTCGATGT TCTCCAGTA 600  
 20 GGTCTGCGAC GAACTGATTA TGCTAACAT CTTGTGGCTG AACAGGGCGG TGAACCTCCG 660  
 AATCGTCTTC TTCTCGTCCG ACAAAGGTA CGCCAGCACC CGCTTGAACA GCGGGTGG 718

25 (2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 724 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1448UP  
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45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GATCTCGCCA GCGCTGGCAT CCGCAGCGCC GCAGGCGCCG CGGCGCGCGG CGCGGCGCGG 60  
 GCCACTGGGC CACAATGCTG TCCCATAGCC CTCAACATCC CAACTAGCTA GTCACCTTGT 120  
 50 GCAATCGGTC TACCGATGGT GTGTGCGGCG GGGACAAAGC CGTGGTGAAA CGGACACTTT 180  
 TCAAAATGGG CTGATCTGCA GCAGTACAG ACCGATGAGC TGCGGCGACG GCGACAGCAG 240  
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TCGCGGTTCG GCGCCTGGCT GCGCATAGGG AACTTACGTA TAGTATAGAA GGGCGGTCTA 300  
 CTTCGGGTAG GCACGGAGGA TGTCGTGTT GTAGCGGAGG TATTTCGGT TCGCGCAGTC 360  
 CCGGATGCT CTCAGCGCCA GGTTCGGCAA GATGGTGGC GGGATCTGG GGTCCAGCAG 420  
 CTGCTGTC TTCTTGAGCT CCGTGAAGC GCGCAGTGC TCGCGCGCA TGCGATGGC 480  
 GAACTTGTG CGGATGTCT TCTGCATCTG CGTGTGACC ACCCGCGCG CCACGGCGAC 540  
 CCGCGCACG GCAGGCTCTT CCGCGGCCAG CGTCATGCA AAGTGGTCA GCGCGGCTT 600  
 CGACGAGCG TAGCGGCCC ACCGGACTG TCTCGAGTT AGTAGCTGC CTGCGCTGC 660  
 TCTGCGTGT ACATACATAT GCTTGTGTC TCGCGCGCA GTCACGAAC ACCACTGTC 720  
 CGCC 724

## (2) INFORMATION FOR SEQ ID NO:675:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1449RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

45  
 50  
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GATCCAAAGA CCGGTGCTC GCACTTCCAC ATGTCTCCAA GCTGGACGG AACAACGATA 60  
 TCTTACTGGC GGTGAAAGAA AGCCGAATC ACAAATGCC ACATGCTGG AAGCAAGCAT 120  
 CTCCCGAGGC CGACGCTCTA TGTAACTGCT GCGCCAGAGT CTTCCAGTAA GCCAAACCTG 180  
 AATTTTTCAA AAATTGAAAA CTTCACCATG GTCACATGC TGACTGCTTT AATATCCTGT 240

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AAATACAACC GGACTCTGCA GGTCGATGCT CCCTCACCTG GGGCCCCAAC TCTCCCTTGT 300  
5 ACCGGGTGCG GGGTGGCTG CCTCATTCOG CCTGCATCTC GCTTCCAGAG GGGGGGCTTC 360  
TGGGGTGGCG GGGGGGCTGC CGGCATTCAT CGGGGGGGCC TACGGCAGCC CACGGGGCGA 420  
10 CGCGAGGCAG ACCCGCGGGT GGACGTACCT CGGGGGGCTG CGGCTCTTCC AGCGCCTTTA 480  
CGCGGGGCTT TCGTTCGGCG CGTACATCGA CGGTCTGCTG GCCAACGGGC CGGTGCCAAC 540  
15 ACTGGCGGCG TTCTGCTGCT TCCATGAGGC CACCGCCATC GCTCCTCTGG CGCTGCTGTG 600  
GTGGGGGGTC TACAGCTGGG AGGTGGTGGC GCTGTGTGGG CAGGGGCTGC TTGACTAAGT 660  
20 GGCCGAAGCA CGCATCCTGC CGTCRAGAGG TTCTGTGG 697

(2) INFORMATION FOR SEQ ID NO:676:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 715 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1449UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

45 GATCGGCTCA ATGGGTGCT GAAGCCGTGT CTTTCGTAAG ATGACCTCAA CTAAAGGCA 60  
GGCTCTCGAT ATCTCGTTTC TTTTMTAAC AGGTGAGCTT TGGAAAATTT TTGGTTCTCA 120  
50 GCTCATCTCA TCTACAATAG TATGTCTAGC ACGCCAGCAA AGCTTGCGTA ACGCTCTAT 180  
TCAATATGAG TAAGCAGGTA AATGATACTA GCAAGAATGG TCTTGACCTA AAGACGCTGT 240  
55 TTGTCCGAA TATTCGGTTT GATGCTACGG ATGCAGAGCT GACAGACTTC TTCTCGCAGT 300

TTGCACCTAT TAAGCATGCT GTGATCGTAA AAGATAATGC GGGCTCGAGC AGAGGGTTTG 360  
 5 GGGTTGTGTC GTTTGCTGTG GAAAGTGATA CACAGGCTGC ATTGGACAAG GGACGGAAAA 420  
 CACAGTTCAA GGGCGGTCTT CTGAGGGTGG ATGTTGCCAA AAGAAGAGAA CGTTGAAAA 480  
 10 AAGGCGATGA GGCCGAGGCA CAGACCTCCG CGGAGGACGC GGAGAAGCCG ACTACTGCTC 540  
 CCGAGGGTGA CGAGGCGCTC ATCGGGGCA AGCCCAAGCT GATCATTAGG AACATGCOGT 600  
 15 GGTCTGCGG CGACCCGACC AAGCTGAAAA AGATCTTCGG TAAGTTCGGA GTGGTTGCGG 660  
 AGGCTCCATC CCGCGCAAAG CGGATGAAA GCTGTGTGGG TTGCATTTGT CACGA 715

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1450RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GATCAATTCT GTCTTGAAGT AGGTATTAAT CAATGGGTCA GGCTGGGTGG AATTGCTTAC 60  
 45 AAAAATACCA ACCCAATCAT CTGTAAAGTT GGTGAGCGAT ACGTAGACAA TTTGCTCAC 120  
 ATCAATCTTA TAATGACAG CATAGGTGAG TTGATTATTA ACCAGTGTCT TTCCGATAAT 180  
 50 GTAGAAATGG GATGGCGTAA GTATAAAGT TTTGGGTAGC CTTTGGGCGG ACCTACCAAA 240  
 TTTTGAATGT AGCGCTTGCC CATTGATAGA GAATACGACA TGATCATTAA TTCCAGCTTT 300  
 55 CCTTTTGACA AACGCACCTT TCGATTTTCTC CTCATTACAA GAAAGGTAGT CTCCAGGAA 360

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TGCCTGTAA CCTAACAAAG ACATTGCACG CCTCTCCTTT CTGCCACCCA ACAACTTGTT 420  
 5 ACOGTAAATCC CGGAGTTGTT CGAATTGGTT CCCATGTTTC ATCTACCGA TAGCAGCTG 480  
 GATACGAATC GCAGAATCGA TACGCGTTG TAAAAACGC CGCCAGGCTC TCTGAATGCG 540  
 10 AGATGCCATA TTATGCCAAT ACTTATCCTT CATGTTTTTC AAAGCAAACA AGGTCTCAGG 600  
 TGTTTTAATA AATACCTTCG TTACACCCAA CTGATATTCA GTCACAGGAA TTGAAGTATC 660  
 15 TCTCAAAATT AAATTGACAG CATCTAAGGT ATTACCTTGC CATGT 705

## (2) INFORMATION FOR SEQ ID NO:678:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 699 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1450UP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

40 GATCGCAAGT TGGAGAGCG AGTATCCATA TGATTACTCG CGGAGACGC CCGGCTCGCG 60  
 CATCAAGCCT CAGACAGTTA TCACTCGGCT CTCGAAATC GCAAACGCCA CCGGAAAGGA 120  
 45 GGTCATCGTG ACGACCGGTG TAGGTCAGCA CCAAATGTGG GCGGCCAGC ATTGGACGTG 180  
 GAAGAAACCA CGCACATTTA TCACATCAGG CGGCTCGGT ACCATGGGCT TTGGTCTACC 240  
 50 GCGGOCATT GGTGCCCAGG TAGCCAAACC CGATGOGATT GTCATGACA TCGATGGCGA 300  
 CGGCTCGCTC AACATGACCT TGATGGAGAT GTCCAGCGCG GTCCAGGCGG GCGGCCAGT 360  
 55 AAAGATATTG TTGTTGAACA ACGAAGAGCA GGAATGGTC ACTCAATGGC AGTCTCTATT 420

CTACGAGCAT CGTTATTCTC ACACCCATCA GCTAAATCCG GACTTGGTCA AGTTGGCTGA 480  
 5 TGCAATGGGG TTCAAAGCAA TGCGCCTAGA GCGCGAGTCG GACATGGAGC CCATGCTGCA 540  
 GGAGTTTATT AATTGCAAGG AGCCCGTGT ACTCGAAGTG GCGTCGAGA AGAAGGTTCC 600  
 10 CGTCTCCCG ATGGTCCCTG CCGTAAAGC CTGCATGAGT TTATCTACTT CGACCCAGAG 660  
 GTCAGCGACA GCAAGCGGAG CTTGCGAGCA GCGTACCG 699

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1451RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

GATCTTGGTG GTAGTAGCAA ATATTCAAAT GAGAACTTTG AAGACTGAAG TGGGAAAGG 60  
 40 TTCCACGTCA ACAGCAGTTG GACGTGGGTT AGTCGATCCT AAGAGATGGG GAAGCTCCGT 120  
 TTCAAAGGCC TGATTTTCCA GGCCACCATC GAAAGGGAAT CCGGTTAATA TTCCGGAACC 180  
 45 TGGATATGGA TTCTTCACGG CAACGTAAC T GAGTGTGGAG ACGTGGCGT GAGCCCTGGG 240  
 AGGAGTTATC TTTCTCTCTT AACAGCTTAT CACCCCGGAA TTGGTTTATC CGGAGATGGG 300  
 50 GTCTTATGGC TGGAAGAGCC CAGCATCTAT GCTGGGTCCG GTGCGCTTAC GACGCCCCCTT 360  
 GAAAATCCAC AGGAAGGAAT AGTTTTCATG CCAGGTGTA CTGATAACCG CAGCAGGTCT 420  
 55 CCAAGGTGAA CAGCCTCTAG TTGATAGAAT AATGTAGATA AGGGAAGTCG GCAAAATAGA 480



TCGGTAACTT CGGGATAAGG ATTGGCTCTA AGGATCGGGT AGTGAGGGOC TTGGTCAGAC 540  
 5 GCGGCAAGTG TGCTTGTTGGT CTGTCTCTGG GGGCTTGCTC CTGGGGAOCG ACTGCTTGCG 600  
 TGCTCTGTGG TAGACGGCCT TGGTAGACCA TCTCTGGTGG TOGCTTGCTA CAATTAAOGA 660  
 10 TCAACTTAGA ACTGGTACGG ACAAGGGGAA TCTGACTGTC TAATTAAA 708

## (2) INFORMATION FOR SEQ ID NO:680:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1451UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGCCATT GAGCTCTTAC GAACTGCACA 60  
 35 AACCTACTOG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTTCAACTGC TTTCGCATGA 120  
 AGTACCCCCC AGGCTATTTT TCTTACCGC CTGGTGTMTG TCTATATACC CGTTGTATT 180  
 40 TTTGATAAAA AACTCAGCTC TTCCTCTACG GCAGAAATAT ATATCCAGTC CTTAGCGCCA 240  
 TCGGAAAATC TGCTTTTTTA CGCTGTTTC TCCAGTCTT AGCACTGGCA GAAAAAGAT 300  
 45 GTATGGCGTA TAGGCGCTGG CCCCOCGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA 360  
 AAAAGACGTG GCGCGCCCGG CGGCAGACG AAGAAAAAAT AGGCGCCAC CCTTCCAAGC 420  
 50 AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC 480  
 CCGGCTCAT AGGCTGCCAT TCTGTTCCAT CCGGCTTGCA AACCCAGTAG TGGCATGTCA 540  
 55

AAGCATTTGCT CCGACGCTCC GCTGCGTTGC AGTGGACATC CTCTTCTTAA CCCCAGCCAG 600  
 5 ACTTCCCATTA CTTTGCACCTT CACATAGCAT ATCACTTTTC AGATCACTAC GTGACATTTC 660  
 GTACGGAATG GCACTCCAAT GCGACAAAC CTCTTCTTAC CCGTGACTT ACCCCGATGT 720  
 10 GC 722

## (2) INFORMATION FOR SEQ ID NO:681:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1452RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GATCAAATGT GGCTCTACAA GGGCGAAGT GGCAGAGAAT ATTAATGAAT CAGTTCCGCT 60  
 35 GACATATTTG TATTGTACG GTATTCCACA TTCTTTGAG TACGTATGTC CGTCTAGGAA 120  
 TGGCTGGCTT AGTAAGGCTT AATATTAAC TAAAAGCGCA GCAGTGTAAAT CCATCTAGTA 180  
 40 ACTAACACAT ATCATTAGC ACATGTTTCG TTCAGTACTA CGTCATTCTT ACGCCGTCCC 240  
 TACTGTGAAT TACACATGGT CCTCGAGAAG CCTCATAAGA TTCTTCACTA GCGATGAGAA 300  
 45 GGCAGCTCCT CCATCGCTTC CGAGAGAAGA GCAGAAAGAG TTCGAACGGC TTCAGAAGAT 360  
 TGCACAGTCA CAAGCTGCCA TCGACGAGTA CAACAGACAG TTGAGAATG ACCATAAGAA 420  
 GGAGTCAGCG AACTCTCCCA TTCTCAAGAC AGAAATAGGC TCGTTCTCAC CGGAATTCAG 480  
 50 CAAGACGTTG CCAGAGTTTG AGGCGGACAA GAATCCCGAG ACAGGGGAGA TTGGCGGGCC 540  
 55

GGCCAAGAC CCACTGCGGT ACGGGACTA CTCATACAAC GCGCGGTGA CGGACTTCTG 600

AGGTATAACT TGTGTTTATA TGTTCGAGG TTGGTTAAAT ACATAGCTTG CGCTCCAAC 660

CTCTCGCAGC TGCAGACAGG TTGTGGTGC ACTCCGTGAT GAATTTGAG TCCAGCTTT 719

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1452UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GATCACCAAC TCTACAGCAA GAAATCCTAC GCGCAGCAA AGCTGTCTC GATGTTCTTC 60

TATTCTGTAA ACAGTTTGT ACTTCTGGTC GCTTGTATCT GCATGCGCTA TCATCTTTTC 120

ATCTGGAGCG TTTTCAGCCC GAAGTTGTGC TACCTTCTGG GCTGGAACAT CCTCATCCAC 180

TTTCTCACTG AGACGGTGCT TGAACCTTTC TTGCTCATGG TGGGGGCTG ACTGTCTCTA 240

GTTCCACTTG TATAATATTC CTTCATCAGT GAGAATCTCA TAGTATTGTC ATATATTAGA 300

TATTATCTAG GTCATGTTT AGAGAATAGG TCTCTCCGA AAAAATTGGC TACCACTGCC 360

AATCATTACA TGTCAGAACC GACCATCTCC AAGTGTGAA CCGTCCCCAC TGCAAATGCT 420

CTCACTTAGA TCCAGCTTCA GACGCTTATT TTCTGTTTCC TGCAGGGTTT ATGACCAGCA 480

GGCGCAGAAG GCGTGTCTT CTGCCCCGC TGGCACCCG CTGAATCTGC TTATAAAGAA 540

GGGGGGAAG GAGCGTTGG CTCTCGAAGA TCCGACTACC CGAGTGGTTA TGGAGGTGC 600

TTGACCTGAG GCGCAAGCOG CAAAGCTGGC AGAGGACCCA TTAAAGCOG GAAGAAGGCT 660

5 CTGCGGCGGA TGAACAGAGA ACACATCCAG CAGCAGAACT TCTGGGCGAA GATGTGAA 718

(2) INFORMATION FOR SEQ ID NO:683:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1453RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

30 GATCTTAATT TAAAATTTTA ATTAAGTATT TATAATTTAG AAATATATAA TCTAGAGATA 60

TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATAAAT TAGTAAATA 120

35 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGCCATCTTA 180

ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAA ATGTTATATA 240

40 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300

AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTA TTAATATTAA GTGATATATA 360

45 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420

TTTCATAATA TTTATTTTTA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCTTTAA 480

50 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540

TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTATTAT TATTTAAATT 600

55 ATTATTAATT AGTAAATTAT ATTTATTTAT TTTATTAACA TAATTTTTTG ATAATAATAT 660

ATCATAATTA AATGGTAATT TATTATAAT TATCTTTAAT GAATTTAATG ATAAACCATT 720

5 ATTA 724

(2) INFORMATION FOR SEQ ID NO:684:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 732 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1453UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

30 GATCAAAATT TCAACAATTT CCATTTCATT TAGTACTACC ATCACCATGG ACCAATTGTT 60  
 ACATCATTTA GTTTATTAGG TTTACTATTA ACTTTAGCTT TTACTATACA TGGTATTATT 120  
 35 GGTAAATATT ATCCTTTATT ATTATCTTTA TTAGTAGTTT TATTACTAAT AACTTTATGA 180  
 TTTAGAGATA TTGTAGCTGA ACTTACTTAT TTAGGTGATC ATACTTTAGC TGTAAGAAAA 240  
 40 GGTATTAACT TAGGTTTCCT ATTATTGTTT GTATCTGAAG TATTAAATTT TGCTTCTTTA 300  
 TTTTGAGCTT ACTTCATTTC AGCTATAAGT CCTGATATTC TATTAGGTAA TGTMTGACCA 360  
 45 CCAGTAGGTA TTGAAGCAGT TCAACCAACA GAATTACCAT TATTAAATAC TATTATTTTA 420  
 TTAGCATCAG GTCTAACTAT TACATATAGT CATCATGGTT TAATTGAAGG TAATAGAAAA 480  
 50 CATGCTTTAT CAGGTTTACT TATTACTTTC TGATTAATIG TTACATTTGT ATTATGTCAA 540  
 TATATTGAAT ATAGTAATAC ATCATTTACA ATTACAGATG GTATTTATGG TTCAGTATTT 600  
 55 TTGCTGGTA CTGGTTTACA TTTCTTACAT ATGGTTATGT TACTAATTAT GTTAGGTATT 660

AATTATTGAA GAATAAGAAA TTATCATTTA ACATCAACAC TCATGTAGGA TATGAGACTA 720

5 CTACTATTTA TT 732

(2) INFORMATION FOR SEQ ID NO:685:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 714 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1454RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

30 GATCATGCGT CACCGGCGTG GAACATGCAG GTGAGGCGTA TGTACCCCAT GTTGCGTTAT 60  
 TTTTTCACCT GAAGCGGATT GGCTCTTGTT TATACAGACT TTTCGTCATC CCTTGGGGGC 120  
 35 CAGAGCTAGG GCTAGAATC CGTGTGTAA GCGTTGGGCA CTGATTCAAC ACGAGCACAA 180  
 TTCCAGTGCT GCTCGTAGAA ACGAGGCCCC TGAAGTATAT GGIGATATCC ACATTGCGGG 240  
 40 AGTATAGTTC TCTGTGGGGG CGACTTCATG CCATGTGCAT CTCGGGCTTA CTCCACAGCC 300  
 GCACACGCTG CATTGTTTTG GGAACATCAT GTGAAATACT GGTATAGAGC GCATTTCATA 360  
 45 GGGGTGCCAG CAGCTGTAAT AGGGCGGCAT ACCCGCTCT ATTTTCATGIG TTCATGTGCT 420  
 AGTTTAGAGG TATTTTGTAG GTGCATGGGT TATGGCTTAC TTTCATATG GAGATCTCAT 480  
 50 TCGCTGTAA CGTATATAAC TGAGGTAGCC GTAAACTTGC ACTGGTTCCC ATTGCCAGAG 540  
 CGAAGCTACA ATAGCACCAT CTGGCTGCAA GTTGTGAACA ATGCATTGGA ATCGCATACT 600  
 55 CTTTGGGGC TGTGCGCTTT TGCTGCAACA ATTAACAAAT GCCTTTGATG AAGGAGTGCT 660

AAGGAAATGT TATGAATCTG GTGTATGCCA CCGGAACAGG CATTACGGAG AGAA

714

## (2) INFORMATION FOR SEQ ID NO:686:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1454UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GATCAAGCGC TGTATGGTTC CCGGAGCGCC AGTAACAGCG GTCTGTACG ATTTCACGA 60  
 TTCCAACATG GACGATGATG GCTCCAAAGT TATGTTCCG ACCACGCTTG AACTCAAAAA 120  
 GGTTTTTCAG GCTATTCTGT TTGAGGCCAT CAAACGGGG CTGCAAGTGT TTCCATTAG 180  
 GAATATTGCT CCTATCTTCC GACAGGTGG ATTCAAGAAC GTAAAATATA CGTTCGTGAC 240  
 ATTCAAGCGC GCGATTTCG TGAATGAAAT GGGTTCGTG AACGAGCTAC TTGCAACGTT 300  
 TCACTACGAT TTTCTAGTGC GAACCTTTTT AACTGATCGT AGTAAGTATC CAGTTGGAAC 360  
 TGACCCACAG ACACTGCOGA GGAGGTACAT TGATGAGCAC ATGGGCCAAA TAGATGACAA 420  
 TGCAGGATGC TTGCGTCTTA TTGCAATCAC GGCGGAAAA CCAGAGTAGG TTTCCACCGT 480  
 TGCTATTGCT ACCCGGGGCA ATTCTCCGG TCATTATATA TGTTAGCAGG TGTCAATACC 540  
 TCCTTACAAC CTAATATTTT AAAACCTAAT ATCTTCTGCT CCTTAGAAAG AGCCACTTCC 600  
 TTATATGTTA ATATCTACCG CTAGTCTAT CTAATAATT TATAATTTTG ATAAATCTTG 660  
 ACGTACATCT TATCACTAAG GAAGATCTCA TCACAAACTC CGCAAAGTGT TTCATATATA 720

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1455RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

GATCTCTTCG ACATAGTGT TTAATAGGCC TGCTGAGGAC TTCACTGAGA AAGCTTCAAT	60
AGCGGGCAAT GGCCCATCTC ATCAACACTT AAAATTTTTC GTGGCAAAG AAACAACACT	120
GGAATCACGT GACCACACAA AACTCAAGAT TTAAGTTTGA AGGGGAGCAG GCTACGACGA	180
CTCTTCTTCG CATGGTAACT CGCTGCTGTC CACTTGCCGC TTGGGAGCCT TCTTTGCTGA	240
CGCTGCTCTT TTCTCTCTTT CTAACAGCCT CTCCCGGTTA GCTGTGATGT AGTGGATGAA	300
GAAGTGGCCA TCCTTGCTGC GTTTCGCATC ACGCAGGAGC GTCTCGACAT CGTCGTATAT	360
ATCAATGCGT CGCTTTGCGA GTTGGTTTAG CAGCTTGTTA TCACGCCCTG CACATTGCAA	420
CTTCGGGATG GCTTTGGTGC ACTTGAACGA CACCTCGCCC GGTTTCATAT ATCCAGATTT	480
GCGCAGGTTG TGCCAGGGCG TGCTCACAAT GCTACATTGT GCGTCTTGT TCCCTTGTTAC	540
AGACTCTGAC TTGCACAAC TGCAGGAGGC ATGCAGCACA TCCCGGGCA CGTCGCTGGA	600
GCTCTGCTGC TTTGCATGTA ACTTGAGATA GACATGTGGC CTGGCATACT TGTCTACGTT	660
GGAAACCAGAA GTAGTTTAAT CCGGTACCC GTGCTTGAAC AAAAGGTGCT TC	712

(2) INFORMATION FOR SEQ ID NO:688:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1455UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GATCCCATCA CATGAAATGT CTAGAACTCC CTGCATGACG CGAATGAGGC CAAGAATGTC	60
TGGTGGGCTT GGCTAACCGA TGTTCGCAAC TGCAACAAGG GGTACCTGGT GTTTATAGCC	120
GTATGTGTC ATCCGGGATT CGTGCAACAG GAGAGAAGAA CCGGACCACA AGGAAACGCG	180
GTAAAGCATC TAGAATCAGC AACCTAGAG AACGTTTGTT CGTCGTTGGC GCAAGAGCAC	240
GGAGCGTAGG GGCTGGGAGT TCCGGTGGCT ATTCAATCGT GGGCACGCGG GGTATATAAG	300
TAGGGTATGC GTCCGTTGAA CAGAATGGAT CCGTCTCAGA ACAATACCAA AATCGCATTT	360
GGAAAAACAA CCACTAATAT GAAGTACACC TCCGCTATTG TACTCGCTCA AGTCGCTTTT	420
GTTGCAGCAC AGTCATCCTC GGGGTCTGTT ACCGGCAGCG CTGCCCCCGC TCCGGGTGCG	480
GGGTGGGGCG CAAGCATTTT TAGCACCAGC ACAGTCACCG CCTCAGGTTC TGGACCAGGC	540
GCGAGTCCG GTGCTAGCTC CGGTGCAGCA GCGGGGGCG CTGGGGGGGC CGCAGGTGGC	600
GCCGCATGTG GCGCCGCAAG TGGCGCCGCG GGTTCCTAACT CCGGCAACTC TGGCTCCAAT	660
GGATCTGGCT CCGGGCCAGA AACTCTGGA ACAGAACACT CCGGCCCAGA AACTCTGGA	720

## (2) INFORMATION FOR SEQ ID NO:689:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1456RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GATCCACGCC GCGCTGCTGA CCAACGTGCT CATCATGGGC GGGACCTCCC TGCTCCAGGG 60  
 CCTGGAGCAG CGCTCGTCA ACGACCTCAG CCTGCAGTTC CCGCAGTACA AGCTCTCTAC 120  
 CTACGCCACG CCGGCCACG TCGACCGCCA GCTGCAGAGC TGGCAGGGCG GCGTCAACAT 180  
 GTGCCACCTC CCGACTGGA AGCTCGGCTC CTGGGTCACC AAGCAGGAGT ACCTGGAGTC 240  
 CCTCGACAAG TAGCTGTGTA GTATGTAACC GTATGCCGCG ACCCTGGGGT TTCTTTCCCG 300  
 CTCCCCCACC CCCATGAGC CCCCCGCGCG CTTCGCGCGC TCCCACGCGC TGGCGCGCGC 360  
 CGCGCGCGCG CGGACACCG TCGAGCTCTA OCTGGACTAC TGCTGCCCCCT TCTCGCGCGC 420  
 CCTCTTCTCT GCGTGGCAG ACGCCCTTTT CCCCCGCGCG CGGCGCGACT CGCGCTTCCA 480  
 GATCGTCTTC AACCACTCA TCCAGCCCTG GCACCCCGCG TCCAGTACA TGCACGAGGC 540  
 CGCCCTCGCC GTGCGCGCG TCGACCCGCG CGCCTTCTCT CCTTCTCTGC GCGAGCTCTT 600  
 CCTCCACCAG GACCGCTGGT TCGACACGCG CACCGCGGAC AAGTCGCGCG ACGCCGTGTA 660  
 CCGCAAGCTC CGGACTTCGC GCGCGACGCC GCGCGC 696

## (2) INFORMATION FOR SEQ ID NO:690:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 739 base pairs

EP 0 866 129 A2

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1456UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GATCTGGAAT ATTACCGCA CAAACTTGGC GCTGTGCTTC CACACCAGCC TCCGGTACCG	60
CTTCACGGCC ACCAGCTCCT GCAGCAAGCG AATGCACACG TATGCCAGCT CCATGCGCTC	120
CAGATTAGTC AGAACCCGCA GGTAGTTGGG GTTCGACACC AGCGCCTCCA CCAGCTCCTC	180
GCTCTGCAGC CCTCCTGGA TCAGCAGCGA GACAAAGTTG AAGCAAGACA GCAGCAAGAA	240
CTGGTCGTCC GCGCGCTGT CGTCAGTGT CGACTCGTAC AGCTTGCGCA CAAGCTCCGG	300
GCCCTTCTTG AAGTACCGCA GCACCTCGTG CAGTACTTGT TGCTCGTGA ACAGCTCCGA	360
CAGCAGGTTT AGCACCGCCC GCTTCGCATC CAGGTTGTTT GACGTGCGCA GCAGGTGCAC	420
CAGCGCCTGC ACGCCCTGTT CCAGCGGCAG ATCCAGCGCG CCGCCGCGCG CGTGTTCCTAA	480
CAACGTCGAC TGAGCTTCT TGGCAATCC CGCGTCAAAC TGCTCAGCT CCGCGGAACG	540
CACCAGCGCG TCCAAGCCA CATGCTCGA GCTGATCGTA TTGCGGATAT CGTTGAAGTG	600
CGTGCTATCA AGCAGAATCT TTTGAACCCC CTGAGCCACG GGCATCGTCA CAGCTAAGAT	660
CTACGCTTCC ACGCCACCGT ACTGCCCACT TTGAACCCG TGGGACTAGT CAATATCTGG	720
CGTGGTCTGG CGGACTCCC	739

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1457RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GATCAATATC GGGACGAAAT CTGTTGTATC TACTACGGC ACGGCGACTG CGCCCAGCGC	60
ACCAGGATCT CAGGCTTGT CAGCGAGTCC GGATTGTGCA GCTAAACAAA AGAAAGATTTC	120
ATCTCCACTA CCTCTTGACT TACCTCCACC GAAGGATTTT AGCAAAGAAA TCGAGGAGAT	180
TATAGAACAC GATTTGACTA AATTGGCCTT TCAGAATCCT CTTTTTAAAG ATGAACTTCC	240
ATATTGGTTA CAGGCCAAGA GGCATTGAT CCAACCGTAC AGCACTATGT CTGAAAGAAT	300
GTTGAAACAG CTGGAATCCT CATTACTTAA CTGCCAGAT TCGCTTGACG CTGACACACC	360
ACATCTCTAT CAACACCCGC TCTCTTTACC GCATCCACC TCCATTTTCT TCCCTAGTGA	420
ACCGATCAGG TTCGTGGCTG CTGGCTGGAA TAACGATAAT ACGTCCACTA AAGATATCTA	480
TGGAAAACT TCTATGGTTC AGATAATGAC CAAGTTCGAT TTGGATACCC TGTTTTTTAT	540
CTTTTATCAT TATCAGGGAA CGTACGACCA ATTCTAGCT GCCAGGGGAA CTAATCATCC	600
GTGGGTGGAT ATTAAATAGA GTCAATCGT GCTGGTTTTA CAAAGAAGTT GAAAAGCTGC	660
CCCTTGAAT GGATCAAAAA GAAGAGGT	688

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

EP 0 866 129 A2

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1457UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GATCGAGGAC TTGAAGCAGT TCCGGCAGGT CCGGTCCAAG ACCCCTGGGC ACCCTGAGTA	60
CGAGCTTCCC GCGGTGGAGG TGACCAACCG CCCTCTAGGC CAGGGTATCT CCAACGCGGT	120
TGGCTTGGGG ATCGGCGAGG CGAACTTGGC TGCCACTTAC AACAGCCCG GTTACGAGTT	180
GTCGGACAAC TATACGTACG TGTCTTTGGG CGACGGCTGT TTACAGGAGG GTGTGTCTTC	240
CGAGGCTTCC TCGCTTGCAG GCCATCTAAA GTTGGGCAAT TTGATTGCGT TCTATGACGA	300
CAACAAGATC ACCATCGATG GCCACACTGA GGTGTCTTTC GACGAGGATG TCTTGAAGAG	360
ATAAGAAGCA TACGGGTGGG AGGTGTTGAA CGTTGCCAAC GGTGACGAGA ACTAGAAGAC	420
ATTGCCAGTG CCTTGGAGCA GGCCAAGAAG AACAGGACA AGCCAACTTT GATCAAGTTG	480
ACGACCACTA TTGGGTTTGG CTCTTTGAAT GCGGGCTCCC ACACTGTGCA CGGCGGCGCA	540
TTGAAGCGGA TGATGTCAAA CAGTTGAAGA CGAAGTTGGG CTTTAACCCA GATGAGTCTT	600
TCATTGTGCC TCAGGAGGTT TATGACCTCT ACCACAACAG CACTATCCAG CCAGGTGCCG	660
AGTCCGAAAA GGAGTGGAAC GCTCTACTCG AGAAGTATGC GGGTGAGTAC C	711

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1458RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GATCCGCAGT AGCTGATTGT TOGGGTGGCC AGGCGAATAT TGCTGGAAGC GGTTCAGGCG	60
CGTATATTTC CTCTGGGAC CGCCAAAGTA CCGGCGAGG TTACTCTTGC TGGTCGTACT	120
AGAGAAGTTG CGCACTGCCC TAGCAAGTGC GGTGCTAGGT ACGGGATTTA GCTTCGCCAG	180
TAATGGTGTG AAGACGTTGC GAAATGGCAC AGACGCGTGT ACTGGTCGCA CTTGCAAGTG	240
GATAGCGTTG CTAAGAAAGA AACACCGCCC ATAAGAGCGC GTGAACGTAG ATAAGCTCAT	300
GGTCAGCAAT CAACAAGCCT AATGATGATC TTCCTTACAA AATGAGGTTT TAAAGCGACG	360
TTAAAAAGGG ATGCCCAACG CTATGTTGCA CACCTATGCA ATATCCGTAT GAATGACTGT	420
GTATCATTAA CGACGGTACT TCCTTACAGG GCAATGGCAG GATGGTAAAG CCGAGTAATG	480
TCCAATAATC ATCATATATA CTCTAGTTAT ACGCTATGAG GGTTCATTTC ATGTATTGTT	540
CGTTGGCCTA TOGGCTATGC TTCAAATTGC ATGAGGTTGG GCAGCTCGCC ATTGTTAOCCT	600
GCGGGTGGCA TGTTCACTTT CTCTAGTCTC TTTTGTGGGC GGTGTCTTTC GCTTGGTCC	660
ATGTCAAGGT CCAAGAGATC ACAGAAAA	688

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1458UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GATCTGTTGC ACCTGCTATT TCAGGCAGAT TTGTGCTGC AGCAGCGCAT GGCCATACTA 60  
TCTGCTTTGG CGCTGCTGC GCGGAGTTG CGGGGGCTGG AAGACAAATA CGTGCTCAAA 120  
CCCGTCCTTG ATTTCCCCAC ACGCGGCTG CCCAGAAATG ACGCACCATC AAGAGCCCTT 180  
GAAAGCCGCG AATCOGGTAC AAGCTCCGAG GGGACCATCT CTGCACACCA CACCGTCTGG 240  
CGGTGCGSCA AACTTGACTC AGCGCCAGCA CCAGAACGTC CGAAGCCCTT TOGGAAGCAT 300  
GCACCTGCGT TTTTCTTCCC GCTGCGGCAC CGGTGGCTGA ATGCCATCGA CCTGGGCACT 360  
TTTGACGCCC TGTTCAAAAA GCACTACCTA AGCACCCCTG GCCTTATTCT TGCAGCCGCC 420  
AACCCGCATG CAGAATTGA CCGATGTCC GAACTCATGA GCTACGTTTT GCAGGACGCT 480  
GAGGCGCAG ATATCAGCAT TGAGTAGCCC GTGCGGCATG TGTGAGCGCA TCTGTGGACA 540  
ACTCCTGCTT GCAAAGTGA TCCGACCAC TACCATGCAT TAGTATGAGA TCTATAGAGC 600  
GCCAATGCA CGCCTAGAGA GATGTGAACC TCGCAATGCA TCTCTTGGGA GTCTCTGTGG 660  
COGGCAGTAT CTGCTAGTAC ATACTCTTTG TAACTCTACA GAGATGTGAA GTCTGTGTAC 720  
COGG 724

## (2) INFORMATION FOR SEQ ID NO:695:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1459RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

10 GATCATGCTG GGGCATATCT GAATGCTCTT GAACAACGGA CTAGATTAAT GGAGCCTTGC 60  
 ACTCAGAGGC TTGGGCAGGA TGCAGCTTAT GCGGGAGCGG CTGTTGGAGC TTTACAATAC 120  
 15 CAAGCAATAT GTGGTGCTGC CCCCAGATGA GACAGTAAAA CTGCAGCGAG AGGTGACGGC 180  
 GAGCCTGAAC TCAGCAGATC CAGGACTCAA CGACGTGAC CGCATGGCCC TAATGGAGAT 240  
 20 GAACTTCTAT TTGTTGGTGT ACATTGGCGA AGAAATAGAA GCAGACGTGC TCTACCGCAC 300  
 ACTTGTGGA CGTATAGGTG AGAACTCGCC CCGGATGCAC CTCATGAAGG CTACGTTACT 360  
 25 GCAGGTTACA GAAGGTGATC CCGCTGCCGC GAAGTACCTG AAGAACTGC TTGAAAAGCA 420  
 GCTTGAATAC GATACAGATT CCGTGGATTA CCTGCAGGTG GGCAAGAAGC TAATTGCGCT 480  
 30 GGAACGGCCC GCGTTGTCCA CCGAGCTGTG GATGAAAAAG CTGCTGTGCG CTGCTAGAGA 540  
 AGTTTCCACT GGACGCCGAA CTATGGTGG 569  
 35

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1459UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:



EP 0 866 129 A2

5  
 10  
 15  
 20  
 25

GATCACGTGC CTGCGACATG GCGACTTCAT CCACTGGGCG CCACTAAGT GGTATATGAC 60  
 ATTATGGCCG AGAGGTTAAG GCGTGAGACT CGAACTAAAT TGAGGGATCT CTGGGGCTCT 120  
 GCGCGGCGAG GTTGAATCC TGCTGATGTC GTTATTTTTT GCTTGCGCGG CCTACGGGG 180  
 GCTGTATTTT GCTGTGTGCT ATTTAGATAA ACGAGATAGC TAACTATGG GTAGAAGTCG 240  
 CGTACTTCC CGTAGTAGTA GGCTGTGCGG AAGCGCGCGA GGGCGGTGAG CACCAGCGGG 300  
 ACGGGTTTGG CGAAACGCGA TGGCAGCCT CTGATGAGG CGGTCAACAG CATCAAGGAG 360  
 CTCGGGCCAA GGGCGAGCTC GAGGCGCGCC TCTGGGTCTT TCGGAGCAA GTACCTGCT 420  
 ACAGCGTAGG TGCTACCAA AACGAGACCT GCAGCCAGCG AGGCACAGA CCTTTTACGC 480  
 CAGTAGCCCA TCGAGCCACC GATGACGGTG AGCGCGGCGA GAGTGAAAGA GGGATGTTCC 540  
 CTTGCGGTGG TGGTGGGTGG TGCTGTGGGG AA 572

(2) INFORMATION FOR SEQ ID NO:697:

30  
 35

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 688 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40  
 45

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1460RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

50  
 55

GATCCGGGTG GAGACACGAA AGTAGACAGA CACGGACGGC TGTTGGGTGG AAGGAAGTAC 60  
 CTGTGGATA CATTCAGCT GCGCCAAAAG ACACATAATT TCTATGTGCT TGTCAGCAG 120  
 CTGATAGAGA TTTTGCAATT CGAGGGGAGC GGCTCTGACT TTTTGCACT GCATAATCAG 180

CTGTACCCGC TGGAGCTCAA AGACAACGAG CGGGCCTTGC TTGCAGAGGC TGGGTTGATC 240  
 5 AAAGGCGAGC TGGGCTCCCC ATACTACGTT ACTGCACTCT CTTCATACAT CATTTTGTGT 300  
 GCTGCTATTG TGGGAGGCGG CTGTAGGATA ATAGATGACT ACTGGGAGCA GGCCTTAAAG 360  
 10 GAGCAGGGAT TCACCATGCA CCACCGTGTA TTCTCTCTGA ACGGCACGCA ACTTTCATTG 420  
 CTACGCCTGC TGAAACCCCC GCGTCCAGAA TCGCATCAGC AGGGTGAGAA GCTGGATACC 480  
 15 AACTGGCTAC AGAAGTGGGA GGATCCATAC CCAACGATCC AGGAACAACC AAATGCTGAA 540  
 GCACGGCGGG AATACGCTAG AGAACACGCG AGAGGTGAGC ACATAACGAT GATTGTTCCA 600  
 20 GGTCAAAGTA TTAGCGGCAG TATAGAACTG AGCCTAAATT ATAAACTTCC TAAGTACCAC 660  
 TACAAAAACT CATTTGCTAA TGGGTTGA 688

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1460UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GATCCAACAA TTCCGCGAGC GCGCTCCAG CGTCTGCTC CGTCGCATCA AATGAGTCCA 60  
 50 CGCCTGCTC AATCCGCGAC AGCTGCGGTC CATGCGCCAC CTCGAAGTGC ATCCGCGAGC 120  
 CAAACAGCTG GATAAACAGC CCGTTCTGCT CGCACCCCGG CCGCAGCTGT CCAAAGAGCG 180  
 55 CCTCCGCACC AGCTGCTATA TCATCGCCCC AGAAACTCTC TACGAATGCC CCATCGCGG 240

TGTACCTCGT CGTAGTTGTG CATGTGCTG CCTCTTCCG CTGAATTTTG ACAGTCTGGC 300  
 5 CCCCCACCCC AGCTCCGGAA CGCTACGTAA TACAACACAC AACCAAATGC CCTACCCGAA 360  
 GGTGCAATC GTCTTCTGCA CCGGCTGCCG CTGGGGCTTG CGCGCAAGCT GGTATGCTCA 420  
 10 AGAGTTGCTA CAGACTTTTG GCGACTCCCT AGCGAGATT GCCCTGTAC CGGTCCGTC 480  
 CGGTCAATTC CAAGTCTCT GTTACGCAAG CCAAGAACA GAGGCCACGG GACAGCGCA 540  
 15 ACACCATCTG GGATGGGCG CCGACAATG GTTTTCTGA TAGTAAATAT CTGAAGCAGG 600  
 CTGTCAAGCC ACTCTTTTGT CAGACAGCG AACCGCTTG GCGCCACAT 649

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1461RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GATCAAACCA CCACGGCACA TCATCATAGT TGATTAAATC AATTAGGTAA GGCAACCATA 60  
 GTTCAGACT TTGTTTCTGT ACCATTTTCT TGGGATTAAA GAAGTAGGGA GTCACGAGGA 120  
 45 AATGCACCGC ACATGCTTTG AGATTGGTGT TTTGGGATTT TAGAAGGCCA GTAAOGAAGA 180  
 CGGTGAACGA GCTGTCCAGC CATAGATTAT TTTTAACTGG ATGAACCTTG TAGCACTOGA 240  
 50 TGTATAGGAC AATCGCCAAC CAGAGCAATG TCTCGTGCAA CCGGTTCCTG ATGACAAGCG 300  
 CACGCGGGGT GCTCGTGAAT GGTAGGAGTT GGTTCCTTCC TATCCACGG TTGCTAAATG 360  
 55

CCATGTACTC TTGGTCTTG GGGTTCGGG CGACGCTGAC CTTTAAAATG TATTTGAGGT 420  
 5 CCAACTGGTG ACCATAGGG TCCACTAGTG ATAGCATGAG TGCTCTAAC GGCAGAAGAA 480  
 GGCCTTGGG AAGCGAAACC ACCTCCCGG ATTTGAGCAC GCGAGACATT AACTCCAAAA 540  
 10 GCGTGTGGC CCAGGAGATC TCTGCTGGG AGTCATCTGC TTCTCATTC TCCCGAGGA 600  
 AGTGTATCAA AAGCCCGGG AAACCCACG GCACAGCCG CCGCACATCC GCGTCCCAT 660  
 15 TACAGTAGTC TATCCACAG TTGTTCAA 688

## (2) INFORMATION FOR SEQ ID NO:700:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1461UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GATCGGCAG TTAAACTTA AAGTTGATAG AGTCCCGTC GTGCTCTCTG GATACAATAG 60  
 40 AGGCCACCGA GTGAGTGG CCTGCACT AGTGCCCGC GTAGCGCTG TGTCCGAGA 120  
 TGGCCCTTC TAGGTTGATC TTGGAGCCAG CTTCCAGCT GCTGACTTCC GTCCGATAAA 180  
 45 CTGTTTCTGG TGCGATCCG ACCTTGAAGC TATCGCCGT GAACTCCGTC ACCGTCAGGC 240  
 AGATACCATT GCATGCAATC GAGTCACGA TGTGGCAATC CGCCAGTATC GGAGCCGCAT 300  
 50 CCTTGATAAG GACTGACACA CGTTGCCG CTGCTCGCT GGCATGTTT TCCAAGTACT 360  
 CAGCAACAGT GCCAATGTGT TCCACTATAC CGGTAAACAT CCTATCAACT TCTATGGCG 420  
 55

# EP 0 866 129 A2

ATATAGGCTT CGGTATGCCA TCTATGCATC TTCTTTTCTG CTACCGGAG CTTTTTAAAC 480  
 5 TOGTAAGACA TGCATAAGGA AATGGCGGTT CGCCATGTAG CTGACTAATA AACTAGAAG 540  
 ATACGACTAA CTATCTGATT ATACTTTAGG ACTATCTCTC CTGCGCTGG TCACAGAAAC 600  
 10 ATCGTTGAGC AAGTCGGTC TATCGGGAAA ATCACTTGGT TCCTTTGTGG TAGAGCTAAC 660  
 TGCTGAGAA GCTGGAAAGC GCTCTTTTAA AGTCTACTTC GAATGGTGGT GTACGTCTGG 720  
 15 GTGCTGGC 728

## (2) INFORMATION FOR SEQ ID NO:701:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1462RP

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GATCTTAATT TAAAATTTTA ATTAAGTATT TATAATTTAG AAATATATAA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 45 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180  
 ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATATAA 240  
 50 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTAATATT 300  
 AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
 55 ATTTAATTA TATAAATTAT TTAATTTACT TCATTTGATAT ATATAATTAT TAAATGTACC 420

TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTAAATAGTC TACCCTTTAA 480  
 5 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540  
 TAATAATTTA TTATCTAAAG TATATAAAAT AATTAAACTT TTTTATTATT ATTAAATTA 600  
 10 TTATTAATTA GTAAATTATA TTTATTTATT TTATTAACAT AATTTTTTGG ATAATAATAT 660  
 ATCATTATTA AATGGTAATT TATTAATAAT TATCTTAATG A 701

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1462UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA 60  
 40 CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT 120  
 ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCAATTCAT TTAATACTCC TCTAATTCAA 180  
 45 TCTTAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG 240  
 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTICAAA ACTGAATATC TACATATTAT 300  
 50 ATCATTAAAT TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360  
 GGIGTGTAAC TTAGCTCTCT AATTAAAGTT ATAAATTTAT CTTAACATAT AAAAATAATT 420  
 55 AATTAAATTA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480

GTTATATTTA AATAGATCAA AATTTCAACA ATTTCATTT CATTAGTAC TACCATCACC 540  
 5 ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTACTAT 600  
 ACATGGTATT ATTGGTAATA TTTATCCTTT ATTATTATCT TTATTAGTAG TTTTATTACT 660  
 10 AATAACTTTA TGATTTAGAG ATATGGTAGC TGAACTTACT TATTTAGGTG ATCATACTTT 720  
 AGCTGTAA 728

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1463RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GATCCCTGAG TCTGCTACCA AGGAGGTGGA GGAGGAGGAC ATCGATATCG AGCAATTGAA 60  
 40 GCAGGAGATG AAAGGCAACA AGGAGGCTC TGCTTTGTAA GCTTGCTGTT TGCCGCTTGT 120  
 GCTAGCCAAT CGTTGCTGAG ACTATCTAAC TTGTATACAT GCGCTATCG CGGCACGCGA 180  
 45 AGCGAACACT ATAATGTATA TGTCAAGTGA AATACATCAT ATATTATCTT GTGCTCAAG 240  
 GGTTCTAAAG ATGTCATAGG ACAGTCGGT GCTCAGACAC ACGAATATAA TCATAATAAT 300  
 50 AATATATGG CGGTCAGCTT CATGACCAGG TCAAGCCTTG ATACCAGAAG ACACTTCTAG 360  
 GAATTCTCA ACGGAGAGA AAACACTAGG GTGTAGGTG TCATTGCTCA AGGACATCTG 420  
 55 CTCTGGGTC CACAAGTTGG CCTCTGGTAC ATAGTCTGGT TCACCGACAC CCAATAAGCC 480

ACCGTGCGCA GCCCAATCGC TGACACGTGG AAGCTGTAGT GTCTTCCAGA CGTCATCCAT 540  
 5 GCGGTCCAAT AGGACATCCG ACAGGTGGTT CGTGTGGCCT GGAGTAGGAA TGATACGGAG 600  
 TCTCTCGGTC CCGGTGGAA CCGTAGGAGT TGAAGGGCCT GTACGTAGAT GCGATGCTCT 660  
 10 CCATCAAAAT GTCGGAAGCA CGCTTGGC 688

## (2) INFORMATION FOR SEQ ID NO:704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1463UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GATCAACAG TAGAAGTATT AGAGCTGCTT GCAAAGGGCG TCATAACAA GAGAGCTGTA 60  
 ATGTGACAA ATTAAACAGA AAAATATCAT TATTAGTGA TAAATAACCA ACTTGCACTG 120  
 40 AGAGTATAGT TCTACATGTT TATTCGTAA CAGAATTTCT ATCCAAATAG TTTAATTCCG 180  
 TTTTACTTAT CTACGGAGTA GCAGTGCAAG AACCTTGTAT CCCAAATGC TAGAGGGACA 240  
 45 TGCAGATGTA TAGTAAAGCA ACGTCTGTTT CTTTGGATTT AGCAGCGTCA GGCGAACAAA 300  
 AAAAATAGAA AGTCAACAGG GATTGGGAAG TTATGAGAGT TGATATGTTT GTCCATTAGT 360  
 50 AAGTCATTCA GTTGATATGA GGTGCTTAAA TGTTTGTAAG AAGCAAGAAC GAAGAGAGAT 420  
 ACAAATGTG CAGTTGTGAA TCGTGAAATT GACACCAGAG GACGTCACCT CCCGTTGCCA 480  
 55 CTGTTTGCCA ATTGCTTCTC GAGCTGCTCA ACCTTGGCCT GTAAATCTCT ATTGACTTTC 540



TTTAGTAGTT OCAATTCAAT ATGCGTTTCC TTCGATCTTC CATAGCTGAG CAGTTTCGCC 600

5 ATCTCCTGGT TCTCTTTTGT CAACATTTTC AGTCGGACAA TCATCTTGTG AGCGAGGGCT 660

TCTTCGTCAT AACGGCCGAA TCGGGTAAAG GAATTAGAGG GATT 704

10 (2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1464RP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GATCGAAATA ACTTCGCTG AAAACGCAGC AGAGGCAGCC AATGGTCAAA TGGAGGAGA 60

35 ATATCCACGA TATTTCTAGG GTACTGTTC TTGCCAGTTG GTGCTCGAA ACATAACCT 120

CAATGGCGCC CAGTGTGTG TACATACCC ACACCGGAA CAGACCATG AATGACCGA 180

40 AAACCACCAG CCACGCGGT AAGCCGCCAT CCGGGTATTC GTTGGAGTTA TCGAGATATG 240

CGCGTCTTC TTCTCTACC TTTTCGTGC TGAGAGGAC AGTCTGCTGA GCGACGTG 300

45 TCGTTGGGC ATCGCCAAA AGCTCTTGT CGCCACAGC TGTGGCTCTG CCGTGTCTG 360

ACGATGGCT GACGTCTAGG GCTACGGCT CATCGCATG CCGTACTGA ACGTGTCT 420

50 TGTGATGAC CACCATGTT CCTAGCACG ATGGGAGATG CTCGAAACG CGTCAGCGC 480

ACCACAGAC ATCTATCTAC TTAAATACCT AATTATCTG TGTCCAGCTA AAAATCCAG 540

55 TATCAGTCAT CCGTGGCGG CCTTATCAC CATTAGGGTC CGCTTTGCG TAGTCATTA 600

CCGTCGGCGG GATTTCATCT CCAAAATGTC TCAAGCGATG CCTTGATTCC GAGTGTACAA 660

5 GGGCCAGATT CCAACGGGCC AGGAGGCAAC TAATAGAGG 699

(2) INFORMATION FOR SEQ ID NO:706:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1464UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

30 GATCTTGGGC TTTTCTTCA GACCGGGTG GGTGTAGTAT TGTTCCTCT TAATGTTGA 60  
 GTTGAGGGCG GACGAAGAGG GCGCAGAGGG GTCTGGCGAG GCACCGGTGG AAAGGGGCT 120  
 35 GTCGGGCGGT TCCAGGGCA GCGCGCGTTC GTGTGGTTC TAGTCGTGAT GTTGGGGCGC 180  
 GGGGGGGGCC GACTGTGGT CCAGCGGGTG GCGTCCGAC GCGAGCGCG AGAACTGGC 240  
 40 GTCGCGGAAC TCGTACTCT TCTGCGGTTC CTGCGGGCG CGCTTGGCG GCGGTTCCAC 300  
 GGCACGGCGC GGGACCTTGA GCGCGTTGA GATAATGAAC TTGTGTTGA CCGAGCCCTT 360  
 45 CGGATGCTTC TTTCGGCCAT TGCGTTTGGG CGCGGGGTC TCGCGTTCG GCACGGGGC 420  
 GCGCGGGCG GCATGCAATT CGTTCCTGTC TGGCGAGACT GGGGGGGAT AAACCTGCCC 480  
 50 AGGATCGCGT CCACGTTAGT GAGGTGCGG TTGCGCTCT CTGCGGCTGC GTGGTGGTGG 540  
 TTGGCGCGGT GAGCGGGTG CACCGGTCC TCTCGTGGG GCTTGGGCTC CTGCTCGGC 600  
 55 ATGCCCCGTT CGGCTGCATG CCTCCAATCG ACTTGCAGT CGTACGATCC CATCCAACGA 660

ACCCCGTAAC TTATCTOGAA GTATGCCTGC ATACCTATAC TGGTCGTTCA

710

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1465RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GATCCACTTC TTGCGGACA AGACATTGGA GGGCGGCAAC GACTGGGAAA TCTACAACGA	60
CCCGGCGACC ATCGGCGACA GCGTCGGCTC CCGCGAGGAC ACGGTGAGGA TCCTCAGAGA	120
GCTGTTCGAC CTGTAGGCGC CGCGCTAGC TAGTTCCTTG TAATTGCTCG ACATTTACAA	180
TGCATATTCC TATATACACC GCGCGCAGCG CTCAGCTGAG CAGCGGTACG TACGCGAGCA	240
CGAGCGCAAA CGTACCGGTG CACACGCGGA TCAGCCACTG CATGACCTGC GTCTTGACCG	300
AGTCGATTTG CATCTTCATA TTAGTGACCT CCTGGTCAAT TCGGTGTCA ATCTCCTTGA	360
TCTGCAGATT GTGGTTGCTG GACTCCTCCC GGATGCGTCC CTTTTCGAAC GAGAGATCCA	420
GCTTGAACCC TCGTTTCGCC TTCTGTATCT CCTCTCGGAG CCGGTTCGCG AGCTGCTCTA	480
GGTCGTTTCG AATCCGCTCC TGTTCGTTCT GGATGGAGTG GATCTGCTG CCGTCGCGCG	540
TCAGCAGTTG GTCCCGCAGT TTTGCAAAAT CCACCGCTG CTGGTACGTC AGCTTCGTAA	600
GCTTCTCGCG GGACGCTAGG TCCTGCGAGA CATGCGTCAC GCGCGCGCG AGTGCGTCCG	660
ACATGATATC CACGATCGCA TTGCGCTGCT GGCTTGCTGA AGT	703

## (2) INFORMATION FOR SEQ ID NO:708:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1465UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

25	GATCCCGCAA TAGCTTGATT CGATCGTCTG GTGCGGTACC TGCTCGACTT CTCCTGCTCT	60
	TCCTATGTT CGTTGCTCAC GCGCGGAAAA CCACTACAGC ACAAAAAATT CACAAGGTCC	120
30	GCGCACCAG CCTTTTAAAT TAGCGCAATG GCAGCGAGTC CTGGTATATA AGGCAAAAGA	180
	CGGGAGGGGG ACAGCTACTA CAGGCTCATC GAGGCATGGT ATGTTGGGGG ACAGTGGGGG	240
35	CAGGGGGCAG GACTAACCTT GATGTTGGAT AGAATGGGTT GTACAACCAC GCGGTGAAAC	300
	AGAAAAAGTT GCTGGAGCAG GAGCTGAATC GATTTGAGCT CGGGGTGGGG GCGCCGGTGG	360
40	GGCTGCAGGG TTCCATATCG ACGGCACTGG TGGGACTGGA GCGCACAATT GAGCAGTATC	420
	AGGCGCAGGT GCGCAAAAG GGCAGCGGGG CGGAAGCCGG CAAGCATGGG CAGCGCGTGG	480
45	GCGAACTGAC GGAGTGGGCA ACGAACGGGC GCGCGGGGTT CGAGGGGGCTG CCGGCGCGCA	540
	GCATGCAGCC GGTGGCGTTC CAGAGCGGGG CGGCAGCGCC GGAGGGGGCC GTGAACCAGC	600
50	CGGCGGGGGG GCGCGGCAC	619

## (2) INFORMATION FOR SEQ ID NO:709:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1466RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

20	GATCTCTTAC TTTTCTACT CACCAATGTC TTTAACAGAC AACCAGAGTC ACGGCOGGCA	60
	GCTTATCTGC CGTGCTGGCG CCATGCCCCG CCGCTGGTAC TGGCCCGCTC GTGCTCGCGG	120
25	TAGTCTCACA GCAACGGAGC TTGCTCCAAT TGGGCTGCAT TCTCCCGACC ACAGTCTGTT	180
	TGTCACGTGA CTCTCAGCCG TCCCGAATGT ACATTTCCTAT TTATCTACTT CTTGCCGCCT	240
30	TGCCGOCACC ACATCCGGTG CCGGGCAGCA CACCGACCGC GCATCGGGC CCTCGCGTTC	300
	GTAGAACTGC GCACAGCACG TGTACAGTGC CTCCTCTGCC GCGCGCAAC GGCCCTCTCT	360
35	GTACCCGTGT CGTTTCAGAC ATGCCCTGGAT CGCACATGCC TGGGCTTGC ATGGGGGCTG	420
	TCCCTCTGGG CTGGCCCGCC TATTGTCCAT GTTTTGTTT CTATCTGTTG GCGGTACCA	480
40	CGTTGTTGTA CCAGAGTACA TTGTGCGGT GACCCCGTGT AATGTCACC CGTGGGCCAC	540
	AGATGACCTT GCCACATGCC TCATTTCTTT GACCGCACCG TGCCGCGAGA CCGCCACAT	600
45	GGGCGGTGG CACTCCGACG ACACCCACGG GCGGCACTG CAAGGCTGC AGGTGGGAT	660
	GAGTCAAAAC AAACCAGGTG TGGGCTGGG CGGGTGAAA TCGACTCATA GAGAC	715

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1466UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GATCTTATTA ATTTTGATGG TGCTATATTC TAAATCAAG TAATGATAGC GCGTGATGCG	60
GTACGTACCT ATACATATAA CGCACAGTTC ACCATCGTCT ATGCGTGTAT GAAAATCACT	120
CCAGCCGTGC GACACGCCAC GTGTAATCTA GTGAGTTTCA AGTTCTTCTT CCTCATGGGC	180
AGAAAGTTGG CCGCGGGGGG TGAGGTTCTT GAGCGCTCC TTGAGCTGCG CGATAAGGCT	240
ATTCTCCCTT TGAGCATGCA TCGGATACC CTCTAGAGAC ATATGAGCCG AATCTGCACC	300
ATCTAAACCA TGTTCGTGT TCGTCCAGT GCGAGCTGCC AGTTTGGGAC TGGACAGACC	360
TGTCGTCCA TCTTTGTAAG AATCTCGGT CGTTGCCGAG TTGGAATICA TGGTTCCCAT	420
AGTGTCGCAAG ATTTTCTCTT CTTCGTGTAG TTCCAGATGG GTACCTGTCA GATTGATCAA	480
GGACCTGCCG CTTTACGGC GCGAGACTT GGGCAGAAGA GAGTGCCCGG TTGGCGTGGC	540
TTCAACCAAGG TTTGTAATGG AGGTGTGAGA TCTGGAGTC CTGGTAGTC TCAGACACGA	600
AGCAACGGCA TCATGTATCC ACTTCGCAAC AAGCGAAGTC CAGCCACACT GGTGTGATGC	660
GCCCAAGCCC CTACCACTGT CACCATOGAA GTAT	694

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 690 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1467RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GATCGCAGAC	TCCGCCGGAG	AGACTTTTCG	ACCTCGGCA	CAGGTCTTGA	AAGAGAGCTC	60
CGGCCGTTCC	GTGCCAGACT	CTGTATTATC	ATGTCGGTAA	GAGCAGCGTT	CGTCCAGGT	120
ACGCCCTTCT	TGTTCTGTGT	TCCACCAATT	GATGGAATTT	GAGACGTGAA	CCTCTCGGGA	180
TTCTRRKCTAT	TGAGCACACC	ATTGGCACCA	CTTGAGCCCC	TTGCTCTGTC	CATCCCTAAT	240
CGTCTATCC	TACGGCCGGC	TAATAAGTTA	CTACCAGACT	CTGGCCCTCA	TCTGGGACTG	300
ATGTTATCGT	CTGCAGCCAG	ATCTGTTTG	TGACCCGATC	GAAATCATCG	AGTACGAATA	360
ACCACGTGAC	CATTATTAC	GTGATGAATT	TGGCGGTCCC	TGTTGCCGAC	TCTTACTCCA	420
GGTTAACCAT	GACTAGATGG	GCATACCTCA	GATACGTTAT	TCATGGGATC	CGGAGTTGCC	480
CGGTGGCCCG	AACCGCCCGG	TGAATCTGTG	CTGACGACCT	AAAAAATAGT	GTGGCAAGC	540
TTCTTAATC	TGTGAGATGC	AACTGACAA	ACTTGAAGGC	TGAACCATCA	AAGCGATAOG	600
CCTCATGCAC	GTGCTCAATA	AGGTCCAGGA	AGTCTCGCAA	TGGGGCAAGC	AGACGGTAGA	660
TTGCAAGACA	CAGACGATTG	GGTGTGCCA				690

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1467UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GATCGTCOGA GTGCAAATCC ATACCAAAAA TGTGGACCCA GGTACGGGAT TCGAACTTCT	60
CGAAGAAAAA TAGCCTCAGT GAAGTGCCCA ATTGCCTTAT AGTCGTTTTC CAGAGCATAT	120
AGAAATGTGG GACAAGGCGG TGGGGGGGCT TGTGGAGCC GACGGAAGAA GGGATCTGGG	180
CGGGAATTAC GCGGTGAGA GGCAGGGGTG CGGAAGAGAA AAAGGTGAAG CGAGTTGTTG	240
CCATGAGOGA GATGCAGCAG CCAATACCTA TCCCAATGGT AAACGAGGCG GTCCAGATGG	300
CCCAATGGCG GAGGGCAACA GGGCCCGGCT CCTTTTTCGG CGGTCTGGG TGTGTTTCT	360
TGGAATTGAC GGTCACTCG GTTTCATAGC CGGACTOGGA CTCGTTGCAA AGTTTGTGCA	420
GGTGCTTGAG CAGGCGGTGC TTCTCGTGGT GGTTGGACAT GATTATAGGG CTGCAGTATA	480
CTCGGATGCA TTTGGGTGCG GTGTAGCGCT TCAGGAGAGC CGCCAGGGTG CTCTTCTGGC	540
CCTTCTGGCA CACGGGAATC ACGGTGGGGC AGGGGGCCTT CTCGCACAGG CCGTCCAAGA	600
GCTCTGGGCG CTGCGCTATG TGTGGAAGA CCACCATAAC CGGAGGTAC CGCTGGCOCA	660
CGTCCAGCG CGTGACCATG CCGAGGTCT TCAAGTCAA	700

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:



(A) ORGANISM: PAG1468RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

10 GATCTCGTCG CTCATTGTCTG ACCTGCAAAA AGTGTTCAGA AGGAAGGCAA CATGTGTTTT 60

TAATCCTACG GCGTGGCCT CAGAGATTGT TCACTCAATG TCGTTCATCA TTATGAATGG 120

15 GTGGCCGGCG CCTGCGCGCC TCGAACCCGC GCCACACGGC CTCGCGCGCG CGCTGCCCCG 180

CTGGGCCACG CAGGGTCCAA AACCACCCCA AACTCACCGC GCGCACCCCG CTACACCGCC 240

20 GCCAGCACGT CAGTGGCGT TACCGGCCCT GCGGCACTG AAAATTTTTC GCGCCAACA 300

CTATCGCGCC CGAAAAGCA ATTTGCGGC CAACCACACA ACGATCTGTT ACGAACAGG 360

25 ACAGGACTCA TGCCCCGTC CCTTCTTTAT TTATTTACTA GCTCCACATA GATATTTTTC 420

ATATTTATAT GGTGTGTTTT CTCCGCAAG CCGCAACCCA GCACTTAGCA GACCACGGG 480

30 GCAGGGACTG ACACCCAGC AGAACAGAAC AACACAGGC GACCTTACAA TGAGCATGGA 540

AACGCCCCCT GTAGATATCG ACAACATCAT CGACCGCTTG CTGGAGGTGC GGGGCTOGAA 600

35 GCGGGGCGAG CAGGTGGACC TCGAAGAGCA CGAGATCCGC TACCTGTGCT CCAAGGGCG 660

CAGCATCTTT ATCAAGCAGC CCATTCCTC 689

40

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1468UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

5	GATCTCAGAA TTATCGGCTA GCAATTGATA TTAGCATACT TAATTOGTGC TAAATACTTT	60
	GGCATCGCAT CTAGACATAG GAAGTAACCT CAAAAAAGCT ACGCAGATAG TAAACCTGGA	120
10	AGAGAGATTG CGCAACAACA ACGGCCAGTT GGAAATAGA CCACCACTTG ACCCTGTCAT	180
	TTGTAGACTC AGCAGTGTTC CTGTGTGTGC GTTCGGGAAT CTCGATGTAC TGTGCTOCT	240
15	TCATTACTTC CATTGTGAGC ATGGAGAGCT TGCGCACCGC ACCCTCTAGC GTCTCCGAGC	300
	TGGAATCAGC GGCATCGGGG GAGAGAACAC CGTAGGTATT AAACGTGACA TCCTTAGTCA	360
20	GGTAGCCCGA ATTGTGTTTC GCAAAGCAGT ACTGGTATTT GCCATCTGTA GCGGCTTCA	420
	AGGTCAACTC ACCGTGGAC GACGCACGCT GCGCATCCAG CACTGACCGT CCGTCAATCC	480
25	CGTACACCAG CAGGTCTCCA GACAGCTGTT GATGTGATTG TGGGTCTCTG TCGCCGAATT	540
	GATAAGTGAT TGTGAGCAG TCCCCGCCCT TCAACTGCTC AAAGAAACAG CCGCGCCCGT	600
30	AGGGGGGAAG AAGTACATTG	620

(2) INFORMATION FOR SEQ ID NO:715:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1469RP

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

55

GATCAACTAC ATCTGGGAGC AGCAGCCGAA TTGTAAAGTG GGCATCATAG CATATGACAA 60  
 GTGGCTGGGT TTCTTCAACC TGGCCCGGA GTGAGCCAG GCACAGGAGC TGATTGTGTC 120  
 CGAGCTCAGA GAAGTCTTCC TGGCGCTGTA CAGCGGCTC TTGTGAGGC CTGGGAGGC 180  
 AATGCATGTC ATACAGGACA CGTTGGTCAA GCTGAGTGG TTTATCCAGG ACGACAAGCT 240  
 CTGCGACGGC GCGAGGGGT GCTTGGGTC GGCGCTGAG GCGCGCTGC TGGCGCTGGA 300  
 CACTGCCACC AATGGTAATG GCGCAAGAT CATTGCGACT CTGAACACGC TGGCCACCGT 360  
 GGGCAACGGC AATCTGAGC TCGGGCGGA GAGCGGCTC AAGAAGAGC TGAAGTGGA 420  
 CAACAGCTTC TACACCGGC TGGCGGACAG GATGCTGAAG GGTACGTCG GCGTGGACT 480  
 CTTCTGCACA GGCAGCGCT TCATGGACTT TGCCAGCTC GGCCACCCG TGCTGGCCAC 540  
 CTCGGGAGG TTCCGCCACT ACTGAACTT CCAGCTGAC GCGACGAGT CCGCTGGGT 600  
 CAACGACATG CTGCAGCCG TCAGCAGCAG CGTCGGCTAC CAGGCGCAGC TCAAGGTGG 660  
 CTGCTCCTCG GGGCTGTGCT CAGTCG 686

## (2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 572 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1469UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

GATCGGGGGA GCAGGACTAG AGATGAGCAG CAATGACAGT GATTATCTCC TGGTTACCTT 60  
 55

CAAACTCTTC ACTCTCTCA AGAACTTGTT ACCTGATGAC TCCTTCTTAT TGTCGTGTC 120  
 5 ACGCGGCCCC GTGTAGGCGT CTTOGTGTC CTCTTCTOG TOCTCAAGAT AGCCAGAGTG 180  
 GGTCCTAGTC AGCTTCAGGT TGGCGTTCTT GGGGTGGGG CCAATGCGG ACGGGACGG 240  
 10 AGGGCTTTTC GCCAGCCTGT GGCTCAGAGA CTCTTCTCTG CCCACCGTC TCTGCTTCAT 300  
 CGCTCTATA GCGACAGGG CCGCGGGCG GCGTGGAGG AACGTGTTG AGCCAAGCCC 360  
 15 CTGTGTCACG GGCCATGCA CAAGGTCCG GGTACCTTG GCGTGAAGT GGTCACTC 420  
 CGAATGGTTC TTGATAGCGT TCACGTGGA GAGGAGCGC TGGCGAGCT CGGGGGGGA 480  
 20 ATACAGGTAC GAGTGTGCT OCTGTGAT GCGAAGACC TGTTCATCG CAGACTTGTG 540  
 TGGGTGGCC CCGACAAGT CGAGTTGGC CG 572

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1470RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GATCTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACRAC GGGGAATTAA GGGCCTTTTC 60  
 CAATATTTTG AGCGTCGTTT CATAGCTCGG AAGAGCAGC AGAAGCCCCC CCAGTAGTGT 120  
 CTGTTTATGT TCGTCATGA AAGGTGCTC TATCAAATCT AGCTCCATCA TCGCAGAGTA 180  
 55 GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCGCAAC TTCGTCAGGA TTACAGTAAA 240

ATAATGGTAG AACCGCGGAC TCACAGAATC GACGACCGCT CGAAATGAAG TCGGCCCCGTA 300  
 5 GAAGATCGTG CGGCGCTGCT TCTCTATCAC AAGATGGAAC TCGGAAAGTC TGTTCACGGG 360  
 GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT 420  
 10 CCGCGCGAGC TCAGTCTCAA GCTCGTGCAT CGGTGCGAGC AGCTCCACAT TGGGCGTTGG 480  
 AGCTGAACAG CTCCCGTGAG TTCACGTGCT GCGTAAACTC AGACAGGTAC ACACACTCGG 540  
 15 GCAGGCCCTT CCCAATACAT TTAGAGCACT TCGGCGCGGC CTGTGTGCAC TTGACGGGCC 600  
 GCTTGCGGCA GAACACGCAC GACTTGCTGA CCTTCGGCTT GGTTTTCACA ATCTTGCCAT 660  
 20 CGGACTCTGC CATCCCGCCA GCTTCAGCAA AATGAGTAG 699

## (2) INFORMATION FOR SEQ ID NO:718:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 655 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1470UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

45 GATCGCGGAC GTGGAACACT GCGCGGAGAT GCGCGCGGCC ATCTGCTGGTGG TTCTGCGGA 60  
 CCGCAAGGAC ACGCCATCGA CGAGCGGTAT GCAGCAGACG GTGCACACGT CGGACCTCTT 120  
 CAAGGAGGCG GTGCGGACCG TGCTGCGCGG GCGGTACCGA GAGATGGCGG CCGCGATCOG 180  
 50 CCGCGCGGAC TTGCGGACGT TTGCGCGCCT GACGATGCAG GACTCGAACT CGTTTCAAGC 240  
 CACCTGCCTG GACTCATTTT CCGCGATCTT CTACATGAAC GACACTTCGC GCGGATTGT 300  
 55

CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATCGTGGCGT ACACGTTTGA 360  
 5 CGCGGGTCCG AACGCGGTGC TCTATTACTT GGGGAGAAC GAGGCGGGC TCTGCGGCTT 420  
 CCTCTCTGCC GTCTTTGGCG CCAACGACGG CTGGGAGACC ACGTTCTCGA CGGAGCAGCG 480  
 10 CGCCACTTCG CCGCGCAGTT CGACGAGTGC GTGCGGGCA AGCTTGGAC GGACCTGGAC 540  
 GACGAGTTGC ACAGAGGAGT TGCCCGCTC ATCTTCACGA AGGTGGGCA GGGCCCCAAG 600  
 15 AACTAAATC CTCGCTCATC GACCCGAGA CGGGCTGCC CCGCTGAGC TATTC 655

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1471RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GATCAATTAA CTATCTAGAT GAGTCTAATT AATTAATATA CTTAAAAGTC CCGTTAATAT 60  
 CATTAGCTAC CCTATCGGAA CAGACCGTCT GCTACTAGGC CGAAAGGGTA AAGCAGTTGT 120  
 45 CAGTCAGTAC TTGCTGTTGC TTATGGAATG CCTGTCATAT GCGGCAGCT TGTTTGTCAC 180  
 TGGAGTACGG CCGTGCCGC CTTCAGAGG GTACCCATGA TTCTGAACGC CAAGGTACCA 240  
 50 CACCTTCTCG CCACATCTCC TCGAAGCTTT CCAAAGTCAA ACCCTTTGTC TCGGGGACAA 300  
 AGAAGAAGAT GTAGAAGAAC GCAAAGATCA AACAACCCAT GAACAGTAG CCGTAGTAAA 360  
 55 ACCTGATCGC ATTGGTAATG TATGGTGTA AGAAGGCGAT CAAAAGCCC CATATCCAAT 420

TCGGGCTGT GCGATAGCC ATGCCCTTGG CTTTGACTCT TAATGGGAAA GTCTCCGAAA 480  
 CAATGACATA CGCAATTGGG GCCCAGGTAG TTGCAAAGAA GAAAAATGTA GAGGCAGGTA 540  
 AAAACAATCA TAGCATTGCC TGCCGGTCTG GAAGAAGGCT GATCGGGTCC ATTGGGOCAT 600  
 AGTCTTGTCA CACCAACGGA GGCAAAAATA ACCATACAAA CGGCCATTGC CGCGGCACCG 660  
 TAGAAGCAAA CATTTCTCTC TGCCAAATCT ATGACAGTGT TTACATTG 708

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1471UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GATCTTGGCC TTCTTCTACA TGTTCTTCTT TGTCCAGAG ACAAGGGTT TGACTTTGGA 60  
 AGAGGTGAG GAGATGTGC AGGAGGGTGT CGTCCCATGG AAGTCCGAGT CCTGGACTCC 120  
 TTCTTACAAG AGAAATGCTT ACGAGACTGA GGAGGTGAAG CCAGAGAAGA CCTGGGCTTA 180  
 AAAACTTTAA ACTACAAACT TTTTGTCTCT GCTAATCATC GGGTTAAAC CTAAACCTAA 240  
 TCTATGTCA TTAATATTGT TATGACGTT ACGAGATAGC ATATGTAAAT TACTATTAAA 300  
 AATATGCGAT TAATCTGTAT TTATTAGTTG TAATTGCAAT GCCATATGAT ACTGCAAGGC 360  
 AATACATGCC GAGATAACCA ACGCACTGA GCGGGACTG GGGCCCTTCT CGGGCCCGGC 420  
 GAACATGCTT GTGTTGGTG GCGCGGTGC CGTCCGCGG CCAGCCGCAT GCGCGTCTC 480

GGTCATCGCC CCACTTTTCAA ACTTTGTAAT CGAGCAGGAA ATTAAGATTC GTTATAAATG 540  
 5 ATATCAAATT TTTCGTGGTT TCTTTTCAGT GAGTAATATT GTTCCGGCAC CGCAGCGCGA 600  
 TGATGCGGCT ACATCGCACA GGGCCAAAGC ACAGGTGCTA AACTATTGCT TAGTTGGGGT 660  
 10 CGTTGAGCTC GTTTATGCTT AGTGAATAT CTGCAGCATA TTCAATATCA AGTCTGAA 718

## (2) INFORMATION FOR SEQ ID NO:721:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1472RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

35 GATCTATCTC CCAGCTTAGA GAGACCGTCC GGATGTAAGT GATACCCAGA CAGCCAATGA 60  
 TACTGGTCAA GTTTTGTAGT TTTATAAGAA AACATATATT AAACGGCTAA AGACAGAAGG 120  
 40 CGAAAAGCCC GACTTTTATG GGCGTAGAAG TCGTGAAAAA GGCGAAAAAC TATATTTCCA 180  
 CTTAGGGCTC CTCCTTCTC ACGTAAACGC GCATCATCAT ACGCCTTCTG TGAGTCAAGA 240  
 45 GCACTACGAC ACGCGGTGCA TTCCCTCATA CAACCTTGCC AACACATGAT CATGTCCAAG 300  
 GATATTGCTA CGACCCAGA ACTGTCCGAA CCAGACAAGT ACTTCGTTGA GCAGCGCGAT 360  
 50 TTGCTGCTAC AAGAAATCAC CTCACGTTA GACTCCATCC TGAACAACCT AAATGGCCTG 420  
 AATATTTCCC TGGAGAACTC CATCGCAGTA GGCAAAGAGT TTGAGAGCGT GTCCGAGCTT 480  
 55 TGGAAGGCTT TTACGACGG ACTCGCGAAC GGAGCGGCTC CTGAGTTGC CGCAGCCAAC 540



CCGTGCTCTC AGGACCTGOC CACTGAGOC C GTGCGCGGC ACCAGAATGC TGCAGCGGC 600  
 5 AATAGTGAAG CACCAGCGOC ATCGCAGTAG CGTTTGCACT CTGCGCTGOC TTTACACCG 660  
 TGCACCCACA TTGCGCTCTA CTTTATGTG TCATC 695

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1472UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GATCTCGATT GAATGCCAAT GAAGGTTTAT GCGCGTCACG GGAGGTATAA CAGACTTGTA 60  
 ACGACTTTTG GTAAGACCCA CGGTGAGGAA GATAGCTGGT TTAGCAGCGA CGATGAGAAC 120  
 CACGCGAGAC CAGTTAGCGA CGACACAACC AACTCAGOC TGAGCCAAGA TCGATGCAGC 180  
 GAATTACCGG AGGAGACGAT AGGTGCGAAT AGAAAACGTC CCGCGGAGOG AACGCAGACG 240  
 GATCGGGTGT GGGAGTTTCT GGAACGCGCG GCATCGGGGC AGAAGCGGAG AAGACGAGCA 300  
 ACATGCGATT CTACAGAATA TAGAGAGAGT GCCAGTCAAG AGTTTCTAAA CGCTGTGAAC 360  
 GTTGTCAGG GCATAGTGTC TTCTCTCAAG CCTGCAAAAG AGGTAGTTGA GCACTGGGCG 420  
 GAGCTTGAGG ATGTGCCAGA GGATCGGGGC AATAACGGGC AGGCGGTCTA TGGCAAAACA 480  
 AGAACATGCT TGCAAAAGCG GAAGAGGATT CTGACACCGA AGCTGCTGCA CATGAGTCTG 540  
 ACGAACCGCT GCACAGGGCG ACGAAGCACT ATCGCGGCAC TTTAATGAGC TCGGTACGAT 600

GGGCGAGACT CTTAAGTACA GCGAAGATCT GGACTTTATA TTGTCCGACA ACTCCATGAC 660

GACACCGGAA CATAGACGCA CCACATGCTG CGCTTGTGTC TGGATATGAT GAACAACGA 719

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1473RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GATCGCATCA TCCTGTACAC CAAGCGGAC GTCTGCGGCG CGCCCACCCC CGCCGGGCTC 60

CACCGCTGGC ACGCCGAGAC CGGCGAGAC TACATGCTCC TCGACGCCCC CAGCGCGCGG 120

GACGCGGGG CGCTGCTGGC CGCCGTGGC GCACGCTACG ACGCGCGCGC TGCCGCGGCC 180

GGCGGCTCC CCTCGGCTA CGCCTGCTC GTTGGGGCA TGCCCAAGT CGGCAAGTCC 240

ACGCTGGTCA ACCGCTCCG CGCCTCGGC ACCGCGGCGC GCGCCAAGT CGCCGCCACC 300

GGGCCCCACC CGGCGTCAC GCGGCTACC AGTGAGTGGC TGGCATGCG CGATCACCGC 360

GCGGCGTCT TCATGCACGA CACCCCGGC GTGGCCCTGC CGCCCGGCGC CTCTCGGTG 420

CGCCGGATGC TGGCCCTTGC TCTCGCGGC TCGTGGGCC CGCCCGTGGT CGACCCCGTC 480

ATCCAGGCGG ACTACTGCTC TACCTCTCA ACCTTCAGGG CCTGGCCCCC TCTACGCGG 540

CCTACAGGCC CCGACCAAC GACATCGCGG CCTGCTGGC CGCGGTGTG ACCCGCCACC 600

GCTACGCTC CGAGACCGCA GCGCCCTGC ACTGGCTTGC CATCGGGGC CGGGGCTCT 660

GCCTGGAACC GGAAG 675

## (2) INFORMATION FOR SEQ ID NO:724:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAC1473UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GATCTAGACG GAGTTATTAT GCGCGGCAC CTCCAGCGAC TGATACTCAA GAATGTGGGC	60
TCCGTGGGGT GGTGGAGGTT CCGAGAGATC CACGAAATTA CGCTAGATCC TAATACGTTT	120
ACCAAGAAAC AGGGCTTTGT GGGAACTATA CACGGGOCAG ATCAGGATCG GGTGGAAGTG	180
CGGCAGATAA ACAGGGCTGT CATGAGTCAG GACACATACT TOCACTTTGA TAGTCTTTTG	240
AGGGCCAGGT TCCAGAACT CAACTACATC AGTCTGCACA ACGTTTCCGA GGAAATTACT	300
GGCATCATAG TGCTCACC GACTGTATTGC AATGGGCGCA TCAGCATTCG AGGCTGGGTC	360
GTGAAGGGGG TTGTAATGAT CTAAACTTGC CCGGATATCC CTATTGAGAA ATAAACACAT	420
GGGTGAAGTT ATACATAGGC GCGGAAGAAG CCGCTTGAAT ATTGATAGAC CGAATAGTGC	480
GATCAATGTA ATTAAATAGA TAGGTTACAG CCTACCGGG CTGGCATTTC GTCCGAGATT	540
GGTCTGCTC TACCAAGTCA GCCAGTTACC GGAGGGTGAA GTAGTAGGAC ATCATAACTC	600
ATAAAAAACG TTACATTGCT TGTGCTTGTC GGGAAATCAG TAATCATGCA GGTGCGTCGT	660
GAAACCGAAG GAAACGTAAT GCGTGGAAT AAGTAAAGA TGC	703

## (2) INFORMATION FOR SEQ ID NO:725:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1474RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GATCGTTCAG TTTAATCACC TGGGACGCAC TGCCCTGCGG TTCCAGCACT GCGTGAACT	60
TGGCCAGGCG TTGCATCAGC GCATTAGCT CCTGTACATC GCGCTCGTGC TGGGCTCCA	120
GCTGCAAGCG CAGTTCAGCG CTGATATGCT TCCCGCCCGG TGTAGACATC TCGGCAAGC	180
TAGGGTAGCT GCGGACCGC CGCAGCGGCG AGCTCGGCGC GCGCTGTCA GCGTCTTCT	240
GTGCCCCCAT TAGTGGCGGT ATCATCGTCT CGATCCCGC GTTGGCATC ATGGGTATGG	300
GGTGTGTGTA ATGTCAATT ACCGCACTCC AGTCTCGTC CAGGTCCGTA AAATACTTGT	360
CTTTTITGCC GCCAGCGTGG TTAGACCGC CGTGGTGTG GCTCCGAGC GGGCTCAAGT	420
GCACGCCGCG GTGGCTGCTG CTGTGGCTCG ACAGGGACGC TGCATAGTCT GCGACCTCT	480
GATGGCGCTA ATATTCCCAT CGCTATCTGC AGGCTCCAGC GATGGCGACG CCAGCTGATT	540
CGACTTGGC GATGACGGCG TCTTCCACGA CTTGATCAGC GAGCCACAA GCGACGAAGA	600
TGATGAATTT GACTTTTGGT ACATTTCTTT GGACCCATTC CCAATTATGGG GAACGCTCT	660
GATAGCCATC ACAATGTATA GCTCGCTACT CTGAACCGCG TGGCAACCAC TGCAAC	716

## (2) INFORMATION FOR SEQ ID NO:726:

## (i) SEQUENCE CHARACTERISTICS:

EP 0 866 129 A2

(A) LENGTH: 699 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1474UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GATCGAATTC TCACAGGCCA GTACCTGGGT ATTACAGGTT TGCCATAGTA TGATTAGAAC	60
CGTAAAGCCC AAGAATGCCA GGGCCAAGAG AGCTCTGGAG AAAAAAGAGC CGAAATTGAC	120
GGAGAACGTG AAGCAAGCGC TTTTAATTCC TGGCCAAACT TCGAATAAGC TCTTGACGA	180
TGTTATGGTG GACCTTGGTG GACTCAAGAA GCTTGATGTG AAGCGCTTCA CGCGGAGAA	240
CGAGCTTCGT CCGTTTGAGG ATGGGTGGG TGTCGAATTT CTCAGCGAGA AGAATGACAG	300
CTCGTTGGTG GTGGTCTGCT CCAACTCGAA GAAGGGGCGC AACAACTTGA CATTCATAAG	360
GACGTTTGGG TACAAGGTTT ACGACATGAT GGAGCTGCAG ATTGCAGAGA ACTACAAATT	420
GCTAGCGGAC TTCCGGAAGC AGACGTTTGC AGTGGGGTIG AAACCGATGT TTCTCTCCA	480
AGGTGGGCA TTGACTCTC ACCCAGTATA CAAGCAAGTC AAGTCTTTGT TCCTCGACTT	540
CTTCGGCGGT GAGGTGACCA AGCTGCAAGA CGTTGCAGGG CTTCAGCATG TGATAGCAAT	600
GACGATCCAG GGCGACTTTG AGGATGGCGA GGCATTGCCC AACGTCTTTT TCGCGTCTA	660
CAGGCTTAAG ACGTACAGAA GCAGCCAAGG TGGTAAGAA	699

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 749 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1475RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GATCCGACCA ACCAGGCGAT CTGCAGGCAC ATCGTTGATA ACCTCACCAT GATCGACGAA	60
ACCGAGGAGG ACCAGGCGCC AAAGAAGGGC GCCTTTGCTG TTTGAAGCCG GATCCTGCGG	120
CGTTCAACCG TAAATAGTCT TATAGCCAGC AGCCAGGGCG CCGGCGGTT CCTATGTAAT	180
CCTGCAATCG CTCGCTTGCT AGCCGACGA TCACAGAATA CAGCTACTTT ATCCTAAATC	240
CACTCCTATC AAAATATCCA GCGCGACAT TTGTTCTCTG TCTGTGGGA TGTGGCGTTC	300
GCCATTGTGG AGTAGGCGCG CAACTCGGAC AGCGACACA GGTGCGCATC ACAGCTGCGG	360
GTCCCGTGTTC CGTCCCTGGA ATCCTGCTCC AAGCCCTTCT GGTCAAAGCC AGCCAAGCTC	420
CCCTGTCTGA TGGCGTCTC GACCGCTGCG TCAGCAAGT CCTGGTATGG ATCTGCGCGG	480
ACGCTTCTGG GGGCGCAGG CGTTGTGTGA AGCCAGTGGC ACAGAGAGGG TGTGCTGTTC	540
AGCGCAACAG ACCAGGCGCC TGTGCGGCGC GCATGGGCGG CCGTGGCGAA TGGGTGCGGG	600
TTTATGTAAT TGCTGCCCTG GTCCGATGTG TATTGTGTCT GCGAAGGGA AATCGGGGAC	660
GCAGGAACGT TCGCTCGCC GCATCGTTC TCGCAGCTCT TCGGTGCGG CACCAAAGCC	720
TCCTTCTGCA GCATCCGCCC TGAGCCGTT	749

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1475UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

GATCTTCGGT CCGAGTACG GTCGTCTCTT CGAGATATNA GCACGCAGCG CAACTGTATC	60
AAGCTAACCA ACACAGTKCG CACGCTTTTC GAGCGAGCT CAGGCGGAG GTGAACAGC	120
TCTGAGACAG ACAGACGCC CTTGTTTACA AGTAGCTCAA TAACAGTCC GCTCGCTCG	180
CGAGGTGCG ACGCGCTAC CTCGTGTAC AGGAAGTTTT CAGGACTCAA TGTCTCATC	240
TCCAGTGTG ATACCGGCAC CTCGCAGCA CGCTGTTTT GACTGTGTC ACCTGCAGCA	300
CCCATAGATC CGTTCATTAT GCACTACGAC CTCGCCCTCA CTCAGGCCA GGGCCGTCTG	360
GAACGCAATA CTCGCTAGTG CTAGTTCCCA CCTAATATCT ATCTCATGCG CCATCGAGCA	420
GCGGGCCAGC TAAAAAATCA CCACTGCGCG CTCACCAGC ACGGTTCACT AAATACGAAA	480
CAGTTGTGTC TCAAGTGTG CTCACGTGAT TTTACCGGC CGGTATAATA TGGGTTCTC	540
AGCGCGCGA GCCAAGGACA CTTCTGTAT CATAACAAAC CAGCACAGC GGTAGGAGCT	600
ATCGGCAGAG TOCCAATACC CTGCTACTG TTGACATTAG GTGGTTCAA TGAGTGTCTG	660
TTTAGTGGTT ACCAAGAGTG TGGCGACAG CACATTGGG ATCTACACG GGATGGTGGT	720
AACGCGCAG TTGGTCTTC	740

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1476RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GATCGTATCG CTAACGTAA TATCGAAAGA AGCACAGACA TCCCGGAAAA ATGACATCTC	60
AGTGACACTC TTCAACAAAT CATAAGAAGA AAAGTATGIG ACTAATGCTT GCAGAAAAAT	120
AAATTGCTCG CTACCACTAA GCGATGTTAG TAGCGTGCCA TGGCAITCAA TAAATCGTAA	180
GAGATACGTG GGTGGTATCT CGATGCTTTT GAGGTACGCA AAAATTGGGC CATATAAATC	240
GATCTTGAAT GGTAGCCTTT TGCATATCGA TTCTTCAAGA AGTCTGTTTA TAAGTTCTTT	300
ATCAGAATGC TGCATAGACT GATGCAGGAG AGCACTTAGC ACATGCCCTT TATTCTTAGG	360
ATAGAGCAAA TATTCTTTGA ACGAAGCTGG GTCTTTCCGG AAGTCAGGCT TCATACCATA	420
AAGGTACATG TATACATTCC TTGCGACATC CATATCTTCA ATACTGCTTT CAAGCATCGC	480
AAGGTAAAAT TCGTAGGAAA ATTCCGGTAC CCAGGAATGC TGTTGAAATT GCGTCCAGAG	540
TTTGTATGCT GTCTTGGGGT GGTTCCTTGC GACGGCCAAC AGGAAGTTGG GACAGAACCA	600
GCGTCTGACA GCGAATCAAG ACCATCTGTT GAGCGAATTT GCGTGAGAAG GCGATCAAGC	660
AGCTTCACAG CAACTTCCAG GGAATCTAAG CTGACAAGCC CAGCTAC	707

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1476UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GATCTGAAAC TAACAACAGC AGTGGGTGAA CCAAGAGGCA TTGGAGGCGT ATGAAGGCGT	60
GTCGCAAGGC AAGTACACTA TGGGCTTGGG CCAGACCAAC ATGAGCTTTG TGAACGACCG	120
CGAGGACATC TACTCGATGT GTTTGACCGC GTGCTCGAAC TTGATGAAGA ACTACGATAT	180
CAAGCCGGAA AGCATCGGCC GCGTCGAGGT GGGTACGGAG ACGTTGCTTG ACAAGTGGAA	240
GTCGTTGAAG TCTATTTTGA TGCAGTTGTT CGGCGAGAAC ACCGACTTGG AGGGTGTGGA	300
TACCGTGAAC GCCTGCTATG GCGGTACTAA CGGTTGTGTT AACTCCTTGA ACTGGATTGA	360
GTCCAGTTGG TGGGACGGTC GTGACGCAAT CGTTGTTTGT GGTGACATCG CAATCTACGA	420
CAAGGGTGCC GCGCGGCCCA CTGGCGGTGC GGGAACTGTC GCTCTCCTGA TGGGTCCAGA	480
CGCCCCCAT TGTCTTGA CTGTGGGTGG CTGTACATG GAGCAGTCT ACGACTTCTA	540
CAAGCCTGAC TTCCGCAGTG AGTATCCATA CGTGGACGGC CACTTCTCAC TAACATGCTA	600
CGTCAAGGGC CGTCGACCAG GCTTACCGCG CCTTA	635

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1477RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

10	GATCTTTGCG AGGGACCACT CTGCAATCCA AGAAGACTAG AGGAGTTGTC TAGGACAACA	60
	AAGTTTATAA GGAGACTTCT GGTGTTTAC CGTCTTTTC GATACCGATT CTOGACAGTA	120
15	TATTCAAAGG CCAATAACGC CAAACAATAC GTTAAAGTTG GCTGCCAGTT TTTCAACACA	180
	CTACTACAAC ATTATGAGGG CATAAAGGTG CTCTAGATG ATAGCAAAT CATTCCTCAG	240
20	CTCGCCAGTA CTCCTATATA GGCTATGGAA GGCATATTT TACCCAGTAA GCTCTTCTCC	300
	TCTTGGGCTC TCCAGAATAC GTTATGTGGC TCTACTTCA AATTCTCGG ATTGCTAATG	360
25	AAATCTAAGG AAGGAATCAA TATATTAGAA AAATGGAACA TGTTCACTGT CATCTATAAA	420
	ATGTTTCAGC CATCACCOCT AGCGGAAGAA TATTTGTTAC TCATGCTTCC AGAGTTGGAC	480
30	CTCTCTCACA GCATACATTG TAGGATTATT TTTAGCAAAG CGCTAGTCGA CAGTAGAGAA	540
	GTCATAAGGA TCAATGCTAC CAGGGTTTTA GCGAAATGA TCAGCAGCGT CAAATTATCT	600
35	GATCCCACTC TGAAGAGTT CATGTAAAC CTGTTGGTGG CTCAGTTGTA CGATTATCG	660
	AGTGAAGTGG TAGCAGTGGC CGACCAGATA CTGTACCATT ACTGTTTAAG TCAAAGTAT	719

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1477UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

5 GATCOGAATG TCCTTAGTCT GTGGGAAGGA ACGATGGTG GTGGTTGGGA ATAGCGGGAG 60  
 CTTGAAAATT GGCTGCTGCT CCTTGAGACG CTCCCGAAT GGTGGGCTC TGTGGATAG 120  
 10 CTTCTGTTT AAACCAGCAA CACGTCCTGG ACAGCAGGAT CGTTGGTGAT CGCAGAGGCG 180  
 GCAGGCGCAG CAATCGAGTC TGCATTTGCC TTCAACTCAG AGGAAAAGTC TTGCCAGAA 240  
 15 GCGTCTTAG CGAGGACAAC AACCTCATGC AGCTTCTGGG TTGCAAAGA GAACAGTCC 300  
 TTGATCTCTG GCTCCAAGGC AGACTCGTTT TCCAAGTCAA CTGGAGTGTG CAACAAGGAA 360  
 20 GAGGACGTGG CAACAATAAC GCGGTCCCTT CTAGTTTCT CAATTGCCTT AGAAATAGTG 420  
 GCAGCGACT TCGCGAAGTC ATTCTTCAG ATGTTCTAC CGTCAACAAC ACCTACAGAC 480  
 25 AACGACTGGT TTTCGCCAAC GATCGCTAGA ACGTGTCCA ACTGCTCTGG GTTCTCACC 540  
 AAGTCGAAAT GTAGGCCAGC CACTGGAAGA TCACAAGCG CCTTCAAGTT CGGAACGACT 600  
 30 GTCCCGAAGT AGGTGGTCAA CACAATGTG AGAGACTTTT CGCACTTAT ATGTCATAA 660  
 GCGTCTTAA ACGCAGACTG TACGTCCTCT GCAAGATCTA AGACCAACAC AGGCTCATCC 720  
 35 AGCTGA 726

## (2) INFORMATION FOR SEQ ID NO:733

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1478RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

5  
 10  
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GATCATTATG	CAITTTTATGA	TATACACTGC	TATCAAAGAC	GACCACTGG	TAGTGAATAC	60
ACACCGGCTG	GCAGACACAA	CCAATGCCGA	GGATGAGGCT	AGTGAGGACG	AGTTAGAGGA	120
GCTCGTTAGT	AGCACTGCAC	ACAGCGGCGA	TGCTACTAGC	GAGTGAAGAG	GTATTTTACC	180
TGAGCTTTTG	AATATATAGG	TAGGTGATGA	GCTTTACAAT	ACGTATTGGC	TAACAATGAA	240
ATGCAGGAAC	TCCTCAAGCT	CTTTAAGTTC	TGTAAAAACG	GTATCAAAAA	CCGTTTTTTC	300
AGCGCTGTCT	GCGTAAATGA	CCTGGATTAT	CGCATTCGAA	TAGTTGCTGC	TCTTCAAGGT	360
CAGATCTATG	ACGCCTTTTG	CGCGGAGGCT	GGTACGCAGT	TGCTGGGTG	GCATGGGGAG	420
GATCTTGTC	AATAGGCTTA	TCTGTTTGTT	TAGGCTAGCG	ATGTTGGCCT	CACGAGCATG	480
GAGCGTATCG	GGCTGGCTTC	GTTGTGGAAG	CAGCTGATG	GACGAACCAG	GAACAATGTT	540
CAAGACGCAC	TCCGTAACAA	CTCTTTTAAC	CACCTGTAAG	TAGTTTCTAT	GCCTTATTCT	600
ACCCAAAACA	GGTCTTAATA	GGAGAAGGTC	ACCATCAGCT	CTATATTTAT	GCTTGAAGT	660
TGCTGGCTTG	AGGCC					675

## (2) INFORMATION FOR SEQ ID NO:734:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 706 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - 45 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- 50 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: PAG1478UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

5	GATCTGAGTA TCAAGATACC ATGAGOGATT CTTGCTCACT CTTGTACGGG ACTGCCCCGC	60
	TTATCCAAGT GCAGACAAGA TGCAACATGC ATACTGGCAG ACCAGGCCCT CTGATCATC	120
10	GAGTTGCTTT AAGCAACATA GTAGGAGGCT TCGAAGGAGG AGTTCTTCGG CTACCTATGT	180
	AAGAGATGCA GCGGATGGTT ACTGCTGGTC ACGTCTAGA ATCATATACC ACGGAAAAGT	240
15	GGATATGTTG CTTGCCCTTT AGATATGGCA GTTTTGCCAC CCTACTTGAC ACAGCTGTAA	300
	CAACGTTGAC TAAGGATAAA CAAGAGCTAC TGTCAACGGG CTATCCATAC AATGACATCT	360
20	GATCTAATGG AGGTGGACTC GGGCCATACA CCGGATGTTT ATAGCGCAAG CAAGGACAAC	420
	GTTGACAAGT TTGTGATCTT GCTTCGCCAG GTCTCCAAGA CTACTATAAC ATTGGACTCC	480
25	CGCTATGTGT GGAAGTCTCT TGGGAGCTA ATGCTTTTGC GCAAGGAGCT GCAGCAGCAG	540
	ACCCTACCA TCCTTATCAC GTCCTATAT CCGGACGACT CGGCATTCAA GGTGCCATTG	600
30	CTTGTGTGG TGAACCAGAA CTCAAAGCA GGTGAGGA TGGGAGGCA TTCCAGGGCA	660
	AGTACCCCGC AGACTTTATC AGCTGACTGC TGACGGCAAG ATTGAC	706

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1479RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

GATCGGCTTA CAGTAGCATT GTCCTCGCAG GTTGCCCTGCC TCAATTTTAT CCGGGCCCTC 60  
5 GAAGAACTCC AACTCGAAGA GGAAGTTCGT GCGGCACTGG CATAAATTGT CTATGCCCAG 120  
CCCTGTTGG CAGAAGCAT GCTTGCACTC TGCAAACTGC TGCACTCGA ATTGGCGGAT 180  
10 CAAGAGCTGT AGCTCCACGA GCGCATCCTT GGTAAAGCCTG CTGCCCTCGG AGCGGTGGC 240  
GCACCGTTTG TCGATGCATT CGTTGATCTC CTCTGTTAGG TTGCGTCTG TGTGGGCGA 300  
15 ATTCTCGAAA AGCGTGGGC GCACTATCTC CCTGCCGTGA GGCACCTTGT TCTCCTTGT 360  
COGCTGTCG TTTTCGTAGG GCGAGGTGAC TGATGATGAA TCATTCATAA AGCTGTTTTT 420  
20 ATTCCGGAGG CTGGGCTTGC GCTGCAAGT CACGTCAAAT TGTTCAACG CCTCTTATA 480  
AGGCTTTTC TCATTATTA TAGCACTATG CCAAGATCCA GATGIGGCAA TCTGGGATTA 540  
25 CTAGACCTGT TGGCCAGCA TGAGTTCCTC TTATATACAC TGCCAGTTTG TGTCTGACAC 600  
AAAGACGTAA AATTGGGACT ACGAAAAGG AGTGGCCAAA CAAGTGGCAA ACGTGTAA 660  
30 AGGATAGTGT ATATTATAC TATTAGTAAT TATGT 695

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 716 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1479UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GATCGGGCA TTACGGTGCC CATCTACGAG GAGGACATTG TCGGGGACCA GGGCGGACG 60

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GACGTAGACG GGCAGCCGCA GAAGCTGGGT TCGTACCGG CGGGGCGCG GCGCTTCTCG 120  
AACACGCTGT CCAACCTGCT TCCAGTATC AGCGGGAAGC TGCAACCACAA CCGGAAGGGC 180  
GGGACGGGA AAGTCGCGC GTCTGCTGCG GACGCGGACG CGGGAGCGCG GTCTACCGTG 240  
GTTGCGGGAG AGATGGCGGG CAGCATCAGC CCTCCGCGG ACCTACATAA CGTGGTCAGC 300  
TTCCCGGAGC CACACGGGCT TGCACAGCCA CGCACTTGA GCGAATCGTA TACGTATGGT 360  
TCTGGATACA GTGGCCACCT GCAGCCACA GTCTCCAACC CTGCTACGCG GACTCGGAAT 420  
AATACTGTAT CTTCGCAGAT TACTTCGCTT TCAAGCATGG GCGAGCTGGG AACCCCGAGC 480  
ACGAGCAACA TCTGGACCAA CAATGGCTCA AGCCCGGCG ATCCAATCAG CAACATGCTC 540  
ACGACGCGT TCAACCCGAT CCCCCTCCCC GACTTTGGCC AGTCGAAC TAACGAGCTA 600  
ATCAGCAGC AGCAGCCTCC GCAGTGCAG AACTCACTGA ATGTCGCC TCAGGGGTAAT 660  
ATTTCTGGGA AAAACGTACT CGTTCTCAAT CTAATGCTTC TAGCATATAC GCAGAT 716

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1480RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GATCCTCTGA GCGAGCCCT ATCCCAAGTT TATTCCAAC TCTTGCCGAA AGGTAACAAA 60  
CGTTTATTT ACATGAGTTT ACACATAACA CCGGAGAATG TTGATGTTAA TGTGCATCCT 120

ACAAAGCGTG AAGTACGATT TTGTATGAA GAAGAGCTAA TAGAGGCGAT TGGTAATTTG 180  
CTCCATGAGC GGTATCTCA GCTGGATACT TCGGAACCTT TTAAACCGGG CTCCTTGACA 240  
CCTGGGAAAC ATAGTTC AAC TGTCCTCC GCATTCGGC AATCAGCGAC CCGGCAAGT 300  
ACACAACCAA AGGCAAAACG TGCAGAAAC ATGCTTGTC GACTGATGG TAGCCAAGCT 360  
AAAATTACTA ATTATGTCAG AGCAAGTCAA AGCTCTACCA GCTCATCCTT TTCACTTCT 420  
TTAAGAAAGA AATCACATGC GGCAGCAAGT GATGAACCTG GCAGCATTGG CGAGGACTCC 480  
CAAGATACAG CAACATCGAT GACAACCTCT ACACAAGAGC CTAATCATAC CAAGTCTAGA 540  
GCCATTTTAA CCTTATTGAA TAATGAGTAT GAAGTCGTAC AGCGGGAAAG AACGGAAGTA 600  
AATCTCACCA GCATCAAAC TCTAAAGCAG GAAGTAGACG AAGATATGCA TAAGGGAATT 660  
AACAGTGTG TTTCAGATA TGACCTATGT TGGTGTGTT GATGCAACAA GCGACTTGC 720  
ATCTATACAG CATGGTTTAA AGTTATTT 748

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1480UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GATCGGCTCA TGGGATACAT AAACCACGGA ATCAATGAAA AGCTCGCTTA CGAACAGTTT 60  
GGATCTGTAC CGGAGAAGGG CTAATATATT CCTCCACAA TATTTCTGGA CGTTCTCAG 120



AGCTCGAGAC TCTGCGTGA AGAGATATTC GGCCTGTGG CCGTAGTTGC GAAATTCAAG 180  
 5 GACTACGATG AAGCTATTTC TTACGCTAAT GACACTAACT ATGGGCTGGC ATCCTGCGTT 240  
 TTCACTGAAA ACATACGGGT TGGCACCGC TTGTCCGTG ATGTCCAATC TGGCACTGTG 300  
 10 TGGGTAAATT CCTCTAATGA TGAGGAGGTG GGAGTGCTT TTGGGGGGTT CAAGATGAGC 360  
 GGTATCGGAA GGGAGCTGGG GAAGGCAGGC CTGCAAACTT AACTCCAGAC TAAAGCAGTA 420  
 15 CACCTGAACT TTGCTTAGAT AGAGCAACTC ATATATTAGA ATCACTTCAT ACATCAACTA 480  
 TATATCATTG TGTATATGAC TATGCCAGAG GTGTAGTGA ACCACTATTT ATCAGTGAT 540  
 20 AGGCGTTGCG CGGTATCCC GCCAGTACCT GCGTTGCAGA ACGGGGGGGA CACATTGAGC 600  
 AGGTGCTATA TACAGTTGTC GAGGACAGTA TGSCAOCAG TACCATTATA GCAAGTAAGC 660  
 25 CGTGTGCTGT TTGCATAAAG CGTAAGGTCA AGTGGGACCG GCTGGTTCCC TGCAAGAACT 720  
 GTGTCAA 727

## (2) INFORMATION FOR SEQ ID NO:739:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1481RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GATCGATAGG CCACACTTTC ATGGTTTGTA TTCACACTGA AAATCAAAAT CAAGGGGACT 60  
 TTTACCCCTT TGTCTACTG GAGATTTCGT TTCTCCATGA GTCCCCCTTA GGACATCTGC 120

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GTTATCGTTT AACAGATGTG CCGCCCCAGC CAAACTCCCC ACCTGACAAT GTCTTCAACC 180  
 5 CGGATCAGCC CGTATAGGAC TTAAATGCT AGAAGGTGGA AAATGAATTC CAGCTCOGCT 240  
 TAATTGAATA AGTAAAGAAA CTATAAGGT AGTGGTATTT CACTGGGGCC GAAGCTCCCA 300  
 10 CTTATTCTAC ACCCTCTATG TCTCTTCACA ATGTCAACT AGAGTCAAGC TCAACAGGGT 360  
 CTTCTTTGCC CGCTGATTCT GCCAAGCCCG TTCCCTTGGC TGTGGTTTCG CTAGATAGTA 420  
 15 GATAGGGACA GTGGGAATCT CGTTAATCCA TTCATGCGCG TCACTAATTA GATGACGAGG 480  
 CATTGGGCTA CCTTAAGAGA GTCATAGTGA CTCGCCCGGT TTACCCGGGC TTGGTTGAAT 540  
 20 TTCTTCACTT TGACATTCAG AGCACTGGGC AGAAATCACA TTGGGTCAAC ATCACTTTCT 600  
 GACCATGCCA ATGCTATGTT TTAATTAGAC AGTCAGATTC CCGTTGTTCG TACCAGTTCT 660  
 25 AAGTTGATCG TTAATTGTAG CAA 683

(2) INFORMATION FOR SEQ ID NO:740:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 657 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1481UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

50 GATCGGGTGG TGTTTTCTTA TGACCCACTC GGCACCTTAC GAGAAATCAA AGTCTTTGGG 60  
 TTCTGGGGGG AGTATGGTGG CAAGGCTGAA ACTTAAAGGA ATTGACGGAA GGGCAACCACC 120  
 55 AGGAGTGGAG CCGCGGGCTT AATTTGACTC AACACGGGGA AACTCACCAG GTCCAGACAC 180

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AATAAGGATT GACAGATTGA GAGCTCTTTC TTGATTTTGT GGGTGGTGGT GCATGGCCGT 240  
 5 TCTTAGTTGG TGGAGTGATT TGCTGCTTA ATTGCGATAA CGAACGAGAC CTTAACCTAC 300  
 TAAATAGTGC TGCTAGCATT TGCTGGTTGC GCACTTCTTA GAGGGACTAT CGGTTTCAAG 360  
 10 CCGATGGAAG TTTGAGGCAA TAACAGGTCT GTGATGCCCT TAGACGTTCT GGGCCGCACG 420  
 CCGCTACAC TGACGGAGCC AGCGAGTATA ACCTTGGCCG AGAGGTCTGG GTAATCTTGT 480  
 15 GAAACTCCGT CGTGCTGGGG ATAGAGCATT GCAATTATTG CTCTTCAACG AGGAATTCTT 540  
 AGTAAGCGCA AGTCATCAGC TTGCGTTGAT TACGTCCCTG CCTTTGTAC ACACCGCCCG 600  
 20 TCGCTAGTAC CGATTGAATG GCTTAGTGAG GCCTCAGGAT CTGCTTAGAG GAGGGGG 657

## (2) INFORMATION FOR SEQ ID NO:741:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 694 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1482RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

45 GATCCATTGG TTAATATGGA TTGTCTACAG TGAGAGCAAA GAGGGGGGGG GATTTAAAGC 60  
 ATGGTGGGGC GACGCTATT TTAATAGGGG GTTGTTTGCA ACGTTTGG CCGGCTTCT 120  
 50 TGTCCTGCAT AGTGAAAAGT TCATTGCCA AAGAACGTAC GAATCTTTC TGATACTGCA 180  
 CAAGCTCTTC AACATTGTCT TTATTGTATG CATGTATATG CACATCAAAA CGCTGGGATG 240  
 55 GCACGGCTGG GTCTGGTGA TGGTTGCCAT CTA CTGCTTTC GAGCGTGTGG CCCGATAGC 300

TCGCATGTGA CTTGCTGGAG GCATCAAGAA GGCCACATTA ACAGATGTTG GGGATCGCGT 360  
 5 GCTCAAGATG ACAGTGGAGA AGCCAAAGCA TTTCAAATAT TACCCGGGGG CTTATGTTTT 420  
 CGTTTATTTT ATTAGTGGGA AGGATGCTTG GTTCTATCCA TTCCAGTCGC ACCCGTTCAC 480  
 10 CGTCCTTAAT ACACCCAAGA TOGATGGCGA CAACTGGTG ATTTATTTCA AAGTGCACAA 540  
 GGGCGTGAAG CAGCAGCTGC TAAACAGGAT CTTTCTATCC GGGAAAGAGT CCATCGAATA 600  
 15 CAAGGTGCTT CTAGAAGGGC OCTATGGAAA CACCATTCGG CGGCTTGCTG CTCTGACCG 660  
 GCGCTAAGTG GCGGCCAGCG CAGGTCTTGG CGTA 694

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1482UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GATCGCGCGG TTCGGCGCGG TGGGCGCAAA GCTGAACCGG TCCGCGCGGA AGGATGCGAT 60  
 GTGGCGGCTG CGGAATTACT CGATGAAGTG CAATGAGGCC AACGATGTGT ATCTGCTGCT 120  
 45 GAACGGGTCC AGCCACGTAG CCTGCGACGT GAGCGACACA CTTCTGATT GGTGGCCAG 180  
 CACCGAGGAT GAGCCGGTGA TGGAGCTGGT GCTGCGAGAG TGGCTGACG TGAACCGGCG 240  
 GCTGGAGTTC CGCGTGTTTG TACGAGGTGG GGAGTCTTG GCGCGTGCC AGCGGGACCT 300  
 55 GAACTACTAT GACTACCTGA AGCCGCTGGA GGAGAAGCTG AGGACGGCCA TTGAAGACTT 360

CGTGCAAGAC GTGATGCTGC AGCGGCTCCC GGACGACACC TTGTGTGGG ACGGTACAT 420  
 5 CCGCGGGCCG TTCACAAAGG TCTGGCTGAT CGACGTGAAC CCGTTTGGC GCGAGACGA 480  
 CCGCTGCTG TTTTCATGGA ACGAGCTGTG CACCTGAAGC CCAACGGCGA AGGGCACCGG 540  
 10 AGCTGGGCTT GGTTCGGGAA AACTACATCG GTGCTTGGC GGAAACAAC ATCGGTGCT 600  
 TCGCAGCGAA AGGAGCACTC GGAACACCAG GTACCTCTGG ACGTGGTGA GGCAGGGCTC 660  
 15 AATCCGCAAA GCATGCAGAA GCTGGTTGAG A 691

## (2) INFORMATION FOR SEQ ID NO:743:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1483RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GATCCAAAAA ACCTCTWAAG GTACAGTCTC TAATTGCTTC CATSTCTTTT TGAACATACA 60  
 40 TGGACCATGC ATCCTCGTTC TTGTACCGA CAGAATCTTG YAATGCAGCA ATGGCACTTG 120  
 GCTCGTTGAC GTGCTTATAA CCACCATCCC TCCAATGGTA TTGCGCGGCT TCAGGCAAGT 180  
 45 TGACAGATCT CTTAATCKTA AACCTCGATG GATAMCCGG CTCGTGCAAT GAAAAGGGT 240  
 CTGSGCAAT GTATTCAAAG GTAACACCTT TAATTCTAGA AGCGGTTCGG GCAAAACACA 300  
 50 AATCAATCAC TGAGTTATCA ATACCTAAAG CTTCAAATAT CTGCGCTCCC TTGTAAGATG 360  
 CCAGAGTAGA GATACCCATC TTCGACATGA CTTTGTAGTAT ACCGCGGTCA ATTGCTTCCT 420  
 55

TGTAATTATG CAACAGTTGC TCATCTGTAA TATCAGAGTA GTCATOGTTA ACATTCCGAA 480  
 5 CTAAACCTTC GTTATTCATT CTGACCAGG TTTCCATGCG TAAGTAAGGG AAAATACCGT 540  
 CACACCCATA GCCAAGAAGA ACACAGAACT GGTGAACCTC G 581

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1483UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GATCATCAGC CCGGCTGCTC CGCCGCAGTA ACGGCTCCAC GTGGTAGTCT GCGGTCCCTG 60  
 CTAGTCGGTG GTCATOGAG AGGTCTCTT CTCAGGCTC GGAGTTGGCC ACGGAGGCAC 120  
 TTGAAAGACT CTGTCTTGA TTCAATCCC CCGCCCCGTA TTCTTGCCC TGTGGGGTG 180  
 GCTTGGTGAG GCCCTCCCCG TGCAGATCTT CAACGTCATC CTTGAGCTCC TGAAGTTGG 240  
 CAAGAATTCC GGTTCCTGA GAGACATAGA ATTGTCAAT TGGCTCAGC TCCTTATCCA 300  
 GCGCCGCAAT GAATCTTTTG ATGTAGCTCT GTGCAAGGG CACCCGCTCG GGGTCTGTG 360  
 CAAACGTCTC ATGCTGGTAC AGCTTGTCTT TCTGAGTGT GTACAGGAGC TTCTTCAACT 420  
 GCGAGTACGC GATATACTTC GACGAACACT CAGGGACCGC GTTGAATTGC AGCGAATGTG 480  
 AGAACTTCAT CTTGGCTTCT ATCGCCTAAC GGCCTGGTC CGTCGCGATA CAGGTCTGTC 540  
 TCATTGAAAG TACGCAGGC AGGCATAGGT TTAATTCCAG GCTCCAGGA GATTTTGGTG 600

CAAGAGGAAG TTTTAATTCT CATTATATCA CGTGCCCTGG CTATATTTAT AAAGTTGCOCT 660

CTAACGGG 668

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1484RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

GATCCTCTTC TATAACTCAA TTAACAATGT TTCTCTCTGT GGAGTCGTTC CTGCATCTTC 60

CGTAACCCCTT TCATTCTGAG GGTAGCCAT TTTTATCTTC TGCGCTGGAA CACTCGGGAA 120

TTCAAATTGA GTTATTGGCA CCTGTGCTC CTCTCTCTTG TCGGTATAC TTTCTTCAGG 180

AGGATAAAGA GGCTCCGATG GTGATGATAG CAGTGTCTTC TTAATATCCG GTTCTGAGAC 240

CTGCGGCTCA AAGCCAGTTA CTGATTGCGA CTGGCGATTC TCCATCGGCG AACTTTGTGT 300

GGTATGTAGG ATTGCTGGAG TGAGTCTGC AGGTTTGAA GAGCTCCTGG CATAGCTACG 360

ATATGTTGGC TCAGGTTGCG TCTTCTCGTA CGGAACAGTG TTGGCTGGAG AGGACTCTGG 420

TTGTGGTGC ATTTGATAAG TGTATGGATC AGAAGGTAAG TGTGCCATGG AATATTGTTG 480

CGAAAGATTA ATATTCTCA ATTGTCTCTC TAACATGGTG TCATAAATGC TCATTATATC 540

CGAAATTTTG GCATTTCATGT CTACCAAGGT ATTATATTG TGAAACGTAT CGTTAAGGGA 600

ATGGTTTAAC CGAGGCCGAG TTCCAAGGAC CTCTGGTAT AGCATCTGCA GCTGTGTATC 660

CTCTAACACG GCATTCATTG GCTGACCCCTT CCTCTTCCTC CACTAGG

707

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1484UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

GATCTGGGAG AACGTGCTAC AACACTCGTG CCGGGTCAAG CCGGACCCGA AGCTGATCGA 60  
CCAGCAGCCG GAGATGAACC CCCAGCACAC GCGGACTGCG ATCGTGAACT TTGGGTTCGA 120  
GCTGGGCGCAG AAGACGCGGG TGACGAACCG GATCTTTTTC CACGCGGTGC GGTGTACGA 180  
CGTTTACTGC TCGAAGCGCG TGGTGCTACG GGACCAGGCG AAGCTGGTGA TTGCGACCTG 240  
CCTGTGGCTG GCGCGGAAAA CGTGGGGGGG GTGCAACCAC ATCATCAACA ACGTGAAGGT 300  
GCTACGGGT GGGCGCTTCT ACGGGCCCAA CCGCGGGCG CGCATCCGC GTCTGTCCGA 360  
GCTGGTGAC TACTGCGGGG GGTGGAACGT GTTTGACGAG TCGATGTTCA CGCAGATGGA 420  
GCGCCACATC CTGGACACGC TGAGCTGGGA CGTGTACGAG CCGATGGTGA ACGACTACGT 480  
GCTCAACGTG GACGAGAACT GTTTGATACA GTAAGAGCTA TACAAAAGGC AGCTGGAGCA 540  
CAATCGGCAG TACGCCAACA AGCGCAACTC GCAGGACAGC AACCGGACCG AGGAGGACGT 600  
GTCCGAGGAG GACGAGGACC TGGATAACAA GATCCAGTTA ATCAACATCA AGAAGTTTCT 660  
GATAGACCTG GCGTCTGGC AGTAAGACCT CTTGAAGTAT GAGGTATTCC GAGCTA 716



## (2) INFORMATION FOR SEQ ID NO:747:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1485RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

25	GATCCCCGCG TTATTAGCAC GGTGCCCTTAA CCAACTGGGC CAAGGAACCA ATTACACTTA	60
	AGATGCTATT TGCAGATAAT TGTAGTCCAC TCAAGTCAAC ACGGGCATAT TTTACTTTCT	120
30	AATTCTTAAA TTCTTAACTC TAAGCCAATC TAAGTAGTTT ATCTATCAT CACTTGATCC	180
	TTGCGTTTGT TTGGTCTATA ACCTTTAATT GGGTAGTGCT TATGGAAATA TATATAATGA	240
35	GATATTACAT GGTGCCATA TAACTTCGGT ATGAGAGTTT GCGCGAGTGG TTTAAGGCGT	300
	CAGATTTAGG TTATTCTCTT AAAATCTCTG ATATCTACGG ATTGCGGGT TCGAATCCCG	360
40	TAGCTCTCAT TATTTTTTGT ATATTGTCTT TCTCAGGCAT GTGACATTTT GCATCATAAT	420
	CATACCGAAG ATATGGCTCC CACCGTGACC TGATACATTC TCGCATCTGA AGGCATGCAA	480
45	TTTAATGCAA CTGTGGCTGC AGATGCTCTA GGTAGGAACT AGCACAACAT CTAACAACCTA	540
	GCTTGCCATA TACAGCGCAA TGACAGCGTC TGAGTGTGTG TGGCACCGAT CATAAGCCAA	600
50	TTCTGATTGT CTGAAGACAG GCTATGAGTC TOCCACAGTC CTCCTTGCTG TCCCATACGC	660
	ATATAAATAC CCTTAAACT CAATTAGCCG GTATTTTATT TGAGCTGCAG AAGGTATCTT	720
55	AACTCAGGTA TAATATACTG TAATGGGG	748

## (2) INFORMATION FOR SEQ ID NO:748:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1485UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

GATCGGAGGT AGTGTMTTTCG GTGGGCACGG AGCTGTAGCA CGGGGGGTCC AAGAGCGGCA	60
TTGTGCTGTG TATGTGTGGTG ATGACCTCGA TGAGCTGCTT GCGAGGTGC TCCACGTAAT	120
CTTCGGTGGC GAGCCACAT TCCTTCGGGT CGGGAAAAT GGTGCAAG TACTCGAGCT	180
GCTGCGAGAC CTTCTGTAT TCTAGCTCGC GGTCAAGCA GACGATGGCG TTGGCTGAA	240
GGATCGTGAG CTCGTGAGC ACGTCAACGA GGTGTCGAA TTGTGCCACC GCGCTCAGCG	300
CGCCGTGAT CGCTTAACA AAGGCGGCG GGGCTTCAG GGCTGTCCA CTAAAGAGAT	360
CACTGGGCTC GAAATGCTG ATTGCCCTGC GCATGTACGG CACAAGCTGG CGGACACGA	420
ACAGATAGCT CATGTGCCGG GAGTTCGAGC TCACGCTAAC TGCCGAGTGC TTGGTTGAGT	480
GGCTGAAGGG CCTACTGCCC CGGTAGGCG ACCCGAGAAA TGCGTCATCA CCTCGTCTTC	540
ATCTGGCTTG AGATACAAAT CCGAAGCGG CAGTTGCCT GTCATGCAG AGTTGTTTGA	600
CAAGAGCAGC TCGTCTAGTC GCTGCTGGAG CTGGCCCACT TTGCTTTTGA GTAGTTCCAC	660
TTCACTGCCC TTTCGGATA GCATGAGCTG CAAGTGCAG TTCTGTTTTT GCAACGCCAG	720
CACCTCATCG GCGCGGTAC CGCTGCTCTT GCAGA	755

## (2) INFORMATION FOR SEQ ID NO:749:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1486RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

GATCCTTCCT	GTACATTTCT	GATTTTAACA	ATGTCCTCAT	AGCGTATATT	TTACCGGTAT	60
CTTTCTTCTG	CACCAGACGG	ACCTCACOGA	ATGCACCCCT	TCCTATGACT	TTAACAGTGT	120
GGAAATCTTC	CAGGGATAGC	CGTGTCTTAC	GCAAGGCGAG	AAACTGGGAC	TCCTTTTTCAC	180
CCAGTGAAGA	AAGCTGTCTG	TTCTTTCTCT	CTTCAGACCA	GCCATGAGAT	AATAGCTGGG	240
ATTCAGTTC	CACGGTCTTT	TGGTTGGGCT	CAATGGCATG	ATTGACAGAT	GATTGGTAGA	300
AATTCTCGAC	TTTCAGCTTC	ACTGCAGCG	CTTTTCTCTG	TGTGGATTTG	CTCAGTAGCT	360
CTGGAAGTCT	CTCGAAGTAC	ATATAGTTCC	CCACTCCCGA	GGTTTGCCGT	TGGCCCCCAT	420
TGGGCGATTG	TGGAAGTGAA	GAGCACTGCA	GGACTGACG	GGATAGCATA	GCGCCCTGGG	480
AGCTCTGGTT	TCCCACTAGC	GTCTGATCGC	CAAGGCTTCC	GTCTAGTAGT	CCAGGTAGAG	540
CTGCAGGCTG	TAAAGGGGAC	TCCGACCCCG	CAAAGTGTTC	ATACGCAGAG	GAAGCAGGCT	600
GCTGCCCACT	GTAGTCCGAG	CTGTTGGAGT	AGTGTCTCTG	TGAAGAATGG	CCGGGGGCAA	660
GAGTAGTGTG	GTTCAAGTTC	CGTAAAAGAG	TGTTGTCTCT	GGCTGTAAAT	GCTGGTGGCC	720
GTAGGGGGG						729

## (2) INFORMATION FOR SEQ ID NO:750:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1486UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

GATCAAAACA GCATGTCTAA GTCTGTTGCG CGCTGCCCCG AGTGCCACAC GGAAGTGGT 60  
 AAGTGCCCTCA TACAGCAGAA CTACAGCATC GTGATTTGCC CGAAGCAGCA GTGCATGTAT 120  
 CCGTTCAATG AGGCGGAGGT GATCCAGCAC CTGGTGCAGA CAAGTGACAA GGAAATCCTG 180  
 GAGGCTGCAA AGGTGCGGCT GAAAAACGAT AATATCACAG GCAGCGGAGG CCGGCTCATG 240  
 GAATAAGGAA CCAACCGTGT GCTATATACG TGTACTGTCT ATGTTAAGTA GGTCTCGTGC 300  
 GCGCGAGGCC CTGCGTGGCT AAAGCTTTAG ATTGGAGTTG TACATGATGT CGCCATCGAC 360  
 GCTGATGCTG ACACTGAACT CAAGGTCTTC GTGGTGGAT ATGTCCACG TTTTATATAT 420  
 CATCATCAAC GCGAACACAT TGCAAATGCT GCGATGAAC AACCGTGA GGTAGTGCTT 480  
 GACGCCCTCG CAGATCTGTT ACGAGATGGT ATACATCAAC ACCTGCCCAG TAGTTATAAA 540  
 AATGACACCC AAAATGGTGG ACCCTGTCAT CCAGAAGTTG GAGAGCAAGA AGATGGAGAC 600  
 CACGAGCTGG CACACCGAGT ACATTAGGAA CCGGAGGCCA TTGAGGCGGT ACATTACAAC 660  
 GAAAAGGCGG TCGTGTTTGT TTTTCATGTC GGGTGGTGCT GAATCCAATT TGGTGAAGG 719

## (2) INFORMATION FOR SEQ ID NO:751:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1487RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GATCGAGCGC GAGCCCATCA ACAACGAGGA GTTTGCTTAC CAGCAGGAGC TGATACGAAA	60
GCGGGACGAG GAGATAGCCA ACATCGAGCG TGGTATCGTT GAACTCAACG AGGTCTTCCA	120
AGACTTGGGG TCCATCGTGC AGCAGCAGAG CGAGCTGGTA GACCACATAG AAAACAACAT	180
ATACACTGCG GTAACGAGCA CGAACCATGC ATCTAACGAA CTGTGCGCGG CACTGAGATA	240
CCAGCGGGGT TCCAACAGGT GGTGCTTATA TCTGCTTCTC GCTCTGCTGG CATGCTCTTT	300
CCTGATCGGG GTGACAGTGC TTTAGAACAT CTCAACTAGT CTACTATGTA ACGCTTTAAT	360
ATACTACTGG CTGACCTACT CCTCCGCGAG TTCCACACAG TTCACGAGC CGTCATCGCC	420
GCCGGTCACC AAAAGAACGC GCGCGTCTAA CGCCAGCCAT TTCACCACAT TGATCTCGTA	480
GACCGTGTGC GCGCAATCTA CGCGGGCTAC CACTTCCAC CGGCCAGCCT GTACCTCTTT	540
GTATACCGCC AACACACCAT CCGAGCCAAC GCTCGCGATA AGCCCGTCCG CCTCCAACT	600
TACGCTGTAC ACAGCCCGCG TATGCACGCG CGGCAGGACC GTCTCTTGGA TCACTCTTT	660
GTCGAAGACG TCGGCGTGGT CAGTGAGGCA CGCCAGATG CGC	703

## (2) INFORMATION FOR SEQ ID NO:752:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1487UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

GATCCCAATA CTGGGACTTT ACTAATACCA GCCATGCGGG CAGCTCTGCA GCAGCTGGTA	60
ATGACAAGGA GGACAAGAAG AACAAATACT GGAACGCAGA CGOOGAGTAT CTGATCGAAG	120
AGGTGAAGAA AAACAAAAAG AGTGTAGTAA ACTACCTTGA ATCGAAGACG AACGACGAAA	180
TGACCCGCAA GGGTCTGATC CGGAACCTGC AACGATTTCG AAAGACAATT CTAATGAAGG	240
AAGGGTTCGA AAACCTGGAG GATATGCTCA CGCTTTCTCA TTTGGAAAAT AGACTGCTGG	300
TAGCCCTAAA ACTTAACGAG ACAAATGAAT TTACCAAATT ATTGAAAGTC TATTGCATCA	360
GCCTAGCAGA AATGGGCTTC AAAAATAGAT TGGATGATGT GCTGAGCTGG CTGTATAACG	420
ATGGAGAATA CAAGGTGGC ACAATAGCTA ACGAGAAGCG GGAGGAACTG CTGAAGCAGA	480
TATTGGTTGC ATGTGCTGAT ATCCGGCAGG TCCAAAGAGT GACAACCAAT TACGCATCTG	540
CTCTTGGTCT TCTTGATGTA TCTTTATAAT TATTGCTAGT CTATAGACAA AGTTGGGAAT	600
CTGAATATAA CT	612

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1488RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

GATCAACAAA TGATTTTTCCT ATTTTCCGCG CACCGATCAA CGAGATATCA TAGGAATCAA	60
TGTTGCAGGC AAATCCCTCA CCGAGTATGA AGCTCTGGTA TGCTGTGGC GTTGTTCCTT	120
TCATTAAC TG CCGTCCCTG GGCAGTCCC TTAAGTTTGG ATGATCGAGA TATCCACAAT	180
TGGCTCATT CATCGTCTCC AATCCAATGA TGCAGTTTTC TTGGAACAAC TCAGGCGGT	240
TGTCCTGAAT GTACTTGTAG AACGTCATTA CGCTTTTCAA GAAGTGCCCC TGGAGGTAGT	300
CTTGAATATT TCTACCAATTA ATTACACATT TAGGGGCAAA TAACTTGCCG CTAAAAAAGA	360
GAGTGAACAT AGTCTGGCAG GCTAGGCGGT AATAGTTTGT GGACCAAATC ATTTCTGGAT	420
ACTGTGCTTT TTCCGCCTGC GTCTCTGAAT CGATATAGTA GTTGTGCAAT ATGGCAGCCT	480
CAGTAGCTAG GAACCTCTTC GGCTGAAAGC CTGCGCAATG CAACTGCCAT AATGGCGCTC	540
CTGATCCCC AGAAAAGCGA GACCACAGT CCTGGTGGG GTCTAGGTAT ACGTACATGC	600
CGCCCGCTC CTGATCTTT TTAAGCACCA TCACCGTGTA CTTCAATGTAT TCCTCATGCT	660
ATATCCCTGG GCGCCATGC TCCAAGGCTT CCAGGTGAA CAAATAACGG ATACA	715

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1488UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

10	GATCTCGTTT AAGCTGCTGG TGAAGTTTGC GAAGGGTAT GAGCTTTCAC GACGCGAAAC	60
	AAACCAGCTG AAGCGGTCTA TGGGCGATGT CTTCCGGTTG GTGCCCTTTT CTGCCTTCT	120
15	GATTATTCOG TTTGCAGAGT TGTGCTGCC CTTCCGCTT AAGCTTTTCC CCAACATGCT	180
	GCCATCCACA TATGTTTCTG GGACGGAGAG ACAACAGAAG AGAGTTAAGC TAGAGGAGGT	240
20	GCGGCGCAAG ACGTCCAAC TTTTGCAGGA GACACTAGAG GAGTCTCAT TGATCAATTA	300
	TAACTCGGTA GAAGGTTTCA AGAAGCGCAA AAAGTTTCTG AGCTTCTTCC AGAAGGTGAA	360
25	CTCCCCAAG GATGGCAAGA CCACTGTTT TACCCATGAA GAGATTTTGT CCATCTCCAA	420
	AATGTTCAAG AACGACACTG TCCTAGACAA TCTCTCCAGG CCGCAATTGG TTGCCATGGC	480
30	GAAGTATATG TCCTTGCGGC CTTTGGGCAC TGACAACATG CTTAGGTACC AAATCCGTTA	540
	TAAATTGAAG AGCATCGTGG AAGACGATAA GAAGATAGAC TACGAAGGTG TTGAGTCACT	600
35	GAGTACAGAG GAGCTCTATA GTCCGCGGC TTCCGCGCGG ATCAAAGCCT TCGGTGTTTC	660
	TAGGGAAGAT TTGGTGGAAG AAAT	684

40

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1489RP



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

5	GATCACGCGG GAGCACGTGC AATCATTTGAA CGAAAGCCCG GGGTTGCTTG CTTTGGCGAT	60
	GGAGAGTCAC AGGGACCCAA TTACCGGTGA GAGTACATTG GTTGGTTTTT CCTACGTTGT	120
10	TCCGGGCGGT CGTTTAAATG AACTTTAAGG CTGGGACTCA TACCTAATGG CTTTGGGTCT	180
	TCTAGACTGT AACAAAGTGG ACATAGCACG TGGGATGGTT GAGCATTTCA TCTTTGAGAT	240
15	AGAGCATTAC GGTAAAATAT TGAACGCCAA TAGGAGCTAC TACCTCTGTC GGTACACAAC	300
	CCCGTTCTTA ACCGACATGG CTTTGAAGGT CTTGAAAAG TTGGGTGGTG ACCAAAATCC	360
20	TACCGCTGTG GATTCTTGA AAAGAGCATT CATGCGAGCC ATTAAGGAAT ACAAGAGTGT	420
	ATGGATGGCA GAACCGCGGT ACGACAAAAC CACGGGTCTT TCATGTTATC ATCCAGATGG	480
25	TATCGGTTTC CCACCAGAAA CCGAGCCTGA CCACTTTGAC GCAATTTGCC GGAAATTTGC	540
	GGAAAAGCAC AATGTAAAGA TTCCGGAGTT CAGGTGCATG TACGATGCGG GCGAAGTACA	600
30	CGAGCCCGAA CTAGATGAGT TCTTTTTCGA TGATGCTGCT GTAAGTGAGA GTGGACATGA	660
	CACCTCTTAC CGTCTAGAGA ACGTCTGTGC TTACTTAGCG ACGATTGATT TGAATCGTTA	720
35	CTATACAA	728

(2) INFORMATION FOR SEQ ID NO:756:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 698 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50	(vi) ORIGINAL SOURCE:
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(A) ORGANISM: PAG1489UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

5	GATCGTAACA TTGCCCCAATA GCTTGTTTAG CTGTCATCG TTCTGATGG CTAGCTGTAG	60
	ATGTCTTGGG ATGATTCTGG TCTTCTTGT GTCTCTGGG GCGTTACCG CCAACTCTAG	120
10	GATTTCGGCG GCCAAGTATT CTAGCACAGC GGTAGGTAC ACAGGCGCG CCGACCGAT	180
	TCTCTGTGG TAGTTCGCTT TTCTGAGCAA TCTGTGGACT CTACCGACAG GGAAAGTCAA	240
15	ACCGGCTTA GCGATCTCG ACTGCGAAGC CTTGGCGCA GAACGAGCTT TACCTCCTTT	300
	ACCAGACATT ATTGTGTGTG TGTTGTGTG TGTGTGTTA GTGTGAAC TGTTGTCTAT	360
20	GAGAAACAC TACGCTGAAA CTGCTAAATA ATCCAGACAG GTCCCCCAC CGCAAAGGAT	420
	CCAGCTATA CTCTCTCTA CATATTTATA CTTGTCTTT TGCTTCTAA TCCTCGATCG	480
25	TACCGGTCTG ACGCTTCAAC AGACCTTAC TAGAGCTCG ACCTGTGCG GCTGGTTTTT	540
	TGCGATGACA TGTCGGTCT GGTTTTTTCG CGCTGAAAAG GAAAGCGGT GGTCCACG	600
30	ACCAGAGCG TACTAGCTCT TTGCGTTC TGTCTATGT GCACGCGAAA TTTCATACTG	660
	TAGAGTGTGC CATCAGCTTC ACAGGTACA ACGGTAGG	698

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1490RP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

5	GATGACCTTC CGATACTATG CGAGGCTTC ACGACATCCA AACTGAAGTC GTTCGAGGAC	60
	CTGAGCCGCA TCCAAACGTA CCGGTTCGCG GGAGAGGCAC TTGCCAGCAT TTCTCACATT	120
10	GCGCGACTAC ATGTGGTGAC GAAAACGAAA GAGAATCAGT GTGCATGGAA GGCTGTCTAC	180
	GAGAATGGGG TAATGGTGGG GGAGCCGAAG CCGACGGCAG GCAAGGATGG GACGACAATC	240
15	CTCGTACAGG ACCTCTTCTA CAATGTGCGG TCCAGGCTGC GGGGCTGGG ATCTCCAAGC	300
	GAAGAGTTTG CGAAAATAGT GGATGTGGTC GGCAAGTAGG CAATCCATTC GGATGGTGTG	360
20	GGATTTCGTG GTAAGAAGTT TGGCGAAACA CAGTACGGT TAAATGTACG TGGGACTTCT	420
	TCAAATCAG ACAAGATACG GGCTGTATTT GGTGCTCCAG TCGTIGCCAA TTTAGTTGAG	480
25	GTAGATATTT CTGCAGACCC TGAGCACGGT CTTACATCCA GTTGGGGCCA GATTACAACT	540
	CCAGACTTTA ACAACAAGAA GTCTATACCT GCTGTGTTT TCATTAAATA CCGCCTTGTT	600
30	TCCTGTGATC CTCTGAGGCG AGCCTATCC CAAGTTTATC CAACTTCTTG CCGAAAGGTA	660
	ACAAACCGTT TATTTACATG AGTTTACACA TAACACCGGA GAATGTTGAT GTTAATGTGC	720
35	ATCCTAC	727

(2) INFORMATION FOR SEQ ID NO:758:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 728 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1490UP

55

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

5	GATCTCAAAG ACCCAGTACG ATCGCGTCAT GGGATACATA AACCACGGAA TCAATGAAAA	60
	GCTCGCTTAC GAACAGTTTG GATCTGTACC GGAGAAGGGC TACTATATTC CTCCCACAAT	120
10	ATTTCTGGAC GTTCTCAGA GCTCGAGACT CTGCGTGAA GAGATATTTC GCGCTGTGGC	180
	CGTAGTTGGG AAATTCAGG ACTACGATGA AGCTATTCTG TAGGCTAATG AACTAACTA	240
15	TGGGCTGGCA TCTGCGTTT TCACTGAAAA CATACCGGTT GCGCACGGCT TTGTCCGTGA	300
	TGTCCAATCT GGCCTGTGT GGGTTAATTC CTCATATGAT GAGGAGGTGG GAGTGCCTTT	360
20	TGGCGGGTTC AAGATGAGCG GTATCGAAG GGAGCTGGGG AAGGCAGGCC TGCAAACTTA	420
	CCTCCAGACT AAAGCAGTAC ACCTGAACCT TGCCTAGATA GAGCAACTCA TATATTAGAA	480
25	TCACTTCATA CATCAACTAT ATATCATTAT GTATATGACT ATGCCAGAGG TGTAGTGGAA	540
	CCACTATTTA TCACGTGATA GCGGTGCGC GGTATCCCG CCAGTACCTG CGTTGCAGAA	600
30	CGCGGGGAC ACATTCAGCA GGTGCTATAT ACAGTTGTTC AGGACAGTAT GGCACGAGT	660
	ACCATTATAG CAAGTAAGCC GTGTGCTGTT TGCATAAAGC GTAAGGTCAA GTGCGACCGG	720
35	CTGGTTCC	728

(2) INFORMATION FOR SEQ ID NO:759:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 716 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1491RP

55

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

5	GATCATCTCC GAATAGGTCT CGGCACGAC GGACACAAAG CGCGGTCCG AGTCACTGCC	60
	GTCTGTCTGG GCGGGTGGG AGAAGGAGAA GATGAACGAC CCCGACTTCG ACTGTGTGCTC	120
10	CGACGCCAGC TCCTGGACGA CCGTGTCCAC CTTGACCTGC ACCAGGTGC CAGGACACGA	180
	CAGAAAGTGG TCCTTATTCT CAGACAGCTT GTTCACAGCT GTAGGCTGGT AGTCCACCAG	240
15	CGCGTCCGCC GCGGGGTGG CCGGTCTGG TCACACCGG ATGTGCTCTG TGTACACGAC	300
	CGTGGCTCC ATGTGCAGGA TCGAGCCGAC CGGCACTGGC GCGCGAAGG TGGTGGAGTC	360
20	CAGCGATACG AACCGCGCA GAGAGTGGG GATCGATGAC GCGGCGAGT ACGCCAGCTC	420
	AAATGTCTGC CGCATCAGGT AACCGCGAA GATCATGTAC GAGTGTGGT TCGGTATTG	480
25	CGGCTGCATG AACATCGTCG ACTTCAGGTT CGTGTCTGTC ATGACACCA CGCGCGCGG	540
	ACGCAGCTCG CGCGCGTCG CGCGCGAGC GCGCACAAAC CCGTGATCA TCCGCGACTC	600
30	CTCCGCGTA GCGGGTTCG TCTCTAGACT CTGCTCTGC GCTGTAGCT TCTTCGCGT	660
	GTGTGGCTC TCCGCGGCC GGAATCCAC CCACTCTGC TGGTCTGCG GTAGCA	716

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 729 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: single   |
| 45 | (D) TOPOLOGY: linear       |

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- |    |                         |
|----|-------------------------|
| 50 | (A) ORGANISM: PAG1491UP |
|----|-------------------------|

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GATCTTGAAC AAAAAGTAGT TTGTTATTCT CCAGCTGCGC AGTCTCTTCC AGGGTTTTAC 60  
 5 TTCCGATGCT TATTAATACT GGTTCTTTAG ATGGTTCTTG ACTTTGGCTA TAGGCCATTG 120  
 GTTCCGGCGA CTTGTGAAGG TATGCATTGA GAGTCTCTTG GGTAGAACGT GTGGTCTCTC 180  
 10 CTGTAGTTTT AGCAGCGGGC TTGGCCGGGA CTGGTACATC AGGCTGAGGT AAAATCTCGG 240  
 CTGGCGTTGC AGGTTCATT TCTGTGGGTG GCTCTACACT AGGATCCAAT ACTTGGGGCG 300  
 15 TACTAGTATC GCATTGGTCA ATATCATCTA TGGCCAGGAT GACAGAACTT TCTTCTTCCA 360  
 TAGGCTGGGA GCATGCAGTA ATCTCGGAAC ATGTGGTAGT ATTATGTAGG TGATCGTCTT 420  
 20 CGAATGTCCC AATCAGCTCC TGGCTGGGAA CGAGTTTGGC CCTTTTGACC TTCAACTCGG 480  
 AGTCTTGATG TGGGACTGGC AGTGACGGTA AAGATTTAGG CAGCATGAGC TCCTGTTTGT 540  
 25 TAAATGCCC GTCCAGTTTC TCTGCTAAAC TTGGGAGGAC ATACTCTTCA TTGTGAAGCA 600  
 ATACAGTCTT CTTATCCGGA GTCACATTCA CGTCTACAAA CTGGGGGGAG AGCTCAAAT 660  
 30 TTAGAATAAT GACGGGATAC TGGACGTTGT TGAAGCTTCG ATATATGTCA TTGCAACACT 720  
 TCAGGACTT 729

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1492RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

EP 0 866 129 A2

GATCTACTTC TCCAACAACG ACCTCCTGTG GTCCAATGGC TACCCCGTGA ACOGCTTTGG 60  
 5 CCAGGGGCGG TTCCGCATGC TTATCGAGCG CCTGTACGGC GAGCTCAACG CCGCTACAG 120  
 CCTGGCCCAT ACCACCTACG GCAAGCCCAA CCGCATTTGC TACGACTATG CTGCCCCGGT 180  
 10 CCTGGGCGCC TGGTCGGGCC TCCAGACCGC ACAGCCGGCC GGCACGGTAT ACATGGTTGG 240  
 CGACAACCCC CACAGCGACA TAATAGGCGC ATACAACTAC GGCTGGGCGA GCTGCTTGGT 300  
 15 GCGTAGCGGC GTCTATCGCG ATGGAGACAC GTTACCATGC CAACCGAACC TCGTGTGGA 360  
 CTCGGTCTTG GAGCGGTAA CCGCGCTCT CCAGCACTCT TCACATTAC TTCTATACTT 420  
 20 TTACGTCTTC TATATACCGG GCTCGTCGGT CCGCAGATGC CTAGATCTGA ATCTTGGCA 480  
 CCACAGTTTG CTCTGAGCC AACTTGTCTG CGTTGGCGCG GGCATATGC TCCTTGACG 540  
 25 TCGGAGGCC GGGCAAGTA TGGTTTCCA TCAGCCGGTG GCGGAACAG AACTGGCCGT 600  
 CACAGAACTG 610

30 (2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 553 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: PAG1492UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

50 GATCATGTTG GTGGCCTCCT GCGTCGGCTG CCGGTGAAG TTGGGGTTTG ATTCCGGAC 60  
 GAGCGCTGC GTGAGCCGGT TGATCTGCC CACGTTGCC TCGAGCGCG AGGCTTGTG 120  
 55

EP 0 866 129 A2

CTCGTGGGCC GACACGTGCT CGTCTAGGGA GAGCTGCTTC GAATTGGAGT TATACTGGAG 180  
5 CATTTGGTGAT CTGCCTGTCC GCAAGAGTGG TGAAGACGT GTTCTTTGGC CTGTTCCGCTG 240  
AACAAAGCAC TCCGTGTTTT TCATGGACGG CGTGGTCCCA GGAGGCGAGA CCGGAGAAGC 300  
10 GAGCGTCAGG GCCGCGGGC AGGGACGTAG GCGGCTGCTC CCCACTATGT AATGCTGGAT 360  
ATGAAGAACA GAAATACTAG ATAATATATT TGTATTAGAC AGTCGTGGG ACCGGCAGAG 420  
15 GGCGGCGTTC ACAAGTCGC ATCGTCTCA TCCGCAACG GCAATGCCGT AGCGCGCTCC 480  
AGCTCTGCT GGTACTGCTG CATCAACTGC TGTCCCCCT GCACCTCTGG AGGCGCCTAG 540  
20 GCAGGCGAGC CAC 553

(2) INFORMATION FOR SEQ ID NO:763:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 719 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1493RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

45 GATCGAATAA AGTAGGTTTG GCGCTGACCG GCATCACCCG CGGACGTAGC GGGACAAAGT 60  
TCCCCGIGTA AATGTTTGCG TAGTCGATGA AGGTATTAGT ATTCACTTC TCCAGCAAAG 120  
50 ACAATTCATA CTGTTGGGCG GGCCGCGAAG AGTTACCACT GTATTCTGCC AACGCTGCGA 180  
CGCTTCGGCA ACTAGATTTC AGTGCCTTCT GGAGCTCTGA AACATTATCT AGGATGTTGA 240  
55 ACGGATCGAA AGCGGTGTG CGGGGCATAG CGGACATGGC AGTTCTCAGA TTCTGCATAG 300



AACCGGCATA TAGAGCCAGT GCCTCCTGAT GCTTGCCCTC CTCTTGGTAA AGGGGAGCGA 360  
 5 GCGCGCGGCC TACAAGCTGC GCACGGTAAA ACACCTTGAC AAGCTTCAGA TATGCAGTGA 420  
 GCTCATOGTC TGAGTAGACA CCGGTAGAC CCATAGCCTC CTCTGCATGG GTGATTATGT 480  
 10 TGTGATGAC GTGGTTCAGC TGCTTGTAAT TGTGAAGCG AGCGGTCTCT CGGCTTCTTT 540  
 GCCATTGAC CCACAGAGGT TGCAACAGCG CAACATGCGG GCCCATGTC GCGCACAAGT 600  
 15 AGTGAATTG GAGGTATGTG AGCAATATCT GGTGCTCTC TCCCTCATAG TGCAACCTT 660  
 CCTCTGTCT GCGCTCATT GACTGCTCT GGCATCAAT TGCCGGTTC CACTTCAGT 719

## (2) INFORMATION FOR SEQ ID NO:764:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1493UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GATCATACTT ATCCACCGGT CAAGCCAGGT CTCATCTTG ACGATGAGCC AGCCGGGGGG 60  
 45 CGTGGCCATC TGGAGCCAGC GCTCCCGGAA GCAATTAGG TACCCTAGAC CAAGCCCGAT 120  
 TAGGTGGCCG ACAAAGCTGG AGCCGGGCAT TAGCAGCGTG ACAAGTACCA GGAACACCAG 180  
 50 CGGGATATAT AGGGTCGGCA TCTTCAGACT TGGAGCTCG TAGTGGGGGC GGAAGCCCCC 240  
 CTCCTGCACT GCGAAGTAGC CACACAGCGT AAAGCAACCAC CCGCTGCCCC CGCCTACGTA 300  
 55 AACGTTTGGG TACAACAACA TGCCAACTAA GCAGTACAG ACGCCCGTCA CAATGGCCAG 360

GAGGTTGAGC GTGATTCCCG TAAACACCGT CCGTGTGAC GCTTGAACA TCGACAGCGG 420  
 5 CACAAACAGC GACATCAGAT TCAACAGCAA ATGGAAGATT GACAGGTGCG CCAGTGGATA 480  
 GAGGGAGAGC CGGTCAGCT GCAGCTTCTT AAGCGCCCCC GGATCCAACA GGATCTTCTC 540  
 10 GTTGATTGGG AACACCCAAT TCAGCACATA CACAAGCGTA AGGGAACACC GACAAGCCTG 600  
 CAGTAAGAGC GCGCGGCTTA TGGACCCCGG TCGTAACAT CGACTTCCAA TCCATCTTGC 660  
 15 TCAATCAAAG TGGCAGTTTG CTTGGGCGTG GCAGTGGACT ATGCTCGCC AGTTGCCCAT 720  
 CAAAAC 726

20 (2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 717 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1494RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

40 GATCTTCGTT CGTGAAAACC TTGCAAGTCT TCATGAGCTC AAGAATTGCC TCTGCATCTA 60  
 TTCTGTCCGG TTGGATTCTG CTTTCCTTAT AGTCTGAAT CATGCGCGCA AAAGCGCGCG 120  
 45 GCGTCAGTC ATGACGGGAT CGGCCCTTAT AGGACTTCCC TGCAAGCGCG ATGAGGCTCC 180  
 GCCAGCCATT TTCTTCAATA ATATTGACAA GTCTTTCGTT TTCCAACAG ACCTTGTTCG 240  
 50 CGAGACTGTG GAACGTGTTT ACGTCTATCT GCTCAAGTAT TTCTACCTT TCTCAGCAG 300  
 ACCATGCAA GTTGCAATCT GCCTCTTGA ATGCTCCAT AAGCTTTTCA TTGATGTTAT 360  
 55

CCACTGCTTT ATTTGTCAAG GAGAGGATTA GTATTCATT AGGAGCTACA ATCCCTTCGT 420  
 5 AAACCAGGTT GTAGACTTAA TGCACTAGTG TCAAGGTCTT GCCAGACCCA GGTCOCGCTA 480  
 CCACATTGAC AGTTGTACAA GGCTCATATG GATGTGTAC TACTCGTGAT TGGGACGTG 540  
 10 TCAGTCTTT CATTATGTA TGATACATG TCGAGCGTG GCGAAGGAAA TAAATTCGTG 600  
 AATTTCCGTT TTAAGATACT CAAAAGAGAT GAGATAACCG CCGCAAGGC GGAGTAGAAT 660  
 15 TACAGCAGCT ATTGAATATA TTTAGTTTAT TTATCTGGCT AGCTTAACCA CTAGTGT 717

## (2) INFORMATION FOR SEQ ID NO:766:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1494UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

GATCCTTTAG GCCATCCTCT CCAAATACCC CGTCTTGGC TTCAGTAGCT CAGTCGGAAG 60  
 AGCGTCAGTC TCATAATCTG AAGGTCGAGA GTTCGAACCT CCCTGGAGC AAGTTTTTTG 120  
 CTCCGGGAAA TAAGTATTTG GAGCTGGACT GAAGCGCCAA CCTATGCAGC TTTGCTGGTG 180  
 CGAAGTGTTT ATTCATGTCT GCGGACTATG TCTATATATC TTGCGGTCT TGTCTTCTG 240  
 CTGGCGAAGA GGAATTGGAT TCTTGGGCGT GGTCTGCAAG CTCTGCTAGC TTCTGGCGG 300  
 GCAGAACTT TTCAAACGCC TCTTTCAGT CATGGTTGTC AAAGTATCTG AGCATGATCT 360  
 55 GGATAACGTG GGTGGTGGTC AGCACCTTCC TGCCGCATAG CTGATGTAC TCTCCTATTG 420

GTAGGCGACG AGTAGGAATG CCCAGTTCTT TGGCCTTATT GTAACAGAGA GCTTTGTGGC 480  
 5 GGTTCCTTGT CACAATGCGG CCCACTATAT ACGTCGTACC GGGTTCACG GTCTCCAGCG 540  
 TCTCATCAGT ATCTGCAGTA AGGTAAACTG CGTTCGTAGT TGGAGGGGGG GATTGCTCTG 600  
 10 TGAAAT 606

## (2) INFORMATION FOR SEQ ID NO:767:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1495RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

35 GATCGAATTA GCGGGTTTTA ATGAACATA AGGAACGAGG TCTAAATGCG CAACATCCTT 60  
 GAATGCAGTG CCAAGATGTA TGCCGTCTCT GGTAAAGAAA ATTGTACCAT CGACATAGTT 120  
 40 AATGCCACAT CCGATCACGT CGTCTCGACC ATAGGGCTTC GAGTACGACT TGAACAAAGA 180  
 GCGTCATTT ATGTAACCGT CCGACCCGTT GTAAATGTAG ACATCCTTAC CAGTCTACT 240  
 45 CTGTTGOGAA GTTGGCCTGG AACCTCAAA AGGCCCTCTT AATATGTTGG AAGTTTGCCG 300  
 GTTCAAGGCA GAAAATTCAC CCGGTCCCT CGAAGGTGGA TCGCTAGTGT TTGCTTGCC 360  
 50 AGCATTGAC GCGACTTTTG ACCAGTCCTT AAATCCAATA TTGATATTGC AGGTTTGCC 420  
 TGACTGCGCG CTGGTCACCG ATAGTACCTT AATTCATAG TAAAAGATAG CCACTTCTCT 480  
 55 ATGATTAAATA CAAGCATTCG CCCAGGTGGA AGCCCACTGC TGCTTCTGGT TATTAACTGA 540

AGTCGGTAGC CTATTATTTA CAATAGGGCT GTGTGCATAG CCAGAGTAGA GCTGCCAGTT 600  
 5 GGGGTTAGGC CGCAAGTTTG TGAAACCGTC TGTGAGACC AAAACTGAGT TGTTCGACTG 660  
 TGTGGTCCAG AGGTGGGGCA AAAGGATACC TATCGAGGAG TATACGTCTG AGAAA 715

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1495UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GATCAGCCAA CAGCTGAGTT CTGATTGGAT GAGAGCTATT AGTAACTTT TTGTGTTTAC 60  
 GGTGCTGGTC CTGGGATCGT TACAGTACTA CTGTGGAGCG TACGGGCGGT GCGCCGCGCA 120  
 GATTGCAGTG ATAAGCCATT ATACGTGGCC TTGCACGTAC GCGCCGCGAG TACGGGATAA 180  
 ATTAGGGAAG GCCAGCGAGT GGTACGGGGC CAATGCGGCT CCGCATGTGT CCGTGGGAG 240  
 CCGGTGGATG CAAGGGAAG TGATGCCCA CCTGACGAAA GTATCCAGT GGACGGAGAA 300  
 GCATGTACAA CCGGGATGC GGCAGGCTGG CCGGAGCGG ATAGTAACAG CCGCGTGGC 360  
 ATGGAATGTC GTACAGCAGT ACCAGCGGG GCATGIGGTG CCTCTGACAG GGCGACTGCT 420  
 GGCGAAGTGT CCGTGTCTCG AGAGGTGGGC CGAACAAAGCT GCGCGCGGCT GGCAGTGGCT 480  
 CTGCAAGCAT GCTGGGCGC TACCACAGCA GTACAGCAGC AGTATCCTGC GTTTGTGGCG 540  
 CATATGGGGG GCATATGGGA GCGTTTGAC GCGCGCTACA ACGGATCTA TCTGGACTTG 600

GGCGGCCAG TGCAGGAGAA GACGTCCGAG GACSCAGTGC GGCGCCCGGG GGGACTCAKT 660

5 ACATCACATC CACTATCACA ATGACCATGA CTGGCTCGAT GAACTC 706

(2) INFORMATION FOR SEQ ID NO:769:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 749 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1496RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

30 GATCGTTTTC TGTCAAACCG CAGTCGGGTT CAAGGAGTAC GTTGAATTTA GCTCTTCAT 60

TCAACAAGTC TTCCCAAGTT TCACAATGT TGTGATAAT GAAGGGTTTA AAGTCTAGAA 120

35 GCTCTTCTTG CGTGAAGCCG TTCTGGTGAA GAATCTTCAG TTGTTCAGT ACGTTCGATT 180

TCCCGCTCTC GCCAGAACC AACACAAAA CCTTGAGCCG GCGATTGCTG GCACTCGGTT 240

40 GCGCCATTGA CCTGGTCCA GCACTGCCG TTGTCTGCTG ACTGTCGCC GATACCACCG 300

AGCGTTTCCT GCGGCCGCT GTAGCGCCG ACGTCTATG ACTGGGTGAC GTCTCAGGTT 360

45 TGACTTCTGC ACCGTAATCT ACCCTCTTTG CTCTGTTC TACCTTCTGA GAAGCACCAT 420

GTCGTCTTG ACGCGCTTT TCCGGGTG TGCTGATCC CTGTCTTC GACGGCACA 480

50 ACGCCATTAT GTGGGCTCT ATATCCACCA GTACTTGAG CACTCTAGG CCTGGCTTTC 540

TTTGAAATAT TACCGTCCG GCAAAAGCCA CTATAGCC CTGATCAATG GATTCCACTG 600

55 CTAGAGGCTA ATTAGGCTGC CGCTGTAC TCGGGGCC ATCATTAT ATCATAGCA 660

AAGTAGGTGC CAACAGAAAA AATCAGCCCG CCTCCTTTAT TGATCAGTG AAGAAATCCA 720

CATGAACAAT CACGTGAACA CACATTGG 749

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1496UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GATOGAAGTC AATGCCAGAC TATCTCGTTC TTCTGCATTG GGTCCAAGG CAACAGGATA 60

CCCCCTGCC TATACTGCCG CTAAGATTGC TCTTGGGTAT ACATTACCAG AGTTGCGCTAA 120

TCCTGTTACC AAGTCGACGG TCGCCAACCTT TGAACCCCTCA CTGGACTACA TTGTGGGOCOA 180

GGTCCAAGA TGGGATCTCT CCAAATTTCA ACACTGGAT AAGACTATTG GGTCTGCCAT 240

GAAGTCGTA GGTGAAGTGA TGGCGATCG CCGAATTTT GAGGAAGCTT TCCAAAAGGC 300

TTTCGGTCAG GTTGATCCAT CTCTACTAGG TTTCAGGGC TCTGACGAAT TCGCAGACCT 360

AGATGAAGCC TTGCAATTTT CTACAGATAG AAGGTGGTTG GCTGTGGGAG AAGCGCTAAT 420

GAACAGAGGT TACTCTGTGG AACGTGTACA CGAGCTTACG AAAATTGATA GATTTTTCCT 480

GCACAAGTGT ATGAATATTG TCCGAATGCA GAAGCAATTA GAGACCCCTAG GATCAATAAA 540

TCGGCTAGAC GAGGTCTGTG TCGGAAGGC TAAAAGCTC GGCTTCTGTG ACAAGCAGAT 600

TGCACGGGCT ATTTTCAGATG ACCTCTCTGA ATTGGATATT AGAGGCTCA GAAAAGCTT 660

TGGCATTITG CCATTITGTA AACGATOGA CACCATGGCG GCAGAAGTTC CTGCGGTAAC 720

5 CAACTACTTG TATGTTACCT ATAATGCGGT CAAA 754

(2) INFORMATION FOR SEQ ID NO:771:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 740 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1497RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

30 GATCATTITG TCTTCTTGGC CTCTACAAAC TGTGAATATC ATACTAGACC TGAAGTCAGG 60  
 TAGGGAGCAA CCCAACCCCTT CGGTGCGAGT AGAGGCTGSC AAATCCATTA AAAAGACCGA 120  
 35 TTGGAATGGG AACTCTAAAA TTGAACTAA GCAATTTCAT GAACTCTCGA CAGTTCTCTG 180  
 TCTTTCCAGT ATTGACTATT ATAACCTTAA GAGAAGGTAT CGAACTTACA AATCTCTGAA 240  
 40 AAGGGCGACT ATTGAAGATA TATTACATGT TGTGTGCGAC AGAGATCTGG CGGAGCGCAT 300  
 TGTTACTCAT ATCCAAAGAG AATCTGAGCT GCAACAATAT GAGGAGGATG GGAGGAATGA 360  
 45 GGTATGAAAT GTTCCCCATT TGGATTAAAG TATCAGGTGG TCACGATATC CACTATATGG 420  
 TGCTATTAAAC GGCATGCAAA GTGTAGAATT AACCTAAAGA ATATGTTATA TATATATATT 480  
 50 ATAACTACA AACTAACGGA CGCAATGAAA TCTAAGTGTG GCAAGGTTAG CCTTAATACC 540  
 GGTACTTGGA TAAAATCTCC TTTTTCAAAT GATACAAGCG TCCCATTTCA AACGCCATGC 600  
 55 CAGAATCACT GGCTGGATTG ATCATGATTG TGATTGCGGT TGCCCTCAGTC GGAAATAAAT 660



TAGCAATACT CATTATACCC TTGCGGACCT CCAGCCGCTT CTCTTGGGTA GGTTCAAATG 720

AGGCAATTG CATACTCTTT 740

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1497UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GATCCTGTCA CAGCGGGCGA CGCCGAGGC CGGTACGGC GACCTGCAGG ACGAGGTGAA 60

GGTAGGAGGG TCCGAGGGG CTTTGGCGA TCGGCGTTG TTGGGGCGA TGGGCGGGG 120

CGCGCCGAG GATGGCGAG AGGGCCACA ACTTGGTGCC GGGGTGGGC CCATGGTGAC 180

GCCGCACTT CGATGGAAC CCTGCGAGC GCACGCGTG CCACAGCAGG CCCCCACTCC 240

GCACCAGCA CAGCAGCCG CCGAGAAGG AATGCACATG CTCCAACAGC TCACGAAGA 300

GCAGAAGAAC TATTCTTACG TGGACCGCA ACCGTCAATT ATGCAACAGC AGCCACACAT 360

GATGCAGCAA CTGCGCAAC AACGGCTCG GATGCAGCAA CTGCGTTGC AGGGCCAGTC 420

CGAGACGCG AAGCCGCGAG GCAGTCTCC AATGGTGGTG CCGTCAACC ATAGGCAGCT 480

GTTCAGAAC CTCGACCCA GCATCCAGAA AAGAGTATCA CAGGATCTGA ACAGCAAGCA 540

GTATGAACTA TTTGTGAAGT CTTTCATGGA ACATTGTAAG CCGTGAATA TTCCGTTTAA 600

CCCAACCTG AGATAGGCG GACGCGGTG AACTTATTCA TTTTATACAT GTTGTACAA 660

AGAATGGGCG GGGCAGATAA TATCAGAGG CTGCAGCAAT GGCGGGCCTT GGCAGAAAAA 720

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1498RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

GATCACTACG TGACATTGG TACGGAATGG CACTOCAATG CCGACAAACC TCTTCTTACC	60
CCGTGACTTA CCCCAGTGTG CCAACTACCA CACATCTGG CCATAGCCCC AGCCATCTGG	120
CACCAAATGT ACTCGATATC GTTATTACAT GTCTACGGCC TCAAGTGCAT CCACCATCTG	180
ATATCATGTC TGCTCTAGGC TATATATTTT GGTTGGGGCC ATATCTACCA GAAAGCACCG	240
TTTCCCGTCC GATCAACTGT AGTTAAGCTG GTAAGAGCCT GACCGAGTAG TGTAGTGGGT	300
GACCATACGC GAAACTCAGG TGCTGCAATC TTTTTTTTTT CCTCTCTCTG CAAGCTGGCC	360
GCCAACACAG GTCACCTAG TATGGCTCAC ATGCAATICA GATATCTACT TCTGACTGGT	420
CTGGTGGGCG ATGGCCATCA TTGCAAACAG TGTGCTGCCA TGGGACTTTA ACGACCTCGC	480
GATAATAATC AGAGATCGTC TACTTATAAA ACATCAGGCA CAAAAAGAAA GGTGCAGCGA	540
AATGGTATAT ATAGGTCTC CAGATCCACC CACCGTACC TCCTACTTGG CGTATCTGC	600
GTCTCCGTGG CGCTTGCCGC TGAGATGCTG TGGGCCCCGAA ATGTACTCTC AAATGGGCTT	660

GTTTCAGTGGC CCATACAGCT CATTAAAGCTC AGTGGCCCCG ATGCTTAGTA GTA

713

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1498UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

GATCTCTTGG TTCTGGCATC GATGAAGAAC GCAGCGAATT GCGATAAGTA TTGTGAATTG	60
CAGATTTTTCG TGAATCATCG AATCTTTGAA CGCACATTGC GTCTCTGGT ATTCCAGGGG	120
GCATGCGTGT TTGAGCGTCA TTCTCTTCTC AAACCCCTGG GTTTGGTAAT GAGTGATACT	180
CGTGTGTAAG ACAAGGTTAA CTGAAAATG CTGGCCATGG GCGGAACCTG CGCGACTGC	240
GGTCTGAGCT AGTTTCTACA CTGCGTATTA GGTTTGACC AGATGTGGA GTGGAGCTGG	300
CGCTTGAAGA ACGTACGACA AACAAAGGCT TCCAGGCGAA TAGTATTCC AAAGTTTGAC	360
CTCAAATCAG GTAGGATTAC CCGCTGAAC TAAGCATATC AATAAGCGGA GGAAAAGAAA	420
CCAACCGGGA TTGCCTTAGT AACGGCGAGT GAAGCGGCAA AAGCTCAAAT TTGAAATCTG	480
GCGCCTTGG CGTCCGAGTT GTAATTTGAA GAAAGTACCT TGGTTGCTAG TCCCTGTCTA	540
TGTTCTTGG AACAGGAGT CATAGAGGT GAGAATCCG TCTGGCGGG GTCTAGTGC	600
CATCTAAGGT TCTTTGACG AGTGGAGTTG TTTGGGAATG CAGCTCTAAG TGGGTGGTAA	660
ATTCCATCTA AAGCTAAATA TTGGCGAGAG ACGGATAGC	699

## (2) INFORMATION FOR SEQ ID NO:775:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1499RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GATCAGCTTC ATGGAATTACC CAGAATTCCG CTTCAACAGC AACGAGGCCA CCGAGATGCC 60  
 CTTCCGCTAC GTAAGTGGAG CTGCTGGCAG GCCATTCTG CCATCAGGCA TGCTAGAGCT 120  
 CATCAAAAAG GACTCCGAAC AGAGTCTGGA TGAOCTACTT TAGGCTCGTT GAACAACAGC 180  
 TTATAGATGA TGTATATATG CCGTCTGTCC GCCAGAGACT GGCATCGGAA GCCACGCAAC 240  
 CTAAAGTCGA TAGAACTCTG TCAACAGAAT CAGTTCTTTT CCTCCTTCAG CATCTGCCA 300  
 AGCAGCTGCT CGAAATCGAT ATCATCAGAA GTGGTTTTTG CAGGAGCAGC TACGGGGGGC 360  
 TGCTGGGACG CACGTCTCTT AGCCTTGTAC AATGACACAC CCCCAGACAG CGTGAATAGC 420  
 GTGCCAAGCA CCAAAACATG AGGCTGAACC GCTTTTCCAA AGATGTTGTA AGCTTGACCC 480  
 ATCGCTAATC ACCGAATCCG CTGCAGATAT GGGTCTGAT GGTCTGGTGT GTAGCGGTGT 540  
 GCATTGTGTA GCTCCTATTG GCGGAGGAGG CAAGTCGATC TAGAGGGCTA CAATGAGGTG 600  
 TTGGGGTGTG TGTACGGGTA CCGAGGAGGT AGCAGGTGAT CGTTCAAATA TCTGTACCGC 660  
 CCCATGAACA TCTATTGGGT GCATTGGGTT TCGAGCACGG GCGATCATTG GAGACTAACA 720  
 CTCACGAATT TTGCTGGCG GA 742

## (2) INFORMATION FOR SEQ ID NO:776:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1499UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GATCGCAATG GAGAAGGTAA CGCTGCTACC GAAGGTTATC AGTGTTTTGA ATAAGGOGAA	60
CCTTGCAGAC ACAATTTTGG ACAATAATTT GCTACAGAGT GTGCGGATCT GCCTTGAGCC	120
ACTGCGGGAT GGATCCCTAC CATCCTTGA GATACAGAAG TCTCTCTTTG CCGCGATTGA	180
GAACCTCCCC ATAAAAACAG AGCAOCTCAA GGAGAGCGGA CTGGGGAAGG TGGTCATATT	240
TTACACCAAG TCTAAGCGTG TAGAACACAA GCTGGCCCCG CTAGCTGACC GCCTGGTTGC	300
AGAATGGACG CGCCCTATTG TOGGGCTTC CGATAACTAC CGGGACAAGC GTGTCTGAA	360
GATGGACTTC GACGTGGAGA AGCACCGTAA GAAAGCGGCA CTTGATTCTG CCAAATCTAA	420
GAAACGGAGA AAGGCTGCAG TGGACGAGGA GAAACACAAG TCACTCTACG AGCTTGCCGC	480
TGCGAAGCGG AACAGAGCCG CAGCGCCTGC GCAGACAACC ACCGATTACA AATACGCACC	540
AGTCAGCAAT ATCTCGAAGC TACAGACCGG GATCGGCACG GCAGGCGTGG GCTCCAAGCT	600
CAACAACAAC GATCTGTACA AGAGACTCAA CTGAGACTT GCCAAGTCTA AACGGTCCAA	660
GTAACCGCTG TGTACTTCAG CTAATAGTAT TATAATAACG TTTAATGATA CTGAAA	716

## (2) INFORMATION FOR SEQ ID NO:777:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1500RP

## (&gt;i) SEQUENCE DESCRIPTION: SEQ ID NO:777:

GATCAGCTAA TGGCTGCTTG TCAAAGACCA AATCCTTCAC CCTAGAACT TTTCCTAGAG 60  
 CATCCATTCG GATAACCTAG GTGCTTTGT GTCTTAAAG AATATTGGTT TAATTGCTTT 120  
 TCGCGGACGG AGTAAAGCGT TATGTAGCAT TTTTCAAAG AGGCTTAATG GACACATCCC 180  
 AGGATAGTAT GAATGAGAA GTCCAATTGG TGGCAACATT GTCTAGTTC TTATATTTAC 240  
 TGTATACAT CTAATGCAGA GTCAAGCATA TATACCAAAT AATTCACAA ATACTAGCTC 300  
 TTCTAAGTCT TCAGCTGATG GATTGCGGC AAGGCGCGC AGAGCTGCAG GTAGGTACCC 360  
 ACACCTTCCA AAATCCTCAT GTGGGGAAT CCTATTCTT TAATCATCTC CAGCCGAGG 420  
 GGTCTTTTAA TCTCTGTCAA GTTCTTCATG ACACGGAAAC ATGTAGTAT TATGTCCACC 480  
 GCGAGTACC TTGCCCCAC AATGCGGTA AGTAATTGAG CGACTCATCA AGAGTAGCAG 540  
 ATAGCAGCAT TTTCTTGATG ACCAGGGGAT GCGGCGAGTC CACTATCTTA AAAACGTTGT 600  
 CGCGTTTAC TAACGTGAAG CCGGCCACGG TGCTCTGCAG ATTGTTGATG GCTTGGCGCA 660  
 TGTACCTTC CGCAGTGAAT ATCAGGGCT CCAGACCATC ATTGGTGTTC TGTACGTTT 719

## (2) INFORMATION FOR SEQ ID NO:778:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1500UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GATCGCGACC CCGCGGTCA CGGCAAGGCC CGCCAACCGC GAGGAGGAGA TCAATGGCTT	60
TGACCTCGAG GCGCGCCCC AAAAGAAGAC CAAATACTA TAGTAGTACG TACATTGTAA	120
TACATGCGCA AGACTTGGCG CCAGTTAGCC GCGCGCTCC CAGGTCTTCA CCAGCGCGGT	180
GCGTCCGCA GAAGTGCTCA GCAGCTGGCG GCTACCTCC TTGTAGACGG TGTCAATGAC	240
TGCGCCGCA TGCAGAGACG CCAGCTGGTC GGACACCACT ACCTGGCTGG TCAAGTCCAC	300
TACGTAGCCG TAGCGCGCAA CATAGCGTTT GTCTCTACG AAAGCGACC GTGCCAGGAG	360
GCGTCCGTG TTCCGCGCAG GGAGGGCAA TCCCGGCTT AGACGCTGTC CGGCTGCTG	420
GCGTAAAAG CTCACACTGT CATCGAAGCC CAGCGCACAC ACCTCTCTC CATGCGCGGA	480
AGTGACACAGC GAGGTCACAC CACTCCGGTG GCGGTCTGC GTCTTCACA CTGGTCTCTC	540
GCTGCGCGC TGCTGTAGG CTGTACCAC TGGCTCAATC CCGAGGTGT ATACCGCGCC	600
GGCGAGACC GGCAGACGG CGGTGATAG CAGCGGAAAG TCGGTGGCCA CAAAAGCGGC	660
CGGG	664

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1501RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GATCTATTTA AATATAACAT ATTATTTTATT TCTTTTTTTA AACATTTTAA ATTAAATTAA	60
TTATTTATTT ATTTAATTAA TTATTTTAT TAGTTAAGAT AATTTTATAA CTTTAATTAG	120
AGAGCTAAGG TACACACCCC TAATGCTTTC AGCATTTCTG TGGTACCACT CTAATTAAAG	180
AGTTATTATA TTAATGATAT AATATGTAGA TATTCAGTTT TGAAGTGAAG ATATATGTCC	240
CTAAACATA TGTTTTACCA ATTAACTAT ATCCACTAAC TTTTATTATA TAATTTAATA	300
ATTAAGAATA TTTTAAGATT GAATTAGAGG AGTATTAAAT GAATGAATAA GAGGTGGTGA	360
ATTTAATATA AACTCAATAG ATGATGATTT AGTAGTATTC ATTAAGAAAA TATTATTTGA	420
TTCAATAAAA TCAGGTAGTT TTATATAATT AATAGATTTA TTATTAACTT TATTAGTTAA	480
ACCATTTATT AATTGATCAT AAATAATATA AAGGAATAAC ATTAATGATA TAATAGTTAT	540
TATAGAACCA AATGAAGATA CTAAATTTCA ACCTAGGAAT AGATCAGGAT AATCAGGAAT	600
TCTTCTTGGT ATACCAATTAA TACCTAAGAA ATGCATAGGG AAGAAAATAA TATTAAGACC	660
TAAGAAAATT AATCAGAATT GAATGTGAT AATTTT	696

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1501UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

GATCAAATAA AAATAGAAAT TAGCTTAATG GTAGAGCATT CGTTTTACAC ACGAATAATT	60
TGAGTTCGAT TCTCAAATTT CTAAATAATA ATTAACAATA ATTTAAATTT GGGTAAAAAT	120
TAATAAATAT TAACGTATAT AATAATTATA TACTTTATAA AATTACTCAA TGTTATTAAAT	180
AAATTTATTT CTATCATTATA ATAATGATGT ACCTACTCCA TATAATATAT ATTTTCAAGA	240
TTCACTACTA CCTCATCAAG AAGGTATTTT AGAATTACAT GATAATATTA TATTCTATAT	300
GTTACTTGTT TTAGGTTTAG TTTCTTGAAT AATAATTATT ATTATTAAAG ATTATAAAAA	360
TAATCCTATT CTTTATAAAT ATATTAAACA TGGTCAAATA ATTGAAATTA TTTGAACTAT	420
TTTACCAGCT ATTATTTTAT TAATAATTGC ATTTCCATCA TTTATTTTAT TATATTTATG	480
TGATGAAGTT ATTTACCAG CTATAACTAT TAAAGTTATT GGTTFACAAAT GATATTGAAA	540
ATATGAATAC TCAGATTTTA TTAATGATAA TGGTGAACT ATTGAATATG AATCTTATAT	600
AATTCCTGAA GAATTATTAG AAGAAGGTCA ATTAAGAATG TTAGATACTG ATACTAGTAT	660
TGTTATTCGG GTTGATACIC ATGTAAGATT TATTGTTACA GCTCTAGATG TTATTCATGA	720
TT	722

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1502RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GATCGCTCC AACCCCTGCT TGATCTCCAT ACTCATCTGG TTTTTCAGGT AGCGCGGGTG	60
GTTGAATACG GACTTGTGCA AAACGAACAC ATAAGAGAAT GACGCCACGA TCAGGTACAG	120
CAGCCAGCCA AACACTGTCTG TCACCAAAAA CAGAGACAAG CTCTGCCCGA ACAGGCTGTA	180
TGCGGCGAGC ACGGACCGA AAGCATGCGG GCTAACCTCG AACATAAAG GTGCATACCC	240
ATATACCTCC AGCGGCTCTT CAAGCGACCT CCCGAACAG CGGCTGGCAT TTACCATCTG	300
CTCCTTAATC ATCGCCTGCT GCCAAGTCCC GCCCATCTTC GCGACAGCG ATGCTGGCAG	360
CAGTGTGGCA TACACATAGT CGAAGAAGTA CGAGTGGCAA AACTCGAGCA CTAAATCCAT	420
GGTCGGAGAA CGCTATAGAC TAGGAGAAAC AATTITAGCT CTAGGTGCC TGCCITCTAG	480
CGTGATAACA GATCTGCTA CAGCTACTAA AGCCCATCTG CCGCTCTCCT CTGGCTTTTT	540
GCACITTTAT ATGGTCCATC CCGGCACTGA CCTAACGTAC GCGCTCTAT ACGACGCTAA	600
AAAATCAAGT TACGAATGCA CTATACGAAT GCGTTGAGCA AGGAACGAAT CCTTTTGG	660
ACGACGATAT CAGTGAACG AAGCCGCAAC GTTGGGGTGC CCGGGGCTTA	710

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1502UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

10	GATCAAAAAT ATTGACGCA TTGCGGCTC TTTAGTGTAC TTCGGTCAT TATGGAGATG	60
	GCCAATTTAC ATCGGTATTT TOGCTTACT CATAAGAGTA TACAGTGCCA ATTTCCGTGA	120
15	ATTGAGGCT ATAAACATCT GGTATGTCTT ATCTTCAGTT CTCTCTGGG ATTGCCCCAT	180
	CACTGGGATT CCATTCAGTT TCAGGCTGCC AGGAGTTGGA ACTAAAACGT GGTTTTTGA	240
20	TCCTCTGAGA TCTCTGTTC CATCAAGGC AAGATAGGCA GCGTGCTTT TGTATGAATA	300
	TGCGGTGAG GATGTCTCAC TCAGGTGG AAACCTATAT TATGGTGCA TATATATTAA	360
25	TGATAAGAC TTCTCTGAC TAACAGCAGT AACTCTTAAT TGAAGTATTT GTTATTTCA	420
	ATCTTCATAC AGTATGTAC CCGTGTGTAT TATAGATTTC GTTACGAAT TGATGTGTC	480
30	TTTCGTGGCT GCGAGGTCAG AAGATGATA TAATAATATA TATATTATTA AATTATGGTA	540
	GGTAGGGAAT TGCTATTTGT GTCTAGTACT CGATGCTTA TCTACAACCT CTAGTTGCAA	600
35	CACATGATAT GCTGTGGACC AAAACGCTAC GCGTTATTG ATTTTATCA AGGTCAAGAT	660
	CATATATTAG CGTAATATCT GTGGAGGTC CT	692

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1503RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

5  
 10  
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 30  
 35

GATCTTGGTA TACATGTGCG AAAGCTCTC CAAAATCTTT TGGTCTCCAT CATGAGAGGC	60
TGCTACAGCT TTTGAGCOGA TAGAATTGGA AATACCATG GAGATTGCTA TTAGTAGGAA	120
GACAATATAA GTACCATCTG TCGATGGGGC AGAGGCTTTA TCAAGAAGGT CCATCAGCTT	180
GTTCTTGGAT ACAGCAGTCT CATTTAATAA TAATGCCTGC TCACCACTGG GCAAAAATTC	240
AGAAACATTG AGCAGTTCAG AGAGTGAAGT CCACTCAAAG TTTTGGTCA TTGTCTCTAA	300
CAAGACAAAA ACAACGTCTT TCTGTCTCTC ATGAACATCA TAAGCCTTGA AAACCTGAG	360
CAAAATAGTA TTGTCTCTGA TCAAGTTCAA AAATACCTCT AGAATTAATG CCTTCTCTCA	420
CAATAAAGTG TCAGATTTAG GAGACAGAGT GTGGATTAAAT AATGATAAAA TAACTTCCAA	480
TTCCAATTCC AGCAATGTCA AATACTGAAC CTTTATGAGA AGTGTAAATAC ATCTGGCGCT	540
ACGAACCACA ATTGCAAAAT TTTTGGATGA GGAAATGTAC CTCAATAGCA GGGGCACCGC	600
CTTTGTTCGC AACAGAAATA ACAGATCTCG GTGTGTCAA AATAATAATT CATAGTTCAA	660
TAAAACCACT TCTAGGAGCT CTAATCCATA CTCTCAATTT ATGCAATTGC TATCCA	716

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1503UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

5	GATCTGCGCG CTTCGAAGGG AAAGGCGGGC CCCAATCCCC AGTCTATGTT CAAGAGGGCG	60
	AACAGCAGGC CGTCATGGCA TTCAATAAGC GAATGGGCAC TCGAGCGTGG GCACATCATG	120
10	TGCTGGATAG CATCATATAC TACACAGACA AGGTGGTGGT GAAGGGGCTT GGAAATTTGT	180
	CCGGAGCTT ACCTTCCAAG ACCTCCTCGG CGACAAGCGT CAGGGGTGGT GTAAGGAAAC	240
15	GCATTGGTCT CGAAGGCGCA AATGATGTCT TTGTATACCG CACAAAAGAC CTGGTATTGG	300
	ATAGTGATGA AGATATACCC AGAACCTAAC TACTTGTGTC GATATTTCTC ACACCGGCTG	360
20	GTGCGGAACC GGGGGCATAC ATTGGTTTTA CACAAGAGGG GTTGATGCAT AAAACGGGCT	420
	TTCAAAAGTG GCAAGCGAGA GCTGCGGACT GTGGTGGCTT TTGGTGGCGC GACTGTAGGC	480
25	AATGTGGCAT CCGTGGGCGC TTCTTTTACG CGAGATCCAG TCTGGCAAGC CTGGCTGTAA	540
	CCAGAACACT CGGCTGAAGC CCGGACAGG TCCCTGGTGG ACCAGGCAGG CAGCCTTGCA	600
30	TCTGATAGGC CGGATACTGG GTATCTGCCA AGAGAGG	637

(2) INFORMATION FOR SEQ ID NO:785:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 708 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1504RP

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

55	GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
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CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT 120

5 ATTGAGITTA TATTAAATTC ACCACCTCTT ATTCAATCAT TTAATACTCC TCTAATTCAA 180

TCCTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG 240

10 GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATWAT 300

ATCATTAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360

15 GGIGGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACTAAT AAAAATAATT 420

AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480

20 GTGATATTTA AATAGATCAA AATTTCACAA ATTTCATTT CATTTAGTAC TACCATCACC 540

ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTACTAT 600

25 ACATGGTATT ATTGGTAATA TTTATCCCTT ATTATTATCT TTATTAGTAG TTTTATTACK 660

AATAACTTTA TGATTAGAG ATATTGTAGC TGAACCTACT TATTTAGG 708

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1504UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GATCTTAATT TAAAATTTTA ATTAACCTATT TATAATTTAG AAATATATAA TCTAGAGATA 60

55 TATAATCTTA AAATCATAGG TAAAATACA TAAGATAGTA AGAATGAAAA TTAGTAAAAT 120

	AAATAGAAAA CCATAAGTTA ATTGATTCAT AAAGAAAAAT GGAATTATTT GTGGCATCTT	180
5	AATTTTATTT ATTTAATTGA TTATTATCTA TTAAACATAA AACATTTTAA AATGTTATAA	240
	AATAAATAAG AAATTACTTA TAGAATATTT ATTAAATAGT ATTTAATTTA ATTTTAATAT	300
10	TAAATATACC ATTTTATTTA ATAAATAGAT TATTAGTTT ATTAATATTA AGTGATATAT	360
	AATTTAATTT ATATAAATTA TTTAATTTAC TTCATTGATA TATATAATTA TTAAATGTAC	420
15	CTTCATAAT ATTTATTTT ATTAGTCTAG TAATATTTCT ATTTAATAGT CTACCTTTTA	480
	ATTGGATATT ACTACCTACT AAATATTTAC CTAATAATAT ATTATTAAGA ATACTTAAAT	540
20	CTAATAATTT ATTATCTAAA GTATATAAAT TAATTAAATC TTTTATTTTA TTATTTAAAT	600
	TATTATTAAAT TAGTAAATTA TATTTATTTA TTTTAATTTA CATAATTTT GATAATAATA	660
25	TACATTATTA AATGGTAATT TATTAATAAT TATCTTTAAT GATTTAATGA T	711

(2) INFORMATION FOR SEQ ID NO:787:

30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1505RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:	
50	GATCATCTTT ATACCATTTG CTCCTGTTCC GTGTGCACCA ACGTAATCAA AAGCGTGTGC	60
	CCCTCGCTA CGCAGGAAGC ACTAGAACTA GCTGAGTAAA GCAACGGTGA AAGTCGATCC	120
55	CTGATATATA TACGAAACCA GAGATACCTT CATCACAAGG ATCTTGTTCC TCGTGGCCCA	180

ATGGTCACGG CGTCTGGCTA CGATAGTAGT TACTTCTGAA ACCAGAAGAT TOCAGGTTG 240  
 5 AGTCCTGGCG GGGAGTCCT TATTTTTTTT GTTCCCTCTT GTTTCAGCTT TTTGICTTAA 300  
 AAGGAGCAGA AAGATTATTT TGCAGCTCTC TTTTGGCGCC AGCTGGCAAA AGCGAACTGT 360  
 10 TGATTGACAA GCTTTTAACC TGTTATTAAC CACCAGCAAC CTCTOGAATT TATCATGTCT 420  
 CCATCAAATA AGGATATTGC TGCCCTAATT GTTGACTTCC TAACTACGTC CGCCAAAAC 480  
 15 GTAGGAGAGG ATTACGAAGA TTCCCTCAAA GTGGCAATTG ATTGTATCAC TGAAGCTTTC 540  
 GAACTTGGAC CAGGCGAAGC TGACACATTA GTTCCGAAA AGTGTGGCGG AAGAAGCCTC 600  
 20 TCTCAGTTGC TCACCACTGG CATGGCTCAC AACTCAGATG CAGGCGAACC GAAGGTAGCC 660  
 GCGAAGAGT TGAAGAAGGA AGCTGAGGCC TTGAAACTGG AAGGTAACAG 710

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1505UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

45 GATCAAGCTG GACAAAAACT TCCGTAAC TA TCTGAACCTA CTGGAAATGG TTCAGGGGTA 60  
 CGTGGAGCTT AACATGTATG AAGATGTCTG GCGAAAGCTC GTTCAATTAA ATGGGAAAAA 120  
 50 TGAGCCTGAT AGAGTTCCAG GATATTATAT TACGAGGTCT ATCTCACTGA ACCAGCTTTC 180  
 CACCAATATA TATCCTGAGG AGTTGGATAA GTTTAATCTA TCTCCTGTCA CCGAGATAGA 240



AAAGAGGGTC GTGCAAGCCA CTGAGTGTTC CTOGAACTA ACATTAACAA ATAGCCATCA 300

5 TGAAAAGGCG CGCATACTGA TATCAACCTT TCAAAAATTG ACAACGAAAA CTTCCTCAAGC 360

TACTTTGGAT CCAATGATTG ACGCAGATAC CTTACTGGGT TTGATGGTTG TTGTAGTTTG 420

10 TCGCGCACAA GTTAAAAACT TGAAGAGTCA TCTAGATTAT CTTAGAGAAT TTGCGCAGAA 480

TTCGGATGAC GTAAAGTTTG GGCTCCTTGG GTATTGCTA TCGAGCTCG AAGCGGTGGT 540

15 CGGATATTC GATATTGGCG GCAGCTCAAT TAACTTGAA AGATTGATCA CACCATGTCC 600

AAGGAATAAG ATCTTCTGGA ACTTGATAGA GCAAGGAATT CCAATAAATT TAAAGGAACA 660

20 TGAAGAAGTC CTCATATGCG GCACTCCGTC CTGTGAATCA TTTTGTCITT ATGTT 715

(2) INFORMATION FOR SEQ ID NO:789:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1506RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

45 GATCTACCGG TTCGGTATCC CCCTTGAAA ATAAATTCTT TGTCITTTGC ATGCAACTAA 60

AATGGGATGA AGATGCAAGG GATGTTATTT TTAAGTATCT CCATCTTTTG GAGCTTTCTT 120

50 CACAGGCTGT AACATTAACA AGGTCAAAAA CTCTACAGGT TATAGAAAGG CTTTGTCA 180

GAAAATTAGC GTATACGAAG TCGGATGAGT CTATTTTCAG CAGCATTAGT GATATTCCGA 240

55 TTGATGGACA TGACTTGTCA ACCGCTGAAA CATCTTCCGA AGAGCAGCCG AAATCTCAAT 300

CTTTGTCGA GCTATTTGAG GAGAAAATAT ACAGCCTAAA CACCGACGCT CCTTATATGA 360  
 CTCACGATGA CCACTTCATC CAATTTGTGG CTCTCAAAT TCAATTGAGC ACTAAGGAAT 420  
 CGCCCGGAAC GTGTGTGCTT GTTACTGCCC CTTCGATGAA ACTGAAAATT ATAGACTTCG 480  
 ATTCAAATAC TTGGACAAT GAGTATWATG AAAATGTCTT TATGACGAGG TACTACTGCAG 540  
 CATTGATTCA AGCAAATGTA TTTATCTTCC AAGAAAGTGA CTATAAAGTC TTTGAGAACT 600  
 CATTGTTTAA TCCCAAAGGC TACGGTGCTA AAAGTACAGA AAATTGGCAA CCTTGGCTAG 660  
 GACTGGAACT ATGTTTTGAA CCGGAGCCCT TGCAAACTAA TAOGGTTATT AAAGAATTTC 720

## (2) INFORMATION FOR SEQ ID NO:790:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1506UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GATCTCCCCA TAAGCTCAAC ATTTTTCGATA TAAGATATTT GCGTCCCCGC CCAAAACACG 60  
 ACGGTCCGTC CCAAACCTCAA TGCCCCATTT GCAACAAACG GCAAATCATG ATTCCATCTG 120  
 TCCCTCTCGT CAATCACCGA ACTTAACAGT AGTTGACGCT TTGTCACTTG GACTAGATAG 180  
 TTGTTGGTAA CGAAGTAGTA TATCGTGGCG CCAGCCAAGT CGCTAAGGAT GCCATCAACT 240  
 TCGTCGCATT CCATGTCCTC TTCGGAAGAA AAATAAGTA CAAACGCCCT GGTATGGTC 300

GCCCCATCAG AACCAATAAC CAAATAACCT TTATAGGGTC TATCATCGCC ACAAAGTCTT 360  
 5 GTATACACTT CTTCGGCAAC GGCATCCAGT CCTATGGTCC ATATGCTGTT AAAACGCAGG 420  
 AATTCTCGCA GSTACAATAT GTTTTAAAA TGGGCTACAT GACCAITAGT TGATATGTTA 480  
 10 GACAGCACGG ATGATGAGCA AGAACATAAC TCTTCTGTA TTGTACCTGA AATGGCAGGA 540  
 GTTTTATGCG GGAAAGAGAT CAGCTCTTCC GCGTATGCAA AGCTGGTATC CTGGGTGTGT 600  
 15 CTTCTAAGAA TATTGACAT AGACTCCACA TAGGCTCTGT CATOGAGGAT TGCAATGCCA 660  
 AGAGAGATCT AGCGTTATCT CAAATACCTT CCAAACTTA TAATCTGTAA TTT 713

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1507RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GATGGGCTGC GCTCCAACGA TGGCAGCATT GCTCCTAACG GGGCTGAAAT ATATGTGGGA 60  
 45 CTCATGGCTG ACTTTAGCGT CGGCGGGCCA GACACGTCCA ATGCGGCGGA GGGCTGTGTG 120  
 CTGCGGATCC ACCTCGAAGG ATGGGGTGC CAGATGGTTC TAGACGGGAT CCATATCCCG 180  
 50 AACGCTATCA ATTGGAGTGC AGATGGCTCG CAATTCATC TGACTGACTC GCTAGCATTT 240  
 ACCATATGGG CGTGCCCGGT AGTGGACGGT AGCCACAAC TCCTCAAGAG AACCCCATTC 300  
 55 TACTGTACCA AAAATACTGG CAATGACTCA CACACTTCG CCGAACCGGA TGGTGGATTT 360

EP 0 866 129 A2

GTGGACTGCT TTA CTGGGCA CACTTTGTG GCGGTGTGGT CCACTGGCAA AGTCOGAGAA 420  
 5 CTGACAACG CAGGCAGACT ATTGCTGCA TATACACTAC CGACGCCAG AGTCAGCAGC 480  
 TGTTGTGGG GCGCCGAGG CGAACTGCTC CTGTCCACGG CGCAGCAGG CGATTTCAG 540  
 10 ACTGGGCAC ACTCTGACG CGTCGGAGG AGCATTTTCA GAGTGGTAAT CCGGGGCGC 600  
 CGGTTATCC CAAGCCGCAT CCGCGGTCT TCGGAAGCA TCCTTTAAAT AATATTTACT 660  
 15 TCTACACCT CTGTCCCT CTACGCCCA GTCATTGAT GGGCGT 707

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1507UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GATCGTACCA GTATAATACT GGAATTGAC GCGGCAGCC AAGGGTGGT AATCATCGTG 60  
 40 CTGATAATTA TGTCATAGC CATCATWAT GGAATTAGCA TCAGCTATTT GCTTACGGTG 120  
 TTGACGAGCG ACTGTTAATC TCCATAGAGA ATTCTCTCA ATAATTTCTG AGACWGTCT 180  
 45 CTTTTTAAA ATCGGCTTTG GCGCGGAGG TTGAGGGGG CCAGTGCTAC CACCAGACTT 240  
 CTTCCTTGAA ACCCGCTTGG AATTTTGTG ATCGGAACCA TAGACAAGCT CTTCATATC 300  
 50 CGCTACGGCA TTGGGTGCA ATGTCTGAGC GTGACCGCTA TCAGTAATA TAGGCCATA 360  
 CAGCCATGTG ACGTCGAGT CCTTGAACA GTGACAACC TCTGGGCTCA CGTGCGTAG 420  
 55

ATTATTCGG GCTTTGGCCC AACTCTOCA GGATGCGTTC TCGAGCCGG CCGCGTTCAC 480  
 5 GAGGTCTGTC TCTCCCTTCT GTCTCTTCTT CAGGATGATG TACTTCCAGG ACTGAGAGAT 540  
 GTCTCACTCA GCCCAGTCGT GCGAAAGGTA 570

## (2) INFORMATION FOR SEQ ID NO:793:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1508RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GATCCACAGG CAAAATTTAT GCATATAGCT TGCTTATATT TATGCGGTGG ATTCTATATG 60  
 TCGCACGCTA AATACTAATA GCGGCGGTA AAAAGTAGTC CTCGGCAAAC TCGGTAAACG 120  
 CAAGGTCCGA ATTATAGAAA CCGGACTCAG AAAAATAAT CCAGAGTAAT TAAGGGACTC 180  
 GGAAAGCGGA GCGGTTCTT ACCGAAAACC TCAACGGAAG TATATGAAAA AATTATCCT 240  
 GCAGATTATA CCCATGCCIG TTTTATCCAA GGTAGCCCAA ATATATACTA CAGGAAATGA 300  
 GTGACTTTTC ACTTCGAGAG CCCAAATAAC AATAATTTTA GTAAAATTTT AGCATTGCTG 360  
 CTACTCCAAC TTCCAATGA ACACTTCTGA AAGCGTAAAT ATATAGCTAT GCGGTTTGCC 420  
 TCCCAGGCTC TAACTACAAA TTCCACCTTA TGTGTGTAT TCAGGAAATG CAGGGGAATA 480  
 GTTGAATCAA CGAAATAGCG TTAATTTGCA ACCGCTTGT ACGTGTATAA AACCCACCCC 540  
 CCTCCGAAAA AGATGACTAT CGTTATAAAC TAAAAACAT CATCAAAAAA GAACTAAGTT 600

ACTGAAAAGA AAATGGTTTA CCGTCTAGCA GTGAATTTC A GCAACCAGCC CACATGGGTA 660

5 ACCAATTTC GAATCTATCG TTGCAGAATA CT 692

(2) INFORMATION FOR SEQ ID NO:794:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 716 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1508UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

30 GATCTGGTAA CGACTAAATA AGAATCCTTA CCGAGCAACG CCGGCCCGGT CTCGGCAGTG 60  
 TAGTGTCTCT CAAGTGCGCG TCTGGCACTA GTTAGGTCTT GCAGGTGCG TTTGAACCAG 120  
 TGGGCTCGG TAAGCACCGA GATGGCGGAA ACTCCCGCT CCGCATATGC AAGCGCTGT 180  
 35 TCTCTGCAA GCGCTCGCT AATATTGCCA CCGACCGAG ACGCAAGTTT TATCTCGCT 240  
 ACCACAGCCA GCGCGGGGC GTCCCGGCC AGCGCTCAT GGAAGTCAC CAGCGCCGC 300  
 40 AGAACCCCCA ATCGAAAGCT CGCTCCAGG TCGGCATAC CAGTTCCCG CATAGCCATC 360  
 TCGCTGCA CGTCTCTG TCGTTGAGCG TATATCTGC TCAGCACAGA GCGCGCGCT 420  
 45 GCGCGCAGT GGAGCTTGT GTTCTCAGC CAGTACGC CTTCAGGC TAGCATGTTG 480  
 CGCACATTA GCTGCCCGTG GTCCGTCAGA ATGACTCG GGTGGAAGT CACACCTCC 540  
 50 ACGGTGTACT TCGGTGCG CACGCCATA ACCAGCGCT TCTCCGTGG CCGCGTCAC 600  
 55 TCCAGCTCG CCGGGAAGT TGACGCCAGT CCAGCCAGG AGTGGTACG TGTCAGTGC 660

ACGGCTGGGG TACCCCTGGA AGAACCGGCG CCGTCGTGAC GCAGCTCCGA CGTTCT

716

## (2) INFORMATION FOR SEQ ID NO:795:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1509RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GATCCAGTTT CTCTGCAATT TTCTGAACGA TGAGATATGA GTCTAAGTTG GCTAGATTAC 60

TATATAGCCA GTTGTTGCTT CGACGGGCCA AAACCGAGAC CCGTTCTTTC CTTTGACAAG 120

AAGAATAATC GCCATCTACT TTGTTTGAAT TCTTTAAACC GTCTAACTCT TGCACTACCG 180

TTTTTGGTAC TACTATGCGA TAGCTGTATT TTGGGGCAAG CACTGGTAGT TCTTCAAGGA 240

TATCCAGATG TGATAACACA TAATTAGTAT CAACGACCAG TGCAATATTA TGCAAGTCTT 300

GCGCACTTC AACCTGGGGC TGAATTACTT TTGCGAAAGT CTCTTGGCCC GGAATATCGA 360

CTCTCTTGTC AGGAATAGTC TTAATGTGTG TAATTTCATG GCTGTGATAT TGTCTATAT 420

CCATCATCGC TTCAGCTTGG TGTTCCCTTA TAATTTCATG TTCAACCAAT GCATCCAATT 480

CTGCAATGCT ATATTTCTTA TTAGAGTCTT TAGGGTTCCA AGTATGCGGC GAGCTTATGG 540

TATGGGTCTT ATTCTGATGC CTACGCTTGC TCTTCTCTCC ATGGTCCCTA GACATCTCTT 600

GTGTAGCTTG GTGCATAGAC TGTATATGAT TGGACTCCAT CGGAAGTAGT GGCACGTTTA 660

AAAGACATTA ATTAGGTATC ACCTCCATTA ACGTACCTTT GATATTTATT ATATGA 716

## (2) INFORMATION FOR SEQ ID NO:796:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1509UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GATCTCGAGT TTCAATGACGA GTGCATGGAA GATGIGTTTC TAAATGCAAC TAAGGTCCGT	60
AAGGTCAGTG AGGTGCAGTC CTTTATCACT CTAAATTCCT CCTCTTCTT TGATGATGAG	120
ATACTCGAGT CATCGATGCC AACTACAAGT CACCATCAAG ACTTAACAAC TCAAGACGTA	180
CTTGGTGGAT TGGTCGATGC TATGGATGAT AGGCGCGACC AAGAAGACGA TATCGATTGC	240
CAACAACCCC TGGATGTACT TCCTTTGATC GGCTGCGACA GTCCAGTTTC CAACTTGCCG	300
CGGATTACGG GGGTTGCTCG TTCCGAGGAT GCAGACGAAT GGGATCTTGG ACAGAGCAGT	360
ATTACTCCTA ACAAACTAGA AATCCATTGC GTCCAGACGC CTACCACACA CCGTGTGCGT	420
GTCCTAGAAG AAGAACAATC GCCTTTGATC ATGCTGCAGA AGCGCAGACT AGCCAGGAAT	480
GGGTCAAGAA CATTAGCCAC AGCTACAATC AACCATGACC AGGAACTGCA ACTAGAAGTG	540
CCAGATAGAG AAGCCGCTTC GCCTGCCATT GAACACGAGC AAGCCACCTC	590

## (2) INFORMATION FOR SEQ ID NO:797:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1510UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GATCAGAATT GGAAGGGATG TTTGCGCGAA GAAGTTGGTG ATATCGAGGA GGGCACTATA	60
CCCGTCATTG GCGGGAAGTT TTTCAAGTAC GAATCTCTTA TAAAGCACTT GCTACCCCCC	120
AACGCCACTA TAAACGACCC CATTCCTCAG CCAACTGAGG GAGCGGTCAA TGCTCCACCA	180
TTGGTTGGCG CCGTTTATCT ACGCCCAAAA ATTAAAAAGG ACGACTTAGG TGAATATTC	240
ACCTCGATG ATTGTCCAG GTACATTATC AGGCTGGTG ACGGCGCTGA GGTGGGTAGA	300
ATCGACCCAG AAACGGGAAC CATCATTAAC AATTCCAGA CCGCAGTGT ACTACCGAAA	360
ATGAATATGT CTACACCAG TCTGTGCTCT TTGAACCGCA ACGGTAGCTA CTGAATTGT	420
ATAGGCGGTT CCGGTAGCCC AATTACATG ACCAGGTCCA CCAATACTT CGCACCAGTT	480
CCTAACGGCG ATCTGAGAAA TCTGCCAATC GTGCAACAAA TACCGAATAG CACTATCCCA	540
TCTGGCAGT CGTCTGAAA AGGCGGCATA CAGGGGGACC ATGGGGGGTT CAATTAAAGG	600
TACTACCCCT GCATACCAAC CCGCTTCAT TATTAATAAC CTAGCCGCC AGGCTAAGAC	660
AAACAATACC GTTCTTGGA ATATCTTGGT CGATACGCC GGTCCTACG TTCTCTATA	720
TCT	723

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 693 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1510UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

GATGCGCGCT ACTGTTCTAC GAACACGGGC GGGGGCTGAA CCTGGCGATG GGGTTCAAGC	60
TGGAGGACCC GCACGCGCGG GGGAAAGAGC GGCGTACTG CCTGGTGCTT ACGGTGGACC	120
TGGGAGAACG GGGCGCGGCA ATGGAGATCG TGTCGAGCA CTGGAAGTTC ATCTGGGGCG	180
CGTTCGAAAA CATGATCGAG TACATCAAGC AGCAGCGCGG CGCGGAGCTG CTGCGGGTGA	240
TGCAGCAGGG GCAGGTGCAG GGCACATCGA ACTTTTGTGTC CATGGTCAGC GGCACCTATC	300
TGGCGGGGAA CAACCTGAAG ATACCGAAGA ACATCAAGGA GCTGACCAAC GATAGACTGC	360
TGTTGCTCAG GATACACAAG TGAATGCAT TTATACTGGA TAGACTGGGA GGGCAGCTGG	420
ACTGAACCTT TGGGGCGGTG GCTGCGCGGC AACAGTTGGA AGATAGAAGA CAGAAACGCC	480
CGGGAAGCCG AGGCGGAGG TCGGAGGCGT TACATAACTT ACATTCTTAA CTAGATAGTG	540
TTGCGCTGTA CATCAAGTTC AGACGTTAAG GTTGAACGG GCATCGGTGA TGTGTTGCT	600
GAAGGGGGCC AATGCAGATT TGACGTCTT GTTGATGAAC TTCTCCACCT GCTGTGGGGC	660
CCTGCCACAA AACGTGGAGG GGTCCAGCAG GGA	693

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1511RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GATCGACCAG CTGGTGATGG ATAGGCGGCT GGTGCCGCTG GGGCGCTTCG TCGGGGGGCC	60
CGATTTTGGG CTGTTGTGCT GGGTGAGGTG GACGCTGCAC AAGGTGGTGG ACCTGTCTGT	120
GAGGAGCCGG GTGCGGGAGA ACGGACGGTA CCTGCGGAAC TGCGCATAAG TGAACATGGA	180
CGTGCTGGCG GCGCGGCACG GCGCGGTGGA GGGGCGCTG GAAGAAAAGG TGGTGGCGCG	240
GCGACGCGA TATACGGACC TTGTGTTCTC GCGGAGGAG TTCTACGCGG TGGTGGCGGA	300
GAGCCTACGG GGACGCGGGG AGTACGATGT GGTGCTGGCG GACCTGGACA AGCACCGCAA	360
GGCGATTCTA GTGACGGAG ACGTTGTGAA GGTGGTGATG CCGCGGTGC GCGCGCTGGT	420
GCAGCCGTTT GGGCCTGAAC GCGTGACCGC AAACGACCGC CACATGCGAG AGTTCAAGGG	480
CTCGCTCGGA TTGGTGGAGC GGCAGGTCCA AGCGATCCAC GGGCAGCTCG AAGAGACAAC	540
CCGGGCGCTG CGTTGGCGCC GTCCCGGCGG GCGCGCACCC CGATGTGCAG CCGCGGTACC	600
TGCGGATGAA CAACTCGCGC AGGCCAGCCT GTCTGCGCGG CTCAACCACT TTACGAACCT	660
AATGGAGATC AAGGAC	676

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1511UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

10 GATCTTGCCC CACGGCCCGT CGCTCAAGTT CCCCCCGTCC GCCACAAAG CCCGGAACAT 60  
 GCGTCATCC ACGCTGGGCT CGCTCCACGG CGTCTCCCCA GTCAGCAGCA CAAACACAAG 120  
 15 CACTCCCGCA GACCAGATGT CCGCCGTGTC CCGGTGGTAC GCGCGCTCGC CCACCACCTC 180  
 CCGCGCCAGG TACGGCAGCG TCCCCCGCGG GTCCGCGCGC AGCCGCGCGG TCCCGTCGCG 240  
 CCGCCGGAAC CCGCTCGCCA GCGCGAAGTC CGCCACCTTC AGGTTCCCGG CCGGTCCAG 300  
 25 CAGCATGTTT TCCGGCTTGA TGTCCCGGTG CGCCACGCGG CACGCTCTGT GCAGGTGTGT 360  
 CAGCGCCCGC ACCAGCTGCT GGTAGTAGAA CGCGCCACTT CCGAGTCCAC CCCCACGTCC 420  
 GGCTCGATCT TGTGGAAGAG GTGCCCCCGG TCCGCCAGCT CCATCGCGAT CCATAGGTAC 480  
 30 TCACGTGACA CATTCGAGTC CAGCACCTTC ACCACATGTC GGTGCCCCGG CACCGGTCTT 540  
 GCAGCACACC TCGCGGTCA GATCCTCGTC CGTCATCCCT CCGCTTTTGC AGCGCTCGAA 600  
 GTGCACGAAC TTCACAGCCA CTATCGTCTG CCGGTCTGCG CGCAACGAAG CGTTTTTGAA 660  
 40 GAACGCAACG TGCCCTGCCC AATGCTCTCC CGAAGCTCTA ATTCTTAAT CTCGGGAAG 720  
 CA 722

## (2) INFORMATION FOR SEQ ID NO:801:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1512RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GATCTTGACT GGAAGGATGA GGAGCAAACC CCGACAGCG GAGAACTGC TATTGCGTG	60
TCTACACGCG GCTCTACTCG CATCCAAGTT TAGCTATACC TGCATTATTA CTAGATATCT	120
AATGCTACC ATATGTTGTG ATGACACTGA CATTACGCT TTAACCACTT CAGCTTATTA	180
AAAGATTCCA GACATACAGA AAAAATCCGG TGTAAAAGT TATACATATA CACCATTTTA	240
OCTATATACG TGTAGACGAG TAGAGCTACT AAGCAGCCCA AGAAACACTA CCATATTCAT	300
AATGGCGAGC CTAAGGACTT TOGATGCGTT CCGTATGTGC CGAGGGTTAT AGTCACACA	360
CGATGCAGTA CTAACAGTCG TAGCAAAAAC CGACCAGCAG CAGTCCGTC GGTCACTCTG	420
CGGGGCGATT ATGTCCATAA TGATGTACCT GTTCTGCTG TTTATCGCGT GGGGGGAATT	480
TGGCAGCTAC TTGGGGGCT ATTGGACGA ACAGTACATC ATCGACCCCG AACTGCGGCA	540
GACAACGCAG ATTAACATGG ACGTGATGGT GCAAATGCG TGCAATACC TCGAGTCAA	600
GGCAACTGAT ATTACCAGG ACATTACGA CGTGTGAAA AGACTGGTGT TCAAGAATAT	660
CCCTTCTTC GTACCGTACG GCACCACATT TGACTCTGTT AATGAGGGTC CGCACCOCGG	720
AC	722

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1512UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

5	GATCGAATGG CATCCCATTC ATCCGATGAG GACGCTATGT TAAATAAATA TTATCTATAT	60
10	ACTCTAAATA CTATATGGTT TCATCOGIGT TACCCGGATT TAGAGATGCG CGTTCCTGTC	120
15	TCCAAGCTTT AACTCGTGTG GCTGACGATT CTACATAACG TGTATTGACC AGGCTGAGCA	180
20	GTAACGTTAG CAACTTGGAC ACCAGTTATG AGTACCGATT TCGACAGAAT TTATTATAAC	240
25	CAGTCAAAGG TGAGCGGTGG CTTCGGTTTG GCGGAAGGTG GCGTGGGATG GAAGGCTTCC	300
30	GCCACTGGCG GGTCGGCTGC CATGCAAAAC AACGAACCAA TTCTCTTGAC TGGGAACGAA	360
35	CTGGCTTCCG TGCAATGGAG TAGAGGGTGC CGTGGCTACG AACTAAAGAT TAACACGAAG	420
40	AACAAGGGCG TGGTGCAGTT GGACGGTTTC TCGCAGGAAG ATTTACATT GTTAAAGAAC	480
45	GATCTCCAGC GCAGATTCAA CGTGCAGTTG GAACACAAG ACCACTCGCT TCGGGGATGG	540
50	AATTGGGGTA CTACCGATCT GACAAGAAAC GAGCTGATCT TCTCCCTAAA CCGGAAACCA	600
55	ACTTTGAAA TACCATATTC GCATATCAGT AACACGAATT TAACATCAA GAACGAAGTT	660
60	GCGCTGGAAT TCGACTTGC	679

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1513RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

5	GATCAACTGT TGCTCCAGTT GCTCCTTGA CTGGTCTC AATTCAAAG CTTTACACC	60
	GGCTGAGAT GAGATGTTAG TACTCCGCGC ACCTATCAAG CTGGGAATGA CATTGCTGGC	120
10	AACCTGGGG GCGCATCTA CCCCTGGCT ACCGCTGCT GGCTAACCG GTATGCGCTG	180
	CTGTGCGCA CTCTGTCCC ACGATTAA GCTCTAACG GTCACCTGA TACCCAACA	240
15	AAAGCTGCAT GCCATCATC CAGCTATAC ACCGCTGAC ACATACCATT ATGATTGATT	300
	TTGCTGTATT TTGACTAAG AGCCACTCA AATGAACTG CTCTCTGTT GAAGATGTTG	360
20	GCTGCTGTG GAAACCGACT GTGCTCGCT CGGTGTGCGC GAGGAGTCT GTCGAAGAC	420
	GCAGAATCTT CAGCTATACA ACCACACAC CTCGGAATGT ACGGATCAA CAGTCAAACA	480
25	CAATTCACAA TCACGTGACC TACAGGTGAA ATTAACGATT TGGCAGATC GCAAAGTGAG	540
	CGCCAAAGC GCGACGGAAC ACCGAGCG GTACACGATG GGTGCGACTT CTTACACTAT	600
30	ATATCGATGG TAACAGTGCA CGCACAAAA AAAGTAGTAT ACTAGGGTCT ACGAGACTTC	660
	GCTAGTTCAT TTACAGCCTA ACCTAAAGAT TAATTATGCC AAGACAGTGA TTGGAAGGAG	720
35	A	721

(2) INFORMATION FOR SEQ ID NO:804:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 726 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1513UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

5	GATCTTTAAA ATTTGGCAAG AACAGCCAAC ACTCCCGTCA AAATAAGAG CAAAGCGCCT	60
	CCACACCTCT ACGAATCAGG TCCGAAAGGC GATCTTGCAA TGACGAGCAA GGTTACAAAG	120
10	AAAGTTAGAG AGTGCACAG TGCATGTGAC GACCAGCAGC ATAGTTCTCG GGCTCGGGC	180
	ACTGCAGCAG AGGGAGCGCC TAGTAACGTG GTTCAACCGT CCCTCGGTGA TTTGAAGAA	240
15	CTGCGAGAAT ACACACTCTC CACCCCTACG TCGAAGAGT GCATTAAATA ACGGCTGGG	300
	TCCACGAACG TGCAGGAGGT GAAGCTGGGG GGA CTGCAGT TTCTGTTTTA CAAGACGCTA	360
20	CTACTGTGTC TTTACATGGC ATATGGGTTT TACCGATACT TCCAATACCA GTACAACAGG	420
	CTGGGTATCA AACTACTGAA TCTGGCCTAC TCGCGGTCCA ATACCCCGCA GCTGATCAGA	480
25	CAGGAAGTGC TAAAGTTGCA GAAGGTCCCT AAGCGGCTGG CAGCGATTTT GGCATACAAG	540
	TCTGAAGGGG AGGTGGGGG TGGCGTCCAC GGCTTGATAA ACGACGGAAG CAACGTANTA	600
30	TGCTGGACTG TGTCTGGGG CATCAAGCAC CTGTGCTTT ATGATCATGA CCGGGTGCTC	660
	AAGGCCAACG TGCACCAATT CCGCCAGGCG GTGTACGATA CCTGGCGCGC TACTACGGCC	720
35	CAACAA	726

(2) INFORMATION FOR SEQ ID NO:805:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 736 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1514RP

55



# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

5	GATCTGGGTG TATATTGGA TGTATATGGA CTTCACTTT TCGGAAGCAA TCGAACTCGA	60
	AAGCTGGTTG ACCACTCTGC TGTATCTCG TAGTCTTTCT GAAACGACGG TAAGAAAATT	120
10	AACCTTCAGC GCGATAGGG AAGATGCAAC TTTAAATTTC TCTACTTGGT TACTCAAATA	180
	CTGATATAAT AATGCAGCCT CAAATATGCT GTGGAAAACA CCACTTTGCG CGTTGGGAAC	240
15	ATTGGGTGGG ATTTCGATAA CCTGATTGGA GATCGGGAAC AAACCTGACG TAGTAGCCAG	300
	TAACGCTAG GAAATATACT TTAAAACGTC GCGCTGGGC ACCATGTTGC TGTAGTATGG	360
20	GTTAGACAGA TATGCCAATG GAGTATCGTG CTGCTGGGC CGCTTGGGA CCGGGCCGCG	420
	GTATGCAGAG GTTACCGCGG ACGGGGCTC TGAAAGCGC TCCACATTCT CGAACGACTC	480
25	TGCATAGACA CTAACCGCCC TCGACGGCGT CATCAGGAG TTGTGCGGTT GCAGCGTGGC	540
	GTTCGTAAGA TATCCAGAG CGGTGGCGCT GTGTGGAAG GCGGTGCTCT CCTGGGCAC	600
30	GCTGTTGAGC ACGTTCAGT ACTTCAGCAC CTGCTCTTG CTACCGAAAC TCTCCAGCAC	660
	TTTCACGAAC ATCTCGAACT TCCCCACTG CTGCGTCTG TCGGGGTCC GCACCATCTC	720
35	CGCCCGGTAC ATGCTC	736

(2) INFORMATION FOR SEQ ID NO:806:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1514UP

55

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

5	GATCTCCACC GCGTCCAGCA CCACGATCCG GTCACCGTCC CACCGCGTCA TCGCCACTGT	60
	CCGCGCGACG CTTTGGAAAA CCGCCCGTCC CTCGCGCGTC GCAGCCCCTC CCGCGCTGTC	120
10	GTCGCTCCGG TGCTCGGCCT CCGCGACCG CAGCGTCGC ACCACCCGCT CTATATTAC	180
	GCCCCGGGC TTCAGCGTGT CGCGCTTGAT GCCAGGGCTG GTGGGTTTCT CTCCACCAC	240
15	CTCCAGGCTC TTGATAAAG TGCTCTTAAT CACCTTAAAG CTCGCAGTAT GGCCCTTGG	300
	CCCACATAGT AGCGTCAGG TATGGTTTCC CGAATCGTAC GCGTATATCT TGCCCTGTGT	360
20	TACACCGTGG AGGACGTTGG TCACCGGCAC CTGAATCCA AGGATATGTT CCAAGTTGAT	420
	GCTCATCTG CTCACTTCCA AGCCACACA GCTATCCTGG CCACCTTAGA ATGCCACGCC	480
25	TGCTCCCCGT CCACTGGCTG ACTCCCAATC GTTCAGTTTG CGGTGTGGT ATTTTTTTGA	540
	AGTGGCGCTC TAGCGATGAA GTAAGATTTT CTATGTATTA CTATGTGCA CAAAGGTTAG	600
30	TTCCAATAGT GCTTGCAACT ATCAGGTGCT GTGGAGTTCC CAAGCAGACG AGTTGCTGAT	660
	AGTGGAGCCG ATAGAGAATC CGATAAAGAT TATTCOCGAA AATCTAAGGA CAGGTGG	717

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1515RP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

5	GATCCTTCGC CGCGTGGTCA AAGCCCGGAT AGGATATCAC AGGGCACTGT GCAAAGGTAT	60
	CGCATATTGT TTCCATGAGC GTTTCGCCCT TCGGTCTCTT CGCCGGCTTC CACTTGCAAG	120
10	TGGCCGCCAG GAGCTTACAG AGCTGCAGAT AGTTATTACT GTCAAAGTC CAGGGTGCC	180
	CGCGCCGTTT GTGCGCCGA GCAGCATCCG CGAAGTGGTC CAGGTGCGCC CGGACAGAT	240
15	GGAACCCGTC CATGGGCACC ACCTCAGCTA TATTGACCGA TGAAGCTGA TCAGGGCTT	300
	CGCTCGGAT GCGCACCGAA TTGGGGAGOC CGCCCGGCC GAAGATAACT GGGTCCCAT	360
20	CCCCATCGTA GAACTTGTGT GCCTTGAACC CCGGGTCTC CAGTGCGOG AAGAACCCOC	420
	GTGCGGCTC CTCGACCAGG GCGCTGAAG CAACCGGCAC AGTCTGTGC AGGCTTTCCG	480
25	CAGCAATGOC CGCGGAAATC CTCAATCCAC CCCCTCGTGC CTTCAAGTGA CTCTGGAATT	540
	CCTGGTTCAG GTCCCGCTTA AGCCTCTGCG CCATCGTAGA CTTGCGGCAC CCAGGATGCC	600
30	CCACCACCAC TACAGCCACC CGATAGTTC TCTCGATATT CTGAGCAAGG AGATCCACA	660
	CTCGCTTCTT TAAGTCTTCG TAGTCCATGC CGCTGCTGT GTATGCTGC TGGT	714

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1515UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

# EP 0 866 129 A2

	GATCTAACGC CGGCTGTCTC CTCCAAGCGT GTTCCTGCCT CTCTTATATC TGTATCTGGT	60
5	AGCTTCAGCA TTAAAAAACC GTCCAGAGAA TTGGCTTTTCG GCCATGCTCG AAAGCTCACT	120
	AGTGGAGCG CAGCATCTAG GACACCAGTA GGATGCAGAC AGTGTTTTAGG CCATTGAGAA	180
10	GTGTGATTCT GACGCCCGCT CGAGGCCTCG CGCGGTCCAG CAGGCTGCAG TCGGGACACA	240
	ACAAGTGGTC GACGATCAAG CACGATAAAG CGAAGAACGA TGCTGAGCGG AACAGGCTTT	300
15	TCACGGGAT GCCCAACCAG ATATCGGTGG CAGTCAAGCA GGGCGGGTCT GCCGACCCGA	360
	CGCTGAACCT GCGACTGGCG GCGGCGATAG AAGCGGCGTC CAAGGCCAAT GTGACCAAGA	420
20	AAGTGATCGA AAACGCAATC CGCAAGGGCG TCGGCGAGGG TGGGGCGCGC GACAACGCCG	480
	AGGCATGCAT GTACGAGGCG ATACGGCCCG GTGGCGTGGC GTTTGTGCTG GAGGCTCAC	540
25	CGACAACAAG AATCGGACCG TGACCTGGTA CGCGCGCGT TCAACAAGCA TGGCGGCAAC	600
	ATGTGCGCCG CTCAGTACTT CTTCGAGCGC CGCGGTACG TGGCAATCCA GCCACCGGCC	660
30	TCGTGCGAGA GTTACAACGC GGIGTTTGAG GTTGTGTCCG AGGTGAGGG CGTAGAAGAA	720
	CTGGA	725

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1516RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

EP 0 866 129 A2

GATCGACCT TTGGTGGCTT GGCTCGAGTC TTCTTCAAT TTAAACCCCT GTTCAACAGC 60

5 AGATGAAATT GTTAGTCTAT CGAGTCCAG TAAAAGACAA TTTTGGACG TTGAGATGAA 120

GGGTACGGCC TCTCCCGACA AGGGCATCG CCTGCACCGA AAAGTATCG GTCACTCCTT 180

10 CATCATACCG TACCTTCACT ATCTCTTTC GCGGAAACT AAATACAGAA ACATACCTTT 240

AACATCCTTA TTCTGTTTAT CCTTCTCTGA TTTGACTGG AATGTAGCG CGAAAGGGAT 300

15 CTGTTTCAA AATTGGAAAC GCTTACCACC TCACCAACAC ACCAGGACTT TATTTCGTAG 360

AAACAGGCGA TCGGCTGAA CAACAGTCAC TAGAAACGT GCAOCAAGC AGCTTGGCAA 420

20 CGAGGAGGCA CCTAGGGCT CAATGGGTG ATAGTAAAGC ATGTACCGA GCTTTGTCTC 480

CGAGAGAAG AACGACGTCT TCACTCCGA CAGTACGAA TCTGAGATC ACCACCAAG 540

25 GTGGTATG GTGCGACGA AAGCCTTCAG TTTGGGGGA CGGCTGGGG ACGGGGAGT 600

ACTTGTGGC AGCCGAAGAT ACGCGATGA GCTGCAGAG CTGGCTCGG AGCTGTCTG 660

30 CTCGGCTGAC GGTCCGGCT TGGAGAC 687

(2) INFORMATION FOR SEQ ID NO:810:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1516UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

55 GATCATTAC GAAATCTTG TGGTTGATTA CGATGTTTGA TGGGAAGATA TAGCTGGTCT 60

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TACAATAGCA AAGAAGTGTT TGAAGGAAAC AGTTGTTTAC CCATTTTTGC GGCCAGACCT 120  
 5 TTTTCGGGGT CTCCGGGAAC CTATCTCCGG GATGTGTTA TTTGGACCTC CAGGAACAGG 180  
 TAAAACGATG ATTGCCAGGG CCGTTCCGAC TGAATCGAAT TCAACTTTCT TTTGCATCAG 240  
 10 TGCTTCTCT TTTTATCGA AATACTTGGG TGAGTCGGAA AAACCTTGTC AGGCCTTATT 300  
 TTACCTAGCC AAACGGCTTT CCCCCTCAAT TATATTCAAT GACGAAATCG ACTCTCTACT 360  
 15 AACTAGCCGT TCAGATAATG AGAAGCAATC ATCCAGAAGG ATTAAGACGG AGCTCTTGGT 420  
 CCAATGGTCC TCCCTAACGA GCGCCACGGC TAAGGAAACA AGAGAAGGCG AAGAGGCCAG 480  
 20 ACGCGTTCTT GTCTTGGCCG CAACCAACTT ACCGTGGGCG ATAGATGATG CTGCTATTAG 540  
 ACGTTTTTCA CGGCGTCTAT ACATTCATT GCGGAATAC GAAACAAGAC TGTATCATTT 600  
 25 GAAGAAGCTT ATGGCCCTTC AAAAGAATGA ACTTTCIGAA TCTGACTTTC AACTCATTGC 660  
 TCCATGACT GAGGGCTACT CCGGATCTGA CATAACTGCT CTTGCCAAAA GAAGCAGCTA 720  
 30 TGGA 724

## (2) INFORMATION FOR SEQ ID NO:811:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1517RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

55 GATCAATGAA AAACATGCAT ACGATTTTAT GAAGCAAAAT TTGGCTTGA ATATTGCCAA 60

EP 0 866 129 A2

CTCTATTTCAC AAAACAGAAA TACTAAAGGA AGAGAACTTC ACGTTATTAT CCAAAGCCCA 120

5 AAGAGATGAC GTGAAAGGAA GAGAAGCGGA GTTATTACTT CCAAGCGAAT TAAATCAATT 180

AAAGATGGTC AATGAGCGTG AGCTGAACGG CCATGCAAGA AAAATAAGAC TACTATCCAT 240

10 GTGGGAAGTC TTCAAAATGC TTTAGGTTCT GCATTATTAT ATACACATTG TAGATACAAC 300

TGAAACTAA TGCAATTCAC GTCAGCAGTC TAAAAGTGGT CATGCAGTAA CTTCAACCT 360

15 TCTTTATTCC AAGGACAAAG GTATATTCCC AGCTGTGTCT TAGACAGTGT CCCAGCTTG 420

AAACATGTGT TACTCAAATG GTTGGCAGTA ACCTTACATT GCCCAGAATG GGTGATGCGG 480

20 TTAGAAGTGG TATAATCCAA CTGCTTCCAA ACATCAGCGT TATTAGGTGT AAAGAAAGCG 540

GATCTCTGCC ACAGAATTTT AGATGGAGCG CGCAAATTCA GTGCTCTGGA AATCTCATCC 600

25 ATGACAAGTG GAACATCTTT GTATTGTGCC GACAGGATGC CTTTAAATGG TAGGTTAGCT 660

AAATCTTTCA TCAAAATIGA AAGTGGTCCA CCTGTCTCTC CATGAGACAA 710

30 (2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: PAG1517UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

GATCCTCAAA ACTACAGAGC GAAGTTGAAA AAGATCATAT TTTGATAGAG CGTAAGCAGT 60

55 GGGATGAAGC ATACGCTCTT CTCAAAGGTG TTGTGGATAG ACATCCACAT CTATATGATG 120

CACATTCAGC ATTGGTTGG TGTCAGCTGC AGTTGGGCGA CACTGAAAGC GCTTTAGAAA 180  
 5 CATTCCAGCT TATTATTAAT AATGTGAAGA GCAGCGACGG CACGTGCTCT CAGTTCATTA 240  
 GCTCAGTACA CTGGCGAACC GCACAAGCAC TTATTACTAA GCAGCAGCAT GAAGATCCTT 300  
 10 CAGGTAATGA GTTTATAAAG ATTGCTTTCC AGCATCTGGT ACAATCCCTG AAGATAACCG 360  
 ATCTTTTTCG TOCAGGTAT TCCCTTCTTG GACACATTTA CGAAGTGTAT TTTCAAGACC 420  
 15 TGA CTGGC ATTTAGGTGT TACGTAAAG CCTTTGAGCT AGATGCCGGC GACCTGCTCG 480  
 CTGCTAAATA CATGGTGGAA TACTATAGTG ACCTGTGCAA TTGGCAGGCG GCGGGCAACA 540  
 20 TCTGTGACCG TGTAATCAAG AATGATATGC ATCTCAATTC CGTCAACTGG CCGTACAGAG 600  
 TTCTGGGTGT TTATTATTTG GAGCTTCAAC AGGAGGCTGA ATCGATCGAA TGGTTCCAAT 660  
 25 CC 662

## (2) INFORMATION FOR SEQ ID NO:813:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1518RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

50 GATCAAATGC CCTTCCCTTT CAACAATTC ACGTACTTTT TCACTCTCTT TTCAAAGTTC 60  
 TTTTCATCTT TCCATCACTG TACTTGTTCG CTATGGTCT CTGCGCAATA TTAGCTTTA 120  
 55 GATGGAATTT ACCACCCACT TAGAGCTGCA TTCCCAAACA ACTCGACTCG TCGAAAGAAC 180



CTTAGATGGC ACTAGCAACC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCTGTTC 240  
5 AAGGAACATA GACAGGGACT AGCAACCAAG GTACTTTCTT CAAATTACAA CTCGGACGCC 300  
GAAGGCGCCA GATTTCAAAT TTGAGCTTTT GCGCTTCAC TCGCGTTAC TAAGGCAATC 360  
10 CCGGTGGTT TCTTTTCTC CGCTTATGA TATGCTTAAG TTCAGGGGT AATCTACCT 420  
GATTGAGGT CAACTTTGG GAATACTATT CGCTTGAAG GCCTTGTTC TGTACGTC 480  
15 TTCAAGGCC AGCTCCACTC CAGATCTGG TCGAAACCTA ATACGAGTG TAGAACTAG 540  
CTCAGAAGC AGTCCGCGCA AGTCCGCGC ATGGGCAGCA TTTTCAAGTT AACCTGTCT 600  
20 TACGACCGAG TATCACTCAT TACCAACCC GAGGGTTGA GAAGGAAATG ACGCTCAAC 660  
AGGCATGCC CTGGAATACC AGAGGACCA ATGTGGTTC 700

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1518UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GATCGTCAGA TACCTTAGTC TCTATACAGC GCAAGACATG GGTGATGGCG GGTGTGTCT 60  
50 ATGCAAAGTC ATTGGGTTTC CCTCTGGCGG CGCATACAAC ACCTGCTAA CTTGAACAGT 120  
CTCATCTGG GCATCTAGCG ATCCATGGG TGAGCAGCGG AGGATTGGT GGATTACTAG 180  
55 CCAATGGCAA TCCAAACCA AGAAACCGAC TTGGGGGAAT GCTCATTTGA ATAGCCGGTG 240

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TTTCGACACT GTGATTCTCT GAGTGTAAACC TCTCTTTGG TTGCGATAT TAAACCTGTT 300  
5 CTGTGAAACA TOGGAGCGGT GTTTAGTGA AAGCAACTAG AGGAACTCAA AGAGTGCTAT 360  
GGCATGGGG CAGCTGTTGC GAAGGTGTAA AAACCCGAGC TCOGGTTCG TTGACACAGA 420  
10 AGTTACTTTC TGTATCTCTA TCAGTCTATC ACCGAAGGAC CCGTGGTGTG CTTTGCGCAT 480  
TTTCGGGTG TTCTTTAAGA TAGTTATCTG GTTGATCCTG CCAGTAGTCA TATGCTTGTC 540  
15 TCAAAGATTA AGCCATGCAT GTCTAAGTAT AAGCAATTTA TACAGTGAAA CTGCGAATGG 600  
CTCATTAAAT CAGTTATCGT TTATTGATA GTTCTTTTAC TACATGGATA TCTGTGGTAA 660  
20 TTCTAGAGCT AATACATGCT TAAAATCTCG ACCTTTGTGA AGAGAT 706

(2) INFORMATION FOR SEQ ID NO:815:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 699 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1519RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

45 GATCAGACTG AACCATATA TCAGCGAGGT ATGGTACGAT TTGGGCACTT TGTATGAGAC 60  
ATGCAACAAT CAGCTCAGCG ATGCCCTGGA TGCATATAAA CAAGCTGTTT GCTTAGATCC 120  
50 GAATAACGTC CACATAAGGG AGAGACTAGA GGCTTTGACT GCCAGCTAG CCAACCCAGG 180  
GGCCCAGCAG CTTAGCAGC AGCCTCAACA GCAACAGATG CAACAGCCTA GAGGGCCAGC 240  
55 ACCCATTTATG TTGCAGCCAA CATTGCAGCA GCAAGACCAA ACAAATCCGT TGAATAACAA 300

ACCTGCGTTC TACCGGTCTT CTCCCCACGG AGTTGCGGTT GCGGGAACAG AGTCCGCAGG 360  
 5 CCACACACCA ATGTCAGGAC GGCTCAGCC GTTGCAGCAG TTGAACAATA ACGGAAGTAT 420  
 CCTGGAACCG TCATTGTGTG CGCAAAGAG GCCTATGGAG GGTGGAATGG ATACATTGGT 480  
 10 AAATGCCATT TCGCAGCAGG AGTTGCAGCA ACATCAGAAG AACATATGC CTTCTCAGAA 540  
 CCATCCTAGT TTGGCCCTGG CTACAGGACA GCGCAGCAG TTACCACCCG ATGCGGCTCC 600  
 15 CATAATACCG CCGGAAAAGA AAGGTGCGGC TCTCCCCCAG TTTCAGAAAA CTGAACCAGA 660  
 GCATGCGGCA AAAAGACTGA AGCCCGAGCA GAATAACGT 699

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1519UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GATCAGGTAT CGGCCAACAT ATCGGTCCTG TCGATAGCGT CGAAGATTAT CGTGATAGAT 60  
 45 ATAGACTATG AAGTGACGGA CGGCAAGGTG ATCGATGTTA AGCTGGTGCT GGCAAGCAAC 120  
 TTGACAAGT TTGACTACTT CAATGGGAG GCGAACATCC TGCAACGGTC ACTTACCAAG 180  
 50 TATAGCGACC TGCACGAGTT CCACCACAAC CTGAAGTTCT TAACCTACT CGACGGGTGC 240  
 TCAAGCATCG ATATCGAGTC CAATGTGTG CAATTGATT TGTTCAGTA TTAATCGATG 300  
 55 CTGCCGCGT ACATGCAGAG CTACCTGGAC GACAATGGCG CGCAGCTCAC GGTGCAGACG 360

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AACCTGAACG ACCGTTTTGG GATCTACTTG CTGACCAATT CCGAAAAGAA GGTCGCCAAG 420  
 CTGACATTTG CCGCTACGCA GGACCOGAAC CAGCGGTATT ACGAATACAA ATACTOGAGC 480  
 GAAACGAAGG AGTGGATCAA CCAGTCGGCC GAGTCCTATA CGACCGGCAT CACGCTGGTG 540  
 TTCGAACTTC TCGGTGACCC TCCGACGTAC CTGCTAAGG ATAGTTTGCC GCCAGAACAC 600  
 CCTGATGAGG GCTTCACGAG TGCTTCGGG TCCGAGCTGC AGCGCCGCTT TGCATTCAAG 660  
 TGTCAAATC CACGAGTCAC CCTCGTAAAT GACTTC 696

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1520RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GATCTTCTGG ACGCTTTCTT TGAGTTGGTT CATCTTGCCA AGCAGTGA CGTTGGGGTT 60  
 GCCCGCAAAA GAGTTGAGCA TCGGCCAAG GCGGCTGCA ATGGCGCAA ACTTGTCTAG 120  
 CACCTTCGTG AGCGTAGTTG GGAGCTGCAA AAAGCGCAAC GTATGGCCCG TGGGCGCGGT 180  
 GTCAAAGATC ACCGTGTGGA AGTCTCGCC GTGCGCTGC TCTGCTTCT TGATGTGTTT 240  
 CATCACCTCC ATGAACGAAA GCGCTCGTC GATGCGCGA ATGACCCCG TGAGATCTGC 300  
 GAGTGGCGCG CCTGTAGCA AGCCGAGAG CCGTCATCA TCGCGCGGT TCGGATGCG 360  
 CATGTGTTT ACGTCTTCA ACGCGCGGA AGGTGCGATT TCATACAG ACAAGTTGTC 420

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CATGCCCCGTC ACCTTGCGCG CGTCCTTCCC AACCTTCTCG TTGAACGCAT CGCTAAGGTT 480  
 5 ATGCGCAGGA TCCGTGAGAG TCAAAAGAAA CTGCTTAGTG GGCTGGGCAA GCGCCATCTG 540  
 GATGGCAATG GAGCACGAAG ACGTGGTCTT GCGCACACCG CCCTTCCCGC CGACGAAAAT 600  
 10 CCACTTGIGT GTTGTAAGT TGATCAACGA GCGCAAAGAG GCCTCTGGTG TAATATCAGT 660  
 CATGGTTGGT GTACCGCGTG AATCTGAGAG TGCAGGCGAT CTGAGATCTT 710

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1520UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GATCAAACAG TAATGACTTT GTTAACGGTT TTGAAGTACT GCACGAGCTG CGACTCCTCA 60  
 40 CTGCCCCTGTG GCGCCACAAG CGCCGAAATC ACAGCAACTT CGCTTTCAA CTGAATGGCC 120  
 TCCTGCATGT TCCGTGGGAA CCCAAGTAGC ACGACGCTGT CCCCAGCCTG GCACACCTCC 180  
 45 TTCAGATAGC GCGCCATCAA CGCAACCAGC GCACCCCTGG GCAGGTGCGC CGAGTAGTCA 240  
 TCGCCATGCA CAGCATGCAA CTCCTCTAAT AGCGGTGGT ATTTGTCTGT CTGTCGGTG 300  
 50 CGGAACCGCT CCAGCGCCTG CTGCACGGT ACGGCGCGGG CCCCCGCTG CCGCCGGATC 360  
 TTCTCTACGG GCACATCGC AAGCACCGCC AGCACCTCCA GTCATCTGG CTTGAACACC 420  
 55 GTCAACCGCC GCTCAGGC GGAGCGGACC TTCTCGAAT CCGCTTCGCT GAACTCTGTC 480

TGCGGCTTGC TCGGTCAAT CGACTTCGCC GCGTCACGA AGATGAGCGT GCTGACCACC 540  
 5 GCAACGCCAA CCATCTTCCA CCGCTAGGT AGATCTTCG AACCAGGGGC CTTGCTGGCG 600  
 TATGGCCGCA AAAGTCCTG CTGACGCCG AGAAGGAACA ATCTAGGCTT ACAAGTCTGC 660  
 10 GAAACATTTG TCCTGCGAGT TAGCC 685

## (2) INFORMATION FOR SEQ ID NO:819:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1521RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GATCGAATCT KGCTGAGGG TCTTCACGA WTTGCAATGC AATCTCCGA TATCCGGCCT 60  
 35 TCTGTAGATA CGAGATGATG TTCTGGCCCA CAAGGTGGA CGTACGAATG AGACGCAAGA 120  
 CTTCAGGGAA GTTCTGTTC ACCAAAGCTT TCTTAAAGCG GFACTCGGTT GGGTCAATGG 180  
 40 TCAATATCTC AATATCGCCG TCTCTGTTC AAGCATATAT ATGCTTGCCA TGAGCTTTGG 240  
 TAAATGTATAG GGTCTTGCTC AAAGTTTTTA TGATCCCGCT GTCACCAITC AATAGGCAGT 300  
 45 ACTWAATATG GTTCAAAGTA GACAAGAGCA GAACACCAGT TTCATCCAC GCGCTGACT 360  
 TGATCCTGAT CGTCTCATGG TTAGACGTAG TAATCTCCAA CTTCCTAGTA GCAATGGTCA 420  
 GCGTGTGTTT ACTCATTAAA GCAACGTATT GCCCATCTGG GGACCAGACT GCATATTTAA 480  
 55 CCATCTTCAG AGCTACCTCC GCCAATTTTT TCCCTGCTG CACGTGGAAC AAGACTACCG 540

CCTTTGGTTT CAAGATGAGT ACCGCACCAG GGCTCCATA GACAATGICT TTAACAGTTC 600  
 5 CTCTATCTT GATCGATTG GTTACCTTGT TGTCCAACC ACGTACTTCA AGAGATTCCG 660  
 ACGCAGAGTT GTAGACAGCG TTACCTATGC CGAGCGACAA AAGTCGCAA GCTTCCCTTA 720  
 10 TC 722

## (2) INFORMATION FOR SEQ ID NO:820:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1521UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

GATCCACTTC CCAGATTACA TGATAACATC GAAGCGAAG GTGCAAGGG AAATGTTGGA 60  
 35 GCAGTATGAC TTTATWCATA GCGGCTTCAT CAGCGTAGAC GCCAAATCAG AAAGCCTCAT 120  
 CTGGGCGATG CCGAAGAAGA CCACCGGCAG TTTGATCAGC TCATCGAAAG TTTTCCTATA 180  
 40 TGGCAGAGCA GCGTCACCA TGAAGACAAG CAGAGGCCCA GCGTCATCA CCGCAATTGT 240  
 ATTCAATGTC TCTACCCAGG ACGAGATAGA CTACGAGTTC GTGGGGAGCG AGCTCCATAC 300  
 45 TGTCAGAGC AACTACTACT ACCAGGGCGA GCTCAACCAC TOGAGAATGC GCGGCCATTTC 360  
 GCTACCCCTC AACAGCCACG AGGAGTACCA CATATAAGAG GTTGAATGGG ATGCCGAACG 420  
 50 CATCCACTGG ATGGTCGACG GCGAGATAGT GCGCACTTG TTCAAGCGCG ACACTGGGA 480  
 CCGGTCCAC AAAATATACA AGTATCCACA AACGCCCATG ATGCTCCAGA TTCCCTCTG 540  
 55

GCCCCGGGGC ACCCCCGATG CGCGGCAGGG CACCATC

577

5 (2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PAG1522RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GATCAAAAGC GAACAGGCA CTTATGTCCT GOCOAACCGA CGGTGCTCC TGAATACCCA	60
ACGAGCACTC CCTGGCCTGC TATCTGCGCG TATTCTGTCA GAACGATCGC CGCTAGAAAG	120
TTACCAAGCG CGTCACACCT GTATTCCCTG GCTTCTCTCT CGGCTTCTGA TGTGCTGGCA	180
AGTAGTTCTC CACGTTCTGC AGCTGCCACT GGAAACGTGC AAACCAAAAC AAACCTGACA	240
CCACTTCTGT CTCTCGATCG CGTCCAGCCT CCAGAACTCC CAGCGCACAG ATTTTGACTA	300
TAGCAACCCC CGCGACTAGC ACTCAAGAAC TTTCAATTTT CGCTTGAGCC CGACCTTGTT	360
TTTGAAGAT TCTGACCTAT CCTCCTATCG ACGTCAGGGA CACAAATCAC ACTATAGTAC	420
CTCGAACAAC AGTACAGAAA AGAAAACCAG CTGCTCCAGC CAAAATTCAC AAGTCCCGTT	480
AGCTGCTAAG GCCAATTGGT GATACTCAGT CTTTAATCTT TACCCAATTG GGAAACTTCA	540
CCAAGGAGAG TCTTGGCTCT TAAGGTTTGG CAGTTTGGTT TAAAAATTTT CTTGCACGAA	600
ATGTCAGAAT GTCTGGGTTC CCTTGTCTGG TCACGTGGGT GTGGTCAAG TGGGTGCTAA	660
TCACGTGACA CGTGGATGAC GACTGAGGCG GAAAATTTGC AGGTT	705



## (2) INFORMATION FOR SEQ ID NO:822:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1522UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

GATCGACAAT ATTCCCCAC CAGGCGCAAG AATCGAGTGC ACACAGGCCA CGCGCGCATC 60  
CGGGCTCGGA TOGGCGGGGC TGGGCTGCAG TGGGCGGCTG GGGGGCGAAG CACACTACCA 120  
CAGTGTGCTG TGGTGGGGG GGGACGCCAC GCCGCGCAGC TGCGGGCTGC ATTCCAGCCA 180  
CGCATGCAAG AAGAGCGGGG TGACACTGCC ACCGCTGGCG TGGCTGCTGC AGTCCAGGG 240  
CTACATGGGG TTCAACAACG AGCCGCGGGC CGTCAAGCGC TCGTGTCTAG GGGCGACACA 300  
TCCGAAGGC CATTACGGCA GGGACATGCT GAGCAGCGCG GTGGGGCAGC CCGGTGTGTA 360  
CGTGGGGGCG CAGAGCCCGT TGCTACCGCT GGGCGACGCG ATTGGCGCGG CGCTCCCAAC 420  
CAAGCCATCG CATCGCTGG TGGGGGGAA CGCGCAGCTG CGCGGGCAG TGCTGCCCAT 480  
CGTGGGGGCC GCGGGGTCCC AGGCTACGAA ACGAACAAGA CATGCTCTGT TTGTGGCAGA 540  
CGATGTACCC GTCCAGCAC GCTCAAGAAC ACATGCTCAT CCACACGGGC GAACTGCTTT 600  
TCAGTGCAGT TGGCCCGGGT GCTCCAAGCG GTTCAACGTC AGGAGCAATA TGAACCGACA 660  
TGTAAGTCC CACAAGCGCC CGCTGATGAA GGAAAGCAAG AAGAAATCCA GTTCTCCC 718

## (2) INFORMATION FOR SEQ ID NO:823:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1523RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GATCTTATCT AAACCGCTCC GCGATGATGC TTTGGTAGCA ACGGAAGCCC GCATTTCAAA 60  
GTCAACATCA GCGGAAGCTT GGATAGATGA GAAAATCACA GGTGTACAT GCGCGAGAG 120  
CTGAATTGGA TTCACCGCTT TGCTATCAST GGGIWAGAGG CGTTCACITGG GCTGTTCTGA 180  
ATTTGAACTT CTGGAGCTAT WCGAGGGGTT ATGAGCAAGT CCAAGTTCCC GCGTGAAGAG 240  
CTGATCCTGG TAATACTCGG TGTAAATCCAC GCTTTTCTGC CAGCAAAAAG CTGGCGAGTT 300  
TGGAATCTTT CCTTTATCGG CGACGTCOGT GCGTACATGG CGTTCAATGG TATTTGCTGA 360  
TGTAAGTGTG GGGAGAAGTC GTAGGGAATG TCTAGATAAG GTTGACGCTG AAAAGCTATT 420  
ACGTTGCAAT AGCTGCGGTT GAGAATGGTG TACTTGGGCA CAGCAACCTG CTGCGCTGCA 480  
TCTGGGTGAG CTATTAAAAA TCTCGGCCAC CGAATAGAAG AGCATCTTTG GGTGAGCGCG 540  
ATTCAGTTCC ATGAGATCAA CAAAGGATAA AATCGGAGG TTATCAAGGG AGAATTGTGT 600  
ATCATAAAG AGCCAATCAT CACTGCAGTT GGCATATTTT GGATTATTGT GATATTGCCT 660  
CACAGCAGTG TTTATCCGGT CTTTTTGGCA GTCATATACC ACAATGGATT GT 712

## (2) INFORMATION FOR SEQ ID NO:824:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 649 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1523UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

20	GATCGACAGA ATGAGCAGAG CCATTCTGAG AAAGCAAACA CGGCCCATTG CGTTTCTGGG	60
	ATCCCTGCCA CAGAGCGAAA TGGGCCCAGA AGGTTTGTAC TCGCGATCA AGGATCATCT	120
25	GGCCTTAGCG CCATGCGACG TAGTAAAAGG ATGGCATGGA TGCTGGTCGG AAATGCGGTG	180
	CGACTGGCGC AAGACATGGA TTTTATCAAC ACCAGCTCCA AGATATTCTG CCAACACAC	240
30	ACTTCGGAGA CGAATTGCGC AATGAACATG GGTGAGAACA GTACATTATC CCATTCTCTG	300
	ATGAACGCAA ATATTATAGG CTCAGAGTCA AGCAGGGCCA TTAGCAATCC ACCTATGCCA	360
35	TCTGAAACTG AGGAACGTTA CAAAAGTGTT TTACAGAGAC TCGGTAAACA TGTCCCTCGG	420
	GGTAGAGGCC TATCTCAGCT TTATAATGAG TTTTGGAGG ACGAGGCGAT CCTCTACGGC	480
40	TTAGGTGGTG GAAGTGAATA TGTTGAAGCA TACTGCGATA GTTTGGATCA AACAAAAAAC	540
	AATGTGAGCA TCGAGACTGC GTATGAATCT TCTTTGCTAG AGCGCGGGGG CCAGCAGGTT	600
45	TTTCTGTCTT TCGCCCAACG CCGAAGATA GAGCTACTGA GGATCATGT	649

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1524RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

5	GATCTTTTGA AACAAGTGAA TTTCTGGAAA TCGAAGTGGC GTGACTTGGA CAAAATTAAAG	60
10	CAGGACTTAC TGGCCAACAT GCGACGAAA GAGACGGACT TCAACAATCG ATGCACCGAC	120
15	TATGAACGTA ATATAGTTGA ACTTCAGCGT CAACTATCAG AAAAGTGGCA CGCTACAAAC	180
20	GAAAGCTCTG TCACTTCAAC CTCTGCGGAT GTACCTGGAG AAACCAAAGA ATATATTGAG	240
25	TCTCTCAAGG AAGTCAACCG TAGACTGGAA GAAGATATGT TTGCTGTTTT TGCGGGGAAC	300
30	ATAGTGTAC TGGAGAACAT CGGCCTGCTT CTTTCTAGAG GGCCTGACAA CAAGTTACAG	360
35	ATTATACGCG TTAAAGGTTT AAGGAAAAAC ATAGATGATA GTATAATAAA GGACAGCAGC	420
40	CCTGTAATAA ATTCACATAT GGTGAAGAGC ACAGTTTCC AGGATGTGAA GAACTTATTT	480
45	GACGAGCTTC AACTGAGCCA AGGTGTTAAC GACCAACTCC ATTTTGTGTAG TGAGCTGGAA	540
50	CGCTTTTATG AAGAGGATCT ATTTCOAAT TCCGTGATCA AGAGGTTTAC CGATGTAGAG	600
55	AACCTGGCTA AGAGCTCAGA AAGGAAAATA AGGCTAAAAA AAGCGTATTG AAAGACACCA	660

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1524UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

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10  GATCTATCGA AAGTGTGAAG CTCTAGACA AGTTGTCCA TCCAAAAC GGGAGAACCT    60
    CTTTGTGCTA CCGTATCAAC TACCACTCCA TGGACAAGAC TGTTACCAAT GCGAGGTCA    120
15  ATGTCTTACA AGAGCAGGTC AGTCGGGAC TAGTCAGGCT TTACAACGTT CAATTGAGAT    180
    AGCCCAATCA GCGGAGACT AATAAACTTG TATATACAGC TTTGGGACA TCGACCCAT    240
20  GTAACGTATA GTATGATATC TGCTTACTCA TATGCACCT GAATGCTAGC AGACTTCGAG    300
    AAATGCCITTA ATACGCAGCA TATCGATAA CTAGTGCTTA AAGCCAAGTT CTTCGATCTT    360
25  CACAGCTAAC CGTTTTCTTT TGCTCTGAT GGCAGCTACA AGAATAGCAA TCCTTTATGG    420
    ATCTGAAACC GGTACTGCAC AGGATTTCGC TAATATACTG TCCCAACAAC TACGTGTTTT    480
30  TCATTACAAG CATACGGTGT GCTCTATTGG AGAATATAGT GCCAGAATA TCCTGCGATG    540
    TCAGTACCTA TTTGTCATTT GCTCCACCAC CGGCGAGGCT GCGCTGCGGC AAAATGCGCG    600
35  GCAGTCTCCG CAGGCAAG TGGAAGGTAC ACCATGGAGT GTGCTCAAAA GAAGCTCTCT    660
    CCCACCAACT C    671

```

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1525RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

5	GATCTTCTCT CGCTGGAAC TGGTATGCGT CCAAAATTTT AACTTAACAA TTTTTCACCT	60
	TGACCTCGCC AAGCATCTAT ATCAGTGAT TCATCTGAC CAACCTCATC CCAAATGCAG	120
10	GCCATTGGCT GCTGCAITTA CGGCTCAGT GCCCGCTAG AGAACTAGCG TTACGCTTTG	180
	GGGTITACTA GCAAGTGGC GTGCGTGGG ATTCGCAATG TGGGCGGCA CCTTATCCAC	240
15	GCGACACAGA AGTGGGTATT TCGCTTGT TACATAGATG TCCAAAACA GTACGCGCAA	300
	AGCACCAAGC AAGCTTCAGC AAGACTCAGG GAGGTGTTAG AGGCGATAAT CCAATCTGTG	360
20	CTGAATGGAG CAGGCGACGG GACCAAAGTG GATATTTGCA GGCGAAAGTG AGACGATGGC	420
	AGCGCAAGAG GGCAATGGAG TAAACGGGCA CCTGGACGGC GGCATGCAGA AGACGTTCAA	480
25	CCCCGTCAAG CCGCTGGA CTAACTGAA TTTGGCGGTT TACCGGGCA AGGCGGGCT	540
	CGGGGAGACC CTGAATGGC GCGCGCGGG GCAAAAGCTC AGGCTGGAG GAGGAGACAG	600
30	ATAGCGAAGC GAGCGGAGC TCCAGCGGG GCGGGGGAG TGCAGACAG TCTAGTCTGG	660
	AGCCCCCGAA GGTGGACCG TCGTTGACG CTGGCGGCT GAAGTCGTG CC	712

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1525UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

5	GATCATCGCG ATTTTCGGTG GCGTTGATGA GAAAGGCCCT CACTTATACA TGCTTGAACC	60
	AAGTGGGGCT TACTGGGGTT ATAGAGGAGC CGCTGCCGGA AAGGGCAGAC MAGCCGCTAA	120
10	AGCGGAGCTG GAGAACTGA TTGGGAACGA TAAGTCAGAG CTGTCAGCTA GCGATGCACT	180
	GAAAGAAGCG GCTCGGATCA TCTAAGTGGC CCATGAGGAT AATAAGGAGA AAGAATTGGA	240
15	AATTGAGCTG AGCTGGTGCT CCGCTTCGGA GACGGATGGC TTGCACAAGG AGGTACCAAA	300
	AGAGCTATTT GATGCAGCGA TTGAGTTTGC GAAGAAGGAG ACGGTCAGG AGAGTGATGA	360
20	TGATTCAAGC GATGACAACG CATCTGGAGG TGAAGAGTCC TCAACAAAGA AGGATGCTGA	420
	CGGTCATGTC CAGCTTTCAT GATAACAGCC CGGCATTATG TGGAGGTTCA TTTCATGACA	480
25	ATTGACGGAT GTTACTAAGT GTATATTAAG TTAATCCACC TATATAAATT AATAACATGC	540
	AAAGCAATTT AGAATTTGTC GGAAAGCAGG TTAAGCATG TCTACTCTCC TTAATCTTTC	600
30	GCGAAGCTGT ACATTTTCTT CTCAAGTGAA CGAATTCCTAT CCACCGGCTG CGTCTGATTC	660
	TAATTTCTTA CGTTCGGGTT CTGTGTACCA TTTCGGGTC AGC	703

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 725 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: single   |
|    | (D) TOPOLOGY: linear       |

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- |    |                         |
|----|-------------------------|
| 50 | (A) ORGANISM: PAG1526RP |
|----|-------------------------|

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

EP 0 866 129 A2

	GATCTGGCCG CGACCTTGAG AGGCGTCTGT ACCTTCCTTC AGCACAACCTA TTGTGGGAGC	60
5	TTGGTTTCCA AAGTTCATCC TGAGCTCGGT GGTGCTTCAG ATATGGTGGG TGATGGCCTC	120
	GTCACGGTCT GTCAGCTTCC TGTACCGACG ATGACGGCAG TTTTGGCCAC TAGGCCATTT	180
10	TTTTTTTCAG CTCTAAGATG GCAGACGGCA AGGAGAATGC TCCAGGACAC CGGATAGAGC	240
	TCCAATCTCA GCAAAACATC GCCTACTGGC CCATTGCTGC TGCTGCATAA CACTTCTATG	300
15	GCCTAGTTTG TGACGTGGT CGGCGCTTCA CATTGTATCT CGTGAATTGC GTACCGGTAC	360
	TATATTACGG TTGTGTGGCC GAGCGGTCTA AGGCGCTGA TTCAAGTGTA TGCTTACAGC	420
20	TGTTACACAGC TGAACACTCA GGTATCGTAA GATGCAGGAG TTGGAATCTC CTGCAACCA	480
	ATATTTTTCG GGGCGTTTTT GGGCGCCAG CGAACTGAA CCGCACACTA TTTCGTGGTA	540
25	CCGTTGGAGG TAAACTGTTG GAATCCGACA GTGGGTACC GAAACCATCC CAGCCTCTTA	600
	TTACTAAGCT GGATCGTGCA CTGCAAGCG TGATATTGGA ATGTTCCCA CGTATTATTA	660
30	CTAAGCCGCC ATCTTCCCGG CCATGAGGAG GTTACCGAAA ACCAATCCCC AATTTCATT	720
	ACTAA	725

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1526UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:



EP 0 866 129 A2

5 GATCGTCACC AGGTCCCGGG TCTTGGGGAA CGTCTTGCCA TGCGCTGGCG ACAGTCTGTC 60  
 GATCTTCACG TTACCTTGA TTACCTCOGA CATGCTCGTT GCTGCTCCCG TGCGTGCCCG 120  
 AGAGTGATCA AGTGGGTGTT ATTAAGGCC CCAACGCCAC CCGCTGGCC GGGTAACACG 180  
 10 TGCCCCGGCG CTCGCCCCGG TGGGGCTGTG CGGCCCGGCC GCCCCATGCA CCGGCACGGC 240  
 GGCCGGTGCA CCGCGTGCGC GCACTTTTGG CCGGCCCGGG CCGCCACTGC CCGAAGCGGT 300  
 15 AAAGTTAGTA CGCAACCGCC CAGCGCCCGT CATAGCATAC GGACGCCAGA CCGGGTAAGG 360  
 CCGTAGCCCA GTCGGGAATG CCGGCACGAT ACCTCTTTAG GCAGGATACT ATTTTAAGGC 420  
 20 GTACAGGGCG GCAGCCCATC GTGCAGGCTG CAGTAGCAAG CTGAGACAGG CTGGGCAAGT 480  
 CTAGACCTGG GACACAGCCC GCAACCTAGA GGCCCGGGTG GCGCGAGGC GTCAGACATT 540  
 25 TTGGGTGCGA GGGCGGTGG CAGCAGGACA AAGAGCCCG AGAGAAGCAA ATGCMCAACT 600  
 AAACGGGGAG GAAGGGCAGC GGATTTCTTT TTGGGCTTCT GTGCGAGGTG GAAATTGTAT 660  
 30 AAATAATGGG AGCGCGGCT GGTCTTGGCG GCTGAGACTG T 701

(2) INFORMATION FOR SEQ ID NO:831:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 705 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1527RP

50  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

55 GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GCGCCTTTTC 60

CAATATTTTGG AGCGTCGTGT CATAGCTCGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT 120  
 5 CTGTTTCATGT TCGCTCATGA AAGGTGTCTC TATCAAATCT AGCTCCATCA TCGCAGAGTA 180  
 GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTGTCAGGA TTACAGTAAA 240  
 10 ATAATGGTAG AACCGGGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCGTA 300  
 GAAGATCGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TCGGAAAGTC TGTTCACGGG 360  
 15 GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT 420  
 CCGCGCGAGC TCAGTCTCAA GCTCGTCGAT CCGTCGCAGC AGCTCCACAT TGGGCGTGA 480  
 20 GCTGAACAGC TCCCGTGAGT TCACGTCGTG CGTAAACTCA GACAGGTACA CACACTCGGG 540  
 CAGGCCCTTC CCAATACATG TATAGCACTT CGGCCGCGCC TTGTTGCACT TGACGCGCCG 600  
 25 CTTGCGGCAG AACACGCAAG ACTTGCTGAC CTTCCGCTTG GTTTTCACAA TCTTGCCATC 660  
 GGACTCTGCC ATCCCGCCAG CTTCAAGCAA AATGATTAGG CTATA 705

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1527UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GATCGCGGAC GTGGAGCACT GGCCGGAGAT GCGCGCGGCC ATCCTGGTGG TTTCTGCGGA 60  
 55 CCGCAAGGAC ACGCCATCGA CGAGCGGTAT GCAGCAGAGG GTGCACACGT CGGACCTCTT 120

CAAGGAGGCG GTCCGGACGG TGGTGCCGCG GCGGTACGGA AAGATGGGGG CCGCGATCCG 180  
 5 CCGCGCGGAC TTCCGGACGT TTCCGGCGCT GACGATGCAG GACTCGAACT CGTTTCACGC 240  
 CACCTGCGTG GACTCATTTC CGCCGATCTT CTACATGAAC GACACTTCGC GCGGATTGT 300  
 10 CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATCGTGGCGT ACACGTTTGA 360  
 CCGGGGTCCG AACCGGCTGC TCTATTACTT GCGGAGAAC GAGGCGGGC TCTCGGCTT 420  
 15 CCTCTCTGCC GTCTTTGGCG CCAACGACGG CTGGGAGACC ACGTTCTCGA CGGAGCAGCG 480  
 CGCCACCTTC GCGCGCAGT TCGACGAGTG CGTGCGGGC AAGCTTCGGA CGGACCTGGA 540  
 20 CGACGAGITG CACAGAGGAG TTGCCCCGCT CATCTTCACG AAAGGTGGG CCAAGGCCCC 600  
 AGGACACTAA ATCTCGCTC ATCGACCCCG AGACGGGCTT GCGCGTGAC GCTATTCTCC 660  
 25 TGCTATTTTC TGCTCTGTAT ACCCTGCCAG AACCGGCTAT ATATATAGAA TATGCATT 718

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 701 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1528RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

50 GATCACTGTA TCGAATTTGA CACCCAAGGA AGCCAAAACA TCGTGGGGG ATCCCGACAA 60  
 TGTGGAACAT ATGATATCGC TTTCTGCAAG GATGCGTGCC TGAGCTTTCC TCTTATCAA 120  
 55 TTCTCTATTT CTATAATTCA CGCATTCCT TTCCCTCAGC TCATCGCGCT GCTTAOCTAG 180

CTCATTAATC TTCTTGCTCA AGTCCCTCAA CTTTAGCTGT ATCTTAGATA TCTCATCAGT 240  
 5 TGAGAGTTTA CTAGTCGGCG AACCATCCTC TTTATTCATC ATATCCCTGA GCTTTCTCCT 300  
 CTCGCTACG GCGTCATGAA AACTCTGATC TAAGTTCGGA TCGTGATTTA TTTCGTACGA 360  
 10 CTGATTCAAA GCTCGCTTGT CAACCAGCTC TTCCAACGTT AGGTCTCTGA TAGCAGCGTT 420  
 AACTGCATCT GATTTACCAA TCCGCACTAA TTTTGGTTTG AACAACTTGC CGTCAGTATC 480  
 15 GACCAAACCT TCTCTCAGAC GCAACACAAG CTCGTCAACG GCTGCATTAC TGGGTGCACA 540  
 TATCAGAACT TTTTGTCTCT GTAGTAACAT CTCAGTAGAG GTAGCGTTCG ATTCTGTGGG 600  
 20 ATTTCTGATA ACATTGATG GTAGTCTTTT TCGGCTAGTT AGGAAAAAGC CGACGACACC 660  
 AAGAATAGTC TTAGTCTTAC CAGTACCAGG GGGTCCCTGG A 701

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1528UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GATCCAGCAT TTCCGGGTAA ATCGCGGTAT TCCGCACCG AAGGTGGGAA GCTTCAACGA 60  
 50 GTTGATCTGC ATGTGGGGGG CGCAGATGGT TCTTCCACTG CTGCGAGACT TTGATGCCTG 120  
 CAAAGTATCA GATGCTGTTA TTCTGGCGAT GTATGAGATA CTGCTGAATC CGCAGATGCT 180  
 55 CCGGTGCTCG CCGGAAGTCA AGTACTACTA TGATCTAGCA TTCAAGGGCA TGTATGAGAC 240

GGGACATGAG CTTTITAGACC ACACAAAAGA ACAAGGTATC AATCTGCTCG TACCTGGAGT 300  
 5 CGTATATTCA CAGATGTACG GCTGCCCTGA ACAGAGTTCT TGGGCAACAC GTCTCTTGCG 360  
 GCACTTCTTC GAGAACGAAT ACTCAATCAC AAATGAAAAC GTGACAACCG AACTGCTTGA 420  
 10 CGAAATCACC TATCATTTTA TTCAGTTACA GTTGAGCAGG AGCAACAGCT CGTATTTGAG 480  
 CATGATTGGA CTATTCTGGA GCAAGATGTG CCGTTCTTT GCGCTGATGC ATGTTGATGT 540  
 15 CTTAAAGGAG TACTTTATTG AGCTCAAGAA TATTAAGTCA TTGCGGTCCA CGACTAATGT 600  
 TCATATTGAA TCTGTTTICA AGGTATTTTA TCACCATCTC ATAATGCAGG TAAGATCAAA 660  
 20 ACCGTTGGAT ATTCTGCTCC GTATTTTGAA ATTATCCTGG AAAAACTAGG G 711

## (2) INFORMATION FOR SEQ ID NO:835:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1529RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

45 GATCAAAAAG AAGGCGATTG CTATGGCGAC GGTGACTGCT GCTACCGGCG TCTACGCTCT 60  
 ATATCCTTCC TCTCGATGT TGGTTGACAG CTCGCGTTG ATCAAGCTAG AAGGCACCAT 120  
 50 TTCTCTCAGT AGCAAAGGTG CTAATAATGA TACTGATGTT TTCATATTAC CAGAAAAACA 180  
 TTCTGCTGTT CCGGGCTACA ACACAATCAT TCGTTTCTC GTACCGGCGA TGAATGCCCT 240  
 55 CAGGCTTTAT GGCAGGCCGA AAACACTATC GCGAGCAAG GATGACACAA ACTCACTCCT 300

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GTTTAGTCTA CCAGCGCTTC CACATGTGCA CTACTTGCTG GTCTAGGATT TGCTTCCATT 360  
 5 AGTGAATTCA GCGTCTGGCT CATGGAAGAC GCAGGAGTGG CGGAGACAAA TCAAGGCTCT 420  
 ATTACAACGG AGGGTAGCGG CTGGCTATCA GGGATGTGGT TCAAGCTCCG GTCTATCCGG 480  
 10 CGCTCTGTCC TCCCTGTCTC TGGGTCCATT GAGTCTACT TCTTTGTCAT CGCCGCATTT 540  
 TGCTCCGTCC ATTGGGTTTT CGCTACTGA GTCCAACTAC ACTTTTATGT CAAGTCACTC 600  
 15 AAGAATAACT TCACTACATG ATAATATCCA GAGACCATAT TGAATACCGT GGCCAGCACA 660  
 TCCGATAATA CWTGCAACC AAACAATATG CTATCTCCCG CAGGCTTGC CCTGATGCA 720  
 20 TT 722

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 691 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1529UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

45 GATCCCGCTC AATGCCAAGT AGAATGTTTC TGGGGGAGC CCATACAGTA CCGCTCTCTC 60  
 CTCATCCCG CTCTCTGCT CCACGTCTC TGTGCAACA TCTAGCAGTT TCCGATAAC 120  
 50 ACTGGGGATG GTCATGCTCA CGGCTCCGGA TATCACGATC AGCACCAAGG CGCATACTAG 180  
 AGACTTGAGC TCAGGCCGG CCAATTGGAA CAGTCTACGC ACATCCTTGG CACCTGATGC 240  
 55 GTTGCCCGTC GCGGTGACA GCTCGAGTCT TTCTTGGTGG GGTTTCTCTT CGTACTTGC 300

CCGAGGGTTT GCTGTTGAGT TTAGCCTCGT TTGAATTCCT GTGATGCGC TGAACGAAAA 360  
 5 GGGGTGCGT TGATGTAGAT GATTGAACGG CGGCCATCGC TGCATCCCA TAACAGGCCT 420  
 CGGCACCTGC TTAACAGCTA GCGATAGCCA CATATATGTT CTCTCGAGG TCATATTCCC 480  
 10 AGTTTCTTC TAACCTCACC AGCCTGTAG GCCTCTGAG TTGCTGTAA GTGGTGAATT 540  
 TCGCATCGG ACTCATTTTT CATGGAGAAT AAATAATTGT ATTACAAAT AGAGATGCAT 600  
 15 GCCAGCTAG TCGAGGCCAG CTAATAACA GCTCTGGAG CTTTGCAGT GTAGCGCAC 660  
 GTTTTGGC TCATGTGAC TACAACATTT T 691

20 (2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1530RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

40 GATCCCTCTG CTACAAACAC ATACCTAGAT TTTCATATT TTATACTGAA TACATATAAT 60  
 ATATCATTTA ACTGTCTTCA TTCATGAGAC GTGCTCTAAG TTCTGTGCTG CTCAACTTGT 120  
 45 TTTTCCACTT GTCAGCCTCT TCGCCCCCA GTAGGTTTAC CACATGCAGG GCTAGCTTCC 180  
 TCATTCCTTT GCTCTCAGC GTATCGTTGA TTGTCTGGC ACGGCCACA GTTTCTTCAC 240  
 50 TCACTACCAG GGCTTCGATA CCAGGTTGCG TACCCGTGGG CCGGCACAG TCATGTAAG 300  
 CAAATATTTT GATTTCAGC CCGGTTTCA GCGTGTGAAG GAAGCTGCAC AGTTATCGC 360  
 55

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ATCGTTGCTC GAAGGACTGA AGCTGCTCCC TGTATTTCCT GTTCGGCAGC AGTTCTTCAT 420  
 5 CTGTAATCCC CACGATCAGC CGGGACGCAG TCACGAGCGC GGCAACACTG AGCAATATTT 480  
 TATGTCCGTC GGTGAAGTGG TCGAAAGTGC CTCCAGCGC GCTAACAGCG TACTTGCTCTC 540  
 10 TACCGCCACT CTGACCGGG CCCGCAGCGG CCATCGCGG ACTATCAAAC AGCTCTATCT 600  
 GCCTGTGGG GAAAGCATCC TGCAGCAGG GATGCTCAG GAATACAACG TCCCACTTCA 660  
 15 TTGGCTGTA CGCTTCCATA CTGACGTGA ACAAACATT TATCGGGTCT GTGT 714

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1530UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GATCCTGGGA CGACATCGAC ACCATTCTTA TCGTAAAG ACTTGTAAC AACGGCCAGG 60  
 CGACCGTGGA CCAGATGGCT GGTACATGA AACTGCGG CAAGTGCTC GCTGAGGCGG 120  
 45 GCTACAAGGG CCAGTTGTT TCCGTGGACA CTTTCATGC TGTAAACAAC AACCTTGGTC 180  
 TATGTGACCT ATCAGACTAC ATGGCTGTCA AGCCCCACC ATACTTCGAC TTCCACACTT 240  
 50 CTGCTGCTAT GGCCGGCCCT TGGTTTTCG ACCAGATCCA GAGAGTCTGG AGCGCCTGCA 300  
 ACGGTAACAA GAAAGTTGTC ATCACCAGGA CCGGCTGGC TACTCAGGT CAGACTTACG 360  
 55 GCAAGGCCAT TCCATCCAAA GCCAACAGA AGATGGCTT GGAATCTATC AAGGCCACTT 420



GTGGTGATAG CGCTATCCTA TTTACTGCTT TCGACGACTA CTGGAAGCCA GATGGGGCTT 480  
 5 ACGGTGTGGA GAAGTTCTGG GGTATGCTAT AAGTTGCCGT GTGCTTCTTT ATGACCTGTC 540  
 TCTTTATTTT GCTCGGAACC CTTACATGCA GATGGGGGGT GCGGTGCAT GGGCCTGCAG 600  
 10 CCTCCGGGCC TGCAAGTTTC TACATGCCC TACTTTAGCT GCCACGGGAC TTTTGAATTT 660  
 CTTTGGCAGG TGGTACTGCT GGCATCCTTC TCATAGAACA CAGTGTGCC ACAGGG 716

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1531RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GATCTGCATC CTCGTGATGG AAAATACGGC CATGCAGCTA ATTTTGGAAT GGTTCCTGCA 60  
 40 TACCGTAAGA GAGATGGCTC CAAATCATAC CCAGTTACTA TCCTGTGAC TAACTTTTCA 120  
 AAGCCGACAC CTACCAGACC TGCTCTTCTG AAGTTGGGAG AACTCACAAC GTTCTTTCAT 180  
 45 GAGTTAGGCC ACGGCATACA CGATTGGTG GGTTCCAATG ACTTGGAGTC GCTCAACGGG 240  
 CCTGGGTCCTG TCCCATGGGA TTTCGTGAG GCGCCCTCTC AGATGCTGGA ATACTGGACG 300  
 50 GCACGGCGTG ACGTTTAAAC TATGTTATCC AAGCACTACG AGACAGGTGA GAAATCCCG 360  
 AAGTCGCTGC TGGATGCTG GTTTAGTGTT GCGGGCTCA ATTCAAGATT GGCCAACTTG 420  
 55 GGCCAACTGA AACTTGGCTT GTTCGACATG TATGTGCACA CCGCGATTGA CAAAGGAGCG 480

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GAGGTACCGA AATTATGGAA TGATCTCACC AGAGAGATCG GGCTCATGAA CTTAAAAAAC 540  
 5 TACACTAGCA CCGGCTATGA CTCCTTTTGA CATATTATGG CTGGATATGC TGCTGGCTAC 600  
 TATGGCTACC TTGTGTCOCA GGTMTTGTCT GCAGATATGT ACGACACAAA GTTCAAGCCC 660  
 10 AACCCATTCA ATGCTACGGT GGGTGTGGAA TACAGGGACA CTATTTTAGC TACCGGTGGA 720  
 CTT 723

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1531UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GATCCAATCC TGGAGGCGGG TTAAAGTGCT CCTCAATGCA GCGCAGCCGG CACTGGAGTA 60  
 TGGCACGGAA ATCGCACTCT GGAGGAGGCG CGTGGTTGGG AACTGGATCG TCCACCTCGC 120  
 40 GCAGAAAGGC CGTTTCGAAG GCGCAGGCGA GGACCGGAAT GAGCATTAAAT AAAGAGGTAA 180  
 CGTGCATGCT GTGAAGAGTT TCACTTTATG CGTTGCATTC CTCCCCCCT GAAGACGAAA 240  
 45 ACACGGCGCA CATGCGCTAT ATATACCCCT CGTGTCTACT ATTGTGCGCT GCGCGCTCTC 300  
 ATGTCAGTTT TTACTTTTGT ACCCGGGGAA CCGACATCT GCCACAAGC ACCAAGCCCC 360  
 50 AGTGACCAGC TCTATGCGC TTGCTCTGCC AATAACCAGC CCGCTACTAG CCGAGCATTT 420  
 TGCCTTAGTC CACCAGATAT TCAATGTATA TGSTTGCTCG CCAGCCTGG GCTGGGACAT 480

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AAAGATCGGA AGCTCCTGTG CAAACCTGCA CAGCGCGCCT TCGAGAATAC TCOGCAGGGA 540  
 5 CCCCCCTCC CATTAGTCCT TGGCAGTTTT TTGCTTTGTC CCGCGATAAT GTATCTAAAT 600  
 ACAGAATATC GATTACGGCG AATAGGCAAG TTTTGTGGTC TGACATGCCG AGTGTCAATT 660  
 10 CATGATTACA TAATGTGTGCG TGCCATATCT GT 692

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1532RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GATCTKTGA AAGAGTAACC AGGATCAAGC CTGCGGTATA GCCAGCGAA TATGCATATG 60  
 35 AAGTCTTTCT GCGTGGGCTG TTTCAATGAC TTCAGTGATA TCGCATGCC AGTTTCTATG 120  
 TCAAACCTGC GCGACTGCAG ATAATCAAAT ATCTCCTGCT GCAACACTGC CTGGTAGTTT 180  
 40 TTGTCACGGA GAGGTGCGG GTGCGGGTA CTCTGCAGCG CACCGTAAGC TGACGGACCC 240  
 CCGCCGGGAA CAATCGAAGG CCGCTGCGAA GATCGCAGAC TCCGCGGAG AGACTTTGCG 300  
 45 ACCTCGGGCA CAGGTCTTGA AAGAGAGCTC CCGCGTTCC GTGCCAGACT CTTGTTTATC 360  
 ATGTCCGTAA GAGCAGCGTT CGTGCCAGGT ACGCCCTTCT TGTTCGTGTT TCCACCAATT 420  
 50 GATGGAATTT GAGACGTGAA CCTCTGCGGA TTCAAGCTAT TGAGCACACC ATTGGCACCA 480  
 CTTGAGCCCC TTGCTCTGC CATCCCTAAT CGTCTATCC TACGGGGGCG TAATAAGTTA 540  
 55

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CTACCAGACT CTGGCCCTCA TCTGGGACTG ATGTTATCGT CTGCAGCCAG ATCCTGTTTG 600  
 5 TGACCCGATC GAAATCATCG AGTACGAATA ACCACGTGAC CATTATTCAC GTGATGAATT 660  
 TGGCGGTCC TGTTCGCGAC TCTTACTCCA GGTTAACCAT GACTAGATGG GCATACCTCA 720  
 10 GA 722

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1532UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GATCATCTGA ACGCTCATGA ACAGTTGCGG GAACATCGTG TOCAAGACTA TGCACTGCTG 60  
 35 GATGTCTTTC TGGCCGAAGT ACGCGGGTC CGGAGCAACA ATGTTGACCA GCTTAGCAAC 120  
 GACCGTGGCC ACACCGCGGA AGAAGCGTGG ACGGGTGGA CCTTCAGCA TCTGCTGAC 180  
 40 GCCAAGCACC GACACAAAG GCGCGGCTG CGCTGAGC TOCAGTGGG TGCGCGCGG 240  
 GTACATTTTC GGGGAGAGG GAGCAAAGAG CAGTCCACA CCGGCTCTT CCAGCAAGC 300  
 45 GCGATCGCT GCCAAGTCC TGGGATAGG GTCAAGATCT TGTTCGGG CAACTGGA 360  
 AGGGTTTACG AAGACTGAGA CAACAGTAA GTCGTTTTC GGCACGATC TCCGACGAG 420  
 CGTCATGTGT CCTCATGTA GGCAGCCAT CGTTGGCACA AACCAATCG TCTGTGCTT 480  
 55 GCAATCTACC GTCTGCTTC GCCATTGGA GACTTCCTG ACCTTATTGA GCAGTGCAT 540

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GAGGCGTATC GCTTTGATGG TTCAGCCTTC AAGTTTGTCR GTGTGCATCT CACAGATTAA 600

5 GGAAGCTTGC GCACACTAT 619

(2) INFORMATION FOR SEQ ID NO:843:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 564 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1533RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

30 GATCACGAAC TCCATCATTA CAAAGTCCAT CGCGTGGATA CGAAAACAAA ATGCACAGCC 60

GCTACCGACC TTCCGAAACC TCGAGAAGAT CAACCAGCCG CCAAGAAGCG CTGACCATGC 120

35 GTGGGAGTAC ATAAAATCGT GAATTATTGG GGTGTATGT ACTATATACT ATCGCTCTGC 180

CGCCCAATGA TGGTTACGCC TCTTGCACTG GCATTCCTGGG TGACGAGGTT GTCTCCGTAC 240

40 ACCTCTACTA TTTCCAGGTT GGGCGCACAT TCGCTGATAT GGGCGAGCAA TTTGTCGTCA 300

ACGCAGCGGA CGAACCTAC ATTCACTTGC TGCAAGTTTG GACAGGACAT TAGCTGGAAC 360

45 CCAGCTGCCG TCAGGTTCCT GGCTGAGTTC AAGTTTAGCT CTTTGAGGAA TTTGGAACAT 420

GGATTCAACC ATATCTCCGC AATTGATGCA TCATCCAGCT GATGGCAGCG CCTCAAGTTG 480

50 AGGTAGTGAA GTCGGGGAAG CTGGACCGAA GAGAAAAATG TAATGAATCC ATCGGACGTA 540

ACCTGGTCCA ATTCCTCTAG GGAT 564

55 (2) INFORMATION FOR SEQ ID NO:844:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1533UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

GATCCGGAGA CAGACGTGTA TCTGAGTTCT ACCGCTGGGC GCTGAAACGC ACGTCGTTAG	60
CGCACATCCT GTGTGCTTGC ACOGGGCCAG AGCAACCAAG TATTCTATA TTCGTGAAAA	120
CTGCGGTAAT AACCATGTAG AAGATTCCGC GCGGAATAC CGTTTACC CCAATATGTC	180
CGTCATGTGA GCTATTGGAT CGAAGAGTTT TTAATGACGT ATCCCTATC ATAAAGCGGT	240
GCTGGATTAT TGGAGCATGC ATCTGGTCA GCTGGGGGT GCCAATATA TGGTGCAAGA	300
AGAACTATC GTACCAACCC CGTCTGTCT GACCTGTGTC CTCTTAATCG GCATGACTAA	360
TATGGGGTAT CCTTAAACCC TTTAAGATGT TACCTCCGGT CTCAGGGCG GTTGTCTAGT	420
TTACAAGAGT AAATACCACC TTGCCCTGG GAGGGTTCTT ACTTTACAGT AGGAAAGAAT	480
CGATACCACT GGTGGGGGGA TTGGTATAT TTGAAAGAT GGATGGAATG GAGGGCTCCT	540
TATTGACAGC AAAGCCACTC CGACAGAATA CCCACCTT GGATTGGAA GCTGGGATC	600
GACAGACAT GGTACGTAA TCGAATTGTC CTGTGGGCC GCCCTCCGG TTAATCAAGA	660
AGAACAACCG CGGGCACGC AGGGAATAT TGAATTCAGT GCTGCCAAGC CTAATTTATG	720

## (2) INFORMATION FOR SEQ ID NO:845:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1534RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GATCCACATT GGAATATGGG TATGGGACTT GATGGTGA ACGCTTGGCTT CAACCACTGC 60  
AACATTGGCA AACCGTTTGA AGTCTGGAT GATTTTCTCC TTCTGGATCG CAGTCAAGAT 120  
GTGGCCGAAT CGTTTTTCTG TGTATAGGOC TTGCTCATCC TGTGCTTCAT CCTCATCAGA 180  
CGCTAATGGA ACGTCTGGCA CAATCTCGAC GCCATCGCAG GATGCGATAC TCAAGGTATT 240  
GAGCATGTTT AAGGCATGTT CCTTGTCTAC TTAAACCCCT GCATCAACTT CCTCTCTGTT 300  
TTTCCATAGG CGAGGGACAT CGTTTGTATC GTAACGAAAC TTAATTTCAA AGCGTTCTCT 360  
CAGTATAGAA ACCACATTGT CTCTCTTCAA ATACTGGTGG ATAATATCAT ACAGAATAGT 420  
CCATGCATTT GACCGGATCT TCAGGTATAA AGCATAATTG TCCTCTCTGA TGAGGTGAG 480  
CTGGAAGTCG TAAGCGGTAC TTTCATCGGT GACATCCCTT AAATTGGGTA GTTTATACTT 540  
TAGAACTGAA CGGCGGAAAA CATCATCAAA GTGGTCCATA ACAAGTTGCC AGACGTTATC 600  
CTGTGGATGG GAGAGTAAGT GGACAATATC GTCTCTAGTA TGTGTGAATT GGTACTTTTT 660  
CGCCCTCAAT ATAATAGCTT TCATCTCTTT ACCACGCTCT CTTTCCGCTA GTTCACTATC 720  
TTCTCCA 727

## (2) INFORMATION FOR SEQ ID NO:846:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1534UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GATCAGCGTG GACTTGATCA TGGTGTGTCT CGTCCGCGCG TTGTTAGGC GGGGACGCT 60  
 GCTGCTGTCC TTTGTGGGC CCGCGGGGC GGCGATCAA GATCGCGAC CACGGTCGC 120  
 GCGGGGGGG CTCAAGACA CACGCGACA GCAGCGGCG CGTCCGGGC AATGCAGGC 180  
 GCACAGCTAT CCTCGCGCT CGTACCGTG GCTGCCCTCG GGCGATTGC GCTGTCAGC 240  
 GGTCAAGTGA CCCGAGATAT GTTGCAAACC AAGCATCGA TGGCATAGG AACGCATTAC 300  
 CAGCGATTTC GAAACCCCTC ACAACCGGC ATCTGCTGGT ACGACCAACG CAAGTCGCTG 360  
 GCACTGGTTG CACAGTGGTA AGGTCTTCTG TCAAAATTAC TCTGCCAGG CCGCTCTCAA 420  
 AACCTGTCAA GTGCAGAGC ACTGACAGTC CGTCAAGATG CGACATTACA ATGCTCTGGA 480  
 AGCTCTCCAG TAGGTCTCTG CCGCGTGTCT AGACAGTCAG GGGCAGGCTT CATCGACAAA 540  
 GACGCGCAAG GATGTGCAA TTGTTTCCA CAGTCCACTC TAGGGTCGGA CGGAAAAAC 600  
 AGCGTACTC TGGTTGACT GGGCGAGAC TGGTAGCCG CTGCGTGGC TCAATGAGGA 660  
 CAGACCAAGG TGATCATGAT AC 682

## (2) INFORMATION FOR SEQ ID NO:847:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs



- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1535RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GGGCTTTTTC	60
CAATATTTTG AGCGTGGTTT CATAGCTGG AAGAGCGAGC AGAAGCCCCC CCAGTAGTGT	120
CTGTTCATGT TCGTCATGA AAGGTGCTC TATCAAATCT AGCTCCATCA TOGCAGAGTA	180
GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCGGCAAC TTCTGCAGGA TTACAGTAA	240
ATAATGGTAG AACCGCGGAC TCACAGAAGC GACGACCGCT CGAATGAAG TGGGCGGTGA	300
GAAGATCGTG CGGCGCTGCT TCTCTATCAC AAGATGGAAC TGGGAAAGTC TGTTCACGGG	360
GGACACCGTG CCCATAAGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
CCGCGCGAGC TCAGTCTCAA GCTGCTGAT CCGTGGCAGC AGCTCCACAT TGGGCTGGA	480
GCTGAACAGC TCCCGTGAGT TCAGTCTGIG CGTAAACTCA GACAGGTACA CACTCGGG	540
CAGGCGCTTC CCAATACATG TAGAGCACTT CGGCGCGGC TTGTTGCACT TGACGCGCG	600
CTTGCGGCAG AACACGCAG ACTTGCTGAC CTTCGCGCTG GTTTTCACAA TCTTGCCATC	660
GGA	663

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1535UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

15	GATCGCGGAC GTGGAGCACT GGCCGAGAT GCGCGCGGCC ATCTGTGTGG TTTCTGCGGA	60
	CCGCAAGGAC ACGCCATCGA CGAGCGGTAT GCAGCAGACG GTGCACACGT CGGACCTCTT	120
20	CAAGGAGCGC GTCGCGACGG TGGTGCCCGG GCGGTACGGA GAGATGGCGG CGGCGATCCG	180
	CGCGCGGAC TTCGCGACGT TTGCGCGCCT GACGATGCAG GACTCGAACT CGTTTCAAGC	240
25	CACCTGCCCTG GACTCATTTT CCGCGATCTT CTACATGAAC GACACTTCGC GCGGATTGT	300
	CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATGTGTGGGT ACACGTTTGA	360
30	CGCGGGTCCG AACCGGGTGC TCTATTACTT GCGGAGAAC GAAGCGCGGC TCTCGCGCTT	420
	CCTCTCTGCC GTCTTTGGCG CCAACGACGG CTGGGAGACC ACGTTCTCGA CGGAGCAGCG	480
35	CGCCACCTTC GCGCGCAGT TCGACGAGTG CGTGCAGGCG AAGCTTGGGA CGGACTGGAC	540
	GACGAGTTGC ACAGAGGAGT TGCCCGCCTC ATCTTCACGA AGGTGGGGCC AGGGCCCAAG	600
40	ACACTAAATC CTGCTCATC GACCGAGAC GGGCTTGGC CGGCTGAC	649

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1536RP

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

10

GATCATTGTGCTTGCAGCA CAAACATCCA CAGCTGTGCG ATTTGCAGTT GCAATCCGGA 60

GCAGCAGCTC CTTCGCAGCA TTTCGAAACG CCAGGCTCTC CCACCTCTTT CGCATGTTCT 120

15

TCTGACATTT TTGTTTGTTC TAAATCGTGA TTTTGAGTGG ATGGTTCCGA GACCGGCGCA 180

GCTGACTATA GGGGGGACCA AGACCCCTTTA TATATTTTCG CAACCAGATA CATTAATGCG 240

20

ACGCCAAAAC ACTATCAAAA ATAAGGTATA GCCTCATTTT TATTGTGACC CATGGGACAT 300

GCTGTAATCG GATTATTCTA ACTAAGCTAG TATTATGTGG GTATCCTTTT ATTAATTACA 360

25

ATCACTGCTG AGTTCCGGTA TCGTGCAACT GCACACCGAG CTCATCAGTG GTTTCGTTCC 420

CGCGCAGATC ACGTGCTGCG GACATGGCGA CTTCATCCAC TGGCGCCCGAG CTAAGTGGTA 480

30

TATGACATTA TGGCCGAGAG GTTAAGGCGT GAGACTCGAA CTAAATTGAG GGATCTCTTG 540

GGCTCTGCCC GCGCAGGTTC GAATCTGCTG GATGTGCTTA TTTTGTGCTT GCGCGGCTA 600

35

CGGGGGGCTG TATTTGCTTG TTGCTATTTA GATAAACCAG ATACTAACT ATGGGTAGAA 660

CTCGCGGTAC TTCCCGTAGT AGTAGGCTGT GCCGAAACCG CCGAGGGCCG TGAGCAC 717

40

## (2) INFORMATION FOR SEQ ID NO:850:

## (i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 710 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1536UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

5	GATCAGCTCG GTACTGGAGA AACAAAGGCTA CTGTCCCTTG CCTTGACGAA GTTACGCGAA	60
	ATCGAAAGCA GCAGCAACAA GCAACATAGC AAGACCGCTA AATACATTCT CAAGTCATTG	120
10	GAATAAGCTC TAAAACTACC GATACGTATA TTACTGCGT TAACGTTTAT ATACATATAT	180
	CTAGGCGTGC GTATGGGTGT TGTAAGTGTA CATCTAACCA AATAACTCCA CTATAGCTGT	240
15	AGTACATGGC ATTCCCTTGT AAGCAACTTC AGGTTCTGGA CTACCCAATT GCTGTCCGCG	300
	ATCCAGCCT TGGGGTGTG GCGCTGTGT GACCTCAATT TAGCGAAGAC CGACTGTAG	360
20	TGCTCTCAT ACTGCTTGAA TTGCGAATG ACGCGGTAG AGTGAAGTC AACATACAG	420
	CGCGTATCGA CTATCTGAA GAGGACATCG TCACACGCA GGAAGAAAG ACTCAAATC	480
25	AGCATACT CGTTCATCAC TCTCACTTA ACATTCAGAA TGCTAATGCC ATTGTCCGCT	540
	AGTTGCTCT CAAATAAAAT CATGTGTCG TAGAAAAGAA TGGGGTCCG GCTCGAAAAG	600
30	CTTCGCCAGA GGCAGCTCCA CGCTGTGTC TCTGACCATC GCGCTGCCAT CTATGGTGCC	660
	CTGGTAGAGC GTGCTGTACG TCCAGTGTA CTGGTGGGAT ATGTTTAGGG	710

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1537RP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

5	GATCTCCGTA CTTTAGGATG GCTTTATAGA GGGCAAGAAT TTCCCTTTGG CCTATAGAGT	60
	TCAGGTGTGT GGATTTCGCA CGTTTTTTGG AGCGTGAATC CTCTTTGTGG CTTAAGCTCT	120
10	GAGCTCCATC TCATTGACG CTATTTTTTA TCTTATTCAG AGCAACATTC CTACGATTCA	180
	TCATTGACAG TTGTTCCCTGG ACATACTCTT CATCCTTCGG CTCTGTCTCT TCGTCTTTGA	240
15	GTTTGGGTAG CTGCTCTTC GGAATGATAT CATCCCATTC CAGTCAGCT TTATAATGGG	300
	TGACTTCAAA CTGTTTTAGG AATTCCTCAC CTCGAGATG AGACTCTCC AAATCTGGTG	360
20	TGGTGACGTG ATCTTCGCA TGATTCAAGA CATCATCCAA GTTCAAATCT TCAAGCTTCT	420
	TTTGATTATC ATGCGCTTTG AACATATTGC CTGCACCAA CTTGAGAATC TCAGACAGCT	480
25	CTCTGCACT AGGTTCCGCT TTGCTCTTGC TCGTATATTT ATTCCCATCT GTAACACCTA	540
	ACGAGATGAT AGCATACTCC AAGATCATCT TTTTGGGTGC TCTTTCTAAG ACTTCTTCTT	600
30	CAACGGTATT CTTAGACACA AAACGGTAAA CCATAACATG ATTCTTTTGA CCAATTCTAT	660
	GCGCGGAGC CATTGCTTGG AGATCGGCCT GTGGATTCCA GTGGGAATCA AATATGATCA	720
35	CAGTGTCTGC CGTCATC	737

(2) INFORMATION FOR SEQ ID NO:852:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 716 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1537UP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

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5      GATCTAGACC ACCCGGGCTC GTTACCGGA TACGAAGTAA AAGCAGTCGG GAGGGTCTT      60
      CTGGCAACGA CGTTTCTTC TACACACCTC CTGGCACAGG ATCCAGCATC CTGCCGCATA      120
10     ACGTCAACGC CGCGTTGTG ATGGTTCCCA GGTGCCACTG GCGCCAAGCG CTGCGTGAGA      180
      AACAGCAGCG CTGCACTTCG CTGCTTCGG GAGGCTCCTG GGAGTGGTCC GGGGGTTTTC      240
15     CCACCGCTCA AACTAGCGGG GCGTGCCTGT GCGGGCTCT CCATGCAACT GGGGCGCTCC      300
      CATGATGGCG GGGGCTTAC CAGGGTGGTG TTGGGGCTGC CTGGCTGTGC GTGGCCACAC      360
20     GATGGCCTGC TGGAGGAGCT GAACCTGCTT CCGTGGTGCA AAGGTGTGTG CGACAGCGCA      420
      CCTGGGTGCA AGCTGTGCCT GCGGGGGCGT GTGATTGCT GCGTCCGGG GTGCAACTGT      480
25     GGTGACAGCG CTTTGCAGGC ACGTGATGGT TGGTGCGGG CCCAGACGTG CTGGGTGTGT      540
      CTCAGACAGC TTTTCCGGG GCTGCGGGC CGCGTTGCC GCCATATGAT TGATTCCGTC      600
30     TCGATTAGTG CATGGTGGTC AGCTTCCAGA TGGCCAGGCT GTACTTGTGC TTGCCCCGGG      660
      CCGGCAGGCT CTTTGGCTGT GCGGTGGGT CTGCTTGTG GGGCTGGGC CGTTCT      716
35

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(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1538RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

EP 0 866 129 A2

GATCCCTCTG CTACAAACAC ATACCTAGAT TTCTCATATT TTATACTGAA TACATATAAT 60

5 ATATCATTTA ACTGTCTTCA TTCATGAGAC GTGGCTAAG TTCTGTCTG CTCAACTTGT 120

TTTTCCACTT GTCAGCTCTT TCGCCCCCA GTACGTTTAC CACATGCAAG GCTAGCTTCC 180

10 TCATTCTTTT GCTCTCAGC GTATCGTTGA TTGTCTGGC ACCGGCCACA GTTTCCTCAC 240

TCACTACCAG GGCTTCGATA CCAGGTTGCG TACCCGTGGG CCGGCACAG TCATGTAAAG 300

15 CAAATATTTT GATTTCAGC CCCGGTTTCA GCGTGTGAAG GAAGCTGCAC ACGTTATCGC 360

ATCGTTGCTC GAAGGACTGA AGCTGCTCC TGTATTCTT GTTCGCAGC AGTCTTTCAT 420

20 CTGTAATCCC CACGATCAGC CGGGAAGCAG TCACGAGCGC GGCACACTG AGCAATATTT 480

TATGTCCGTC GTGTAAGTGG TCGAAAGTGC CTCCAGCGC GCTAACAGCG TACTTGTCTC 540

25 TACCGCCACT CTGACCGGC CCCGCAGCGG CCATCGCGG ACTATCAAAC AGCTCTATCT 600

GCGTGTGGG GAAGGCATCC TGACGAGGC GATCGCTCAG GAATACAAG TCCACTTCA 660

30 TTCGGCTGTA CGCTTCATA CTGACGTTGA ACAAACATT TATCGGGTC GTGTACAGCT 720

TCTGCTTCAG AAG 733

35 (2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 725 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: PAG1538UP

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

EP 0 866 129 A2

GATCCTTGGG ACCGACATCGA CACCATTCTT ATCGGTAACG AACTTGTGAA CAACGGCCAG 60  
 5 GCGACCGTGG ACCAGATGGC TGGTTACATG AAAACTGGCC GCAAGTGCCT CGCTGAGGCC 120  
 GGCTACAAGG GCCCAGTTGT TTCGTGGAC ACTTTCATCG CTGTAATCAA CAACCCCTGGT 180  
 10 CTATGTGACC TATCAGACTA CATGGCTGTC AACGCCACC CATACTTGA CTTCCACACT 240  
 TCTGCTGCTA TGGCCGGGCC TTGGGTTTTC CACCAGATCC AGAGAGTCTG GAGCGCCTGC 300  
 15 AACGGTAACA AGAAAGTTGT CATCACCGAG ACOGGCTGGC CTACTCAGGG TCAGACTTAC 360  
 GGCAAGGCCA TTCCATCCAA AGCCAACCAG AAGATGGCCT TGAATCTAT CAAGGCCACT 420  
 20 TGTGGTGATA GCGCTATCCT ATTTACTGCT TTCGACGACT ACTGGAAGCC AGATGGGCCT 480  
 TAAGGTGTCC AGAAGTCTG GGGTATGCTA TAAGTTGCCG TGTGCTTCTT TATGACCTGT 540  
 25 CTCTTTATTT TGCTCGAAC CCTTACATGC AGATGGGGG TGGGGGTGCA TGGGCTGCA 600  
 GCTCCGGGC CTGCAAGTTT CTACATGCC CTACTTTAGC TGCCACGGGA CTTTGAATT 660  
 30 TCTTTGGCAC GTGGTACTGC TGGCATCTT CTCATAGAGC ACAGTGTGCC ACAGGGTATC 720  
 ACTGG 725

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1539RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:



EP 0 866 129 A2

	GATCAGACAT GGTGTTTTGC GGCCCTCGCT CCTGTGGGT GGGGTCACCG CAGTTCACCTG	60
5	GGCCAGCATC AGTTTTGGTG GCAGCAGAAA CCCTTAGGAA TGTGACTTTC TCTTCGAGG	120
	AAGTGTATA GCGTAAGGTT ATACTGCCAA CCGGGACTGA GGACTGCGC TTGGGCAAG	180
10	GATGCTGGCA TAATGGTTAA ATGCCGCCCG TCTTGAAACA CGGACCAAGG AGTCTAAGGT	240
	CTATGCGAGT GTTTGGGTGT AAAACCCGTA CCGTAATGA AAGTGAACGT AGGTGAGGGC	300
15	CTCTTTAGAG GTGCATCATC GACCGATCCT GATGTCTTCG GATGGATTTC AGTAAGAGCA	360
	TAGCTGTGG GACCCGAAAG ATGGTGAAC ATGCCTGAAT AGGGTGAAGC CAGAGGAAAC	420
20	TCTGGTGGAG GCTCGTAGCG GTTCTGACGT GCAAATCGAT CGTCGAATTT GGGTATAGGG	480
	GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTTCCTGCC GAAGTTTCCC TCAGGATAGC	540
25	AGAAGCTCGT ATCAGTTTTA TGAAGTAAAG CGAATGATTA GAGGTACCGG GGTTGAAATG	600
	ACCTTGACCT ATTCTCAAAC TTAAATATG TAAGAAGTCC TTGTGCTTA ATTGAACGTG	660
30	GACATATGAA TGAAGAGCTT TAGTGGGCCA TTTTGGTAA GCAGAA	706

(2) INFORMATION FOR SEQ ID NO:856:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 743 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1539UP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:
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55	GATCACTACG TGACATTGG TACGGAATGG CACTCCAATG CCGACAAACC TCTTCCTACC	60
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COGTGACTTA CCCCAGTGTG CCAACTACCA CACATCTGGG CCATAGCCCC AGGCATCTGG 120  
 5 CACCAAATGT ACTCGATATC GTTATTACAT GTCTAGGCCC TCAAGTGCAT CCACCATCTG 180  
 ATATCATGTC TGCTCTAGGC TATATATTTT GGTGCGGGC ATATCTACCA GAAAGCACCG 240  
 10 TTCCCGTCC GATCAACTGT AGTTAAGCTG GTAAGAGCCT GACCGAGTAG TGTAGTGGGT 300  
 GACCATACGC GAAACTCAGG TGCTGCAATC TTTTITTTTTT CCTCTCTCTG CAAGCTGGCC 360  
 15 GCCAACACAG GTCACCCCTAG TATGGCTCAC ATGCAATTCA GATATCTACT TCTGACTGGT 420  
 CTGGTGGGGC ATGGCCATCA TTGCAAACAG TGTCTCGCA TGGGACTTTA ACGACCTGGC 480  
 20 GATAATAATC AGAGATGTC TACTTATAAA ACATCAGGCA CAAAAGAAA GGTGCAGCGA 540  
 AATGGTATAT ATAGGTCTTC CAGATCCAAC ACCGGTACCT CCTACTTGGC CGTATCTGGC 600  
 25 TCTCGTGGC GCTTGCCGCT GAGATGCTGT GGGCCCGAAA TGTACTCTCA AATGGGCTTG 660  
 TTCAGTGGCC CATAAGCTC ATAAGCTCAG TGGCCCGGAT GCTTAGTAGT AGCTGGGCGG 720  
 30 CTCTTCATAC TGCTGTCTGT ATA 743

## (2) INFORMATION FOR SEQ ID NO:857:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1540RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GATCTTTTCT TTGTCAAAGT TCAACACCTG TAAGCCGGCT CTAGATACCG CTCTAGAAAG 60  
 55

EP 0 866 129 A2

GGCCACATAC GCTTGGCCCT TTTCAAAAAC ACGTCTGAGA TCCACTTTCA CTTTGTTTAG 120

5 TGTTTGGCCT TGAGATTTAT GAATGGACAA GGCCCATGCA AGCATGAGTG GCAATTGAAC 180

TCTCGTTACT AGAGGCTTCT CATTTTGTCT CTOGATAGCC CATGCTCTT CTOGAACTAA 240

10 AACTGTTCTG GTGGTATTGT CGGCTGGAA GAATGCACT AATGGCACT TCTTACCCTT 300

TGAGCTCATG TGAACCTCCT GTAAGAGCTG CTCTTTCGGT TCTAGATTGG CCTTCACTTC 360

15 AGGATCTGTG ACTTCTCGAT CATCCTTTAA GAAATOGAAT ATGTGTGTC CCAAGTGGTC 420

TACAGTGICA TCTGTGTCTA TCGTCTTAAA CTCTCTCGC AGAGCTTCT TGACCATGCT 480

20 TGTGCGGGTC TCCTTCTTGG GCTCCTCATC CTCATCAAGC TCGGGGGGGT TCCAGTCGTT 540

TTTGGCTAAT GCATCCCGAT ATTTCTCCCA TTCTGCAACG TCAAGATCAT CATGGCGAAC 600

25 ACTTTGATAG AACATAAATG TTGCCTCATC GATGAAGTCA ATGACCTTCC CCAGTGATCC 660

GTTTACGAGT GTATCATCGA AGTTCTTAAT GTTCATAACC TGTGCGCGA CTTTAA 716

30 (2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: PAG1540UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GATCTCCTGC GCGAAGAGCA CGCCCTGCGC CCATCCGGCA TAGGGGCCCC ACTTTTGTAT 60

55 GAACATTTCC CGCACAAGCT CCAGCTCCAT GTTCAGTTTC TTGCGCACAC TGGGAAGGTC 120

EP 0 866 129 A2

CTTGTATCGC GCTTTCAGCG CAGCGATCTT CGCTGCOGAT GCATTGAACT TGTAGTCTCT 180  
 5 TTGTGOGATC CTGTTGATGT GCACGTCTAC AGGCACATGG TGTCCATCT GCATGCCCAT 240  
 GAGGCAGACG CAATCTGCGA CCTTOGGACC CACCCCOGGA ACCTCCATAA ACOGCTGACG 300  
 10 GATCTCCTCC CGCGATATCA TGTCTAGCCA GGATTCCAGG TGTTCAGTAT CGTCATGTG 360  
 TCCCGGTTTA CTTGAATCCA TCCATTCTGC CGCAGCCATG ATATACTTGG CGCGATACCC 420  
 15 AAACCCCAAA TCCCGCAGTG CGTCTCGCT AGCGCCTTC ATCAGCTGCT TGCTGGTGGG 480  
 GAATGAGTAG TATGGAGTAC CGTCGAGCTC GCCGAGGAAG CTCCCGTACT GCGAACACAG 540  
 20 TGCATGGCAC ATCTTCGTGA TGCGCCCGAT ATTGTGTGTG CTAGAGCAAA TAAACGAGCA 600  
 CAGTGTCTCC CAGGGTTCCT GTGCGAGTAT TCGCAGGCCA CGA 643

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1541RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GATCGAACAA CCATACTTTA GCGCCACACG ACGTTCCCC TCGGGGATAT CCTGCCGCC 60  
 50 CTCTACAAGA TTGGATTCAA TCATCACCCC ACAAATGGCA TTCTCACTT TACTCAGCTG 120  
 CTCATAGATA TCTTGGGCGA CTTTCGGCTG GTTCGGGTAA TCCTTGTGTG AATTTCATG 180  
 55 CGAGCAGTCA ATCATAATCC TCCGCTGGAC CCCAGCGCTG TCAACTAGCT TGCATTGAC 240

EP 0 866 129 A2

CAAGTCCTGC TTAGCCTGTT GTACACTGGC AGCGTCATAG TTTGTGCCAT CTTTACCACC 300  
 5 GCGTAGAATG ATGAAGGTGT CCTCGTTACC TTCAGTCCCA ACAATGCGAG TCACTCCAGG 360  
 CTTGGTAACC GAAAGAAAGT AATGAGAGTG AGCAGCGGCA CGCATAGCGT CAATAGCAAC 420  
 10 CTGTAAGCAG CCATCTGTCC CGTTCTTGAA TCCGATCGGG AACGATAGTC CAGAAGCCAG 480  
 CTCACGGTGC AGCTGCGATT CTGTGCTCCG GCGCCAATG GCGCCCAAGG AGAAGCAGTC 540  
 15 GCTTAAGAAC TGCGGOGATA TGGTGTCTAG CATTTCGCCC GCAATTGGAA TGTGCTCCAC 600  
 CAGCTGCGTG TACATCTCCC GCGAGATACG CAATCCCTTG TTTATTGGA ACGAATTATC 660  
 20 GATGTCGGGG TCGTTGATGA GCCCCTTCCA CCCCACCGTG GTCCGCGGTT TTCCAGATAC 720

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1541UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GATCAGCTGA TGAAGATTGT ACGTCATCAC TGCTATTTAA CACAAACATA ACATAATTCA 60  
 TCCGCGATAG TTAAATGTTT AGAATTGCGG CTGTGCGCGC GCGGGATCGG GGTTC AATTTC 120  
 CCGTGC GCGG AGCTTTTTTGT GACATTATTT GAAACGGTTG TCGTTATAAC CGTTCCGATG 180  
 GAATGTGGCA GGACCCTGTA ACGGCGACGT ATCCTGCAAC TTGACCGTGT TGTGCGGTCT 240

EP 0 866 129 A2

ACGCCAGGGC TTGGGCTTCC AGAAATTGGC TTTCCCGAG CCCAGTTTTT TGTGACCCAA 300  
 5 TATTTGAGCT GCTGATCATC AAGCTCTAGT CGCACACAGG GGGCCCGAGT ATCCATTGAC 360  
 AAAGGTGGC GCAACATCCG ATCGCCGGT CCTTTTATAT ATAAATATAC ACTAATGACA 420  
 10 CATGCGAATA CCCGACTGCC GTGGATAGG GACGTTTGAG GCTCATACC CCTCAATACA 480  
 GATAACAAA TTGGAATATA GGAGAAGAAA TGTTCGAGAG GCTAAACTT AGGTTCGGC 540  
 15 GATGCAGAAG ACTCAGAGC AACCGTTTAG CAGACGTTCC ATACCGAAT CCCACGTGA 600  
 ATTCCGCAAT CATTTCCAGA ATCGACACAA TCACGGTGTC AATCTCGGGT CGCTATCGTC 660  
 20 CTTGAGAAGT GGATATCGAG TCGATGTTCC AATGTGGCGG CGAGACCGAG CATGCGGGGA 720  
 TCAGGAAGAT GA 732

25 (2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 614 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1542RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GATCATGTGG AGGAACTCGG GCAGCGTCTC GGAGCCGGCG TAGTGGGCTA CTGTGGCGGC 60  
 50 GCGGGCAGCC GACTGCTCGG GGTATTTCGG CGCCGGCGCA GCGGCGTGTG AGCCGATGCT 120  
 GCTTCGGGG TGGCGGGCGG CGAAGGCGTC TGGCGGGCGG CGACGGGGCG AGGGCGAGCC 180  
 55 CCCGTCCGAG AGCGCGAGCA CAAGGCAGTC GAGGGCGAGG AGCATGAGG TGGTGGCGAT 240

GGTGGGGGCG TTGAGGCGGT CCTGGACGAC GCGCTCGGC AGGTGGGGG GCTGGAAGAC 300  
 5 GGTGATCAG TGATGCGGC GCGGGCCAG CGTCCAGGC GGATGCGCG TGACGGCGAT 360  
 GAGCGGCTG GCGGGTGGG AGCGCGGCT GCGCAGGTAG GCGGCGAAGT GCAAGAGCTC 420  
 10 GTCAGTCTCG CCGGAGTGG AGCAGAGCAG CAGGGCGTCG CCGTGGCGA CGATGCGGAT 480  
 GTCGCGTGC ATGGCCTCG TGGGTGGAA GACGGCGCG GGGATGCCA ACGAGTGGCA 540  
 15 GGTGGGACA GTCTTGGGA TGATGCGAA GGAATTGCG CAGGCGACA ACACGAGCTT 600  
 GCGGCGTCC GCGA 614

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1542UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GATCATTTAC CTACGCATCG GCGTCCGCG CATTGCCGA GACGGATCG TGCGAGACGG 60  
 45 CTACCTGGAA CACTACTACG AGAACCGTA CCGCGCGCC CTCTGGACG GCTGCCGTGT 120  
 GCAGCGCTG ATAGGACTCC ACGCGCTGCC GCTGTAGGA GTCATGCCG TGTGCCGGAC 180  
 50 CCGAGCGGTT TGCCGTCTCG GGAGCCTCCG GGTTCGCACC GCTGGA AAAA GGAGGGCCAC 240  
 GCTGGTATAT AAACGGCACA CGAGCCATCC GCGTCAGGA ATAGCGTGAG TCGACAAGAT 300  
 55 GGTGCGGAA CACGGTCTTA AGGACCTTCA GAAGAAGCCT GTGAGCTTTT CCAACATTGC 360

EP 0 866 129 A2

CCTGGGAGCG GCGTTGAATA TGTCGAGGT CACGACGCTT GGCAACCGC TTGAGGTCAC 420  
 5 CAAAACGACC ATGGCCGCAA ACCGGCAGTT CGGCTTTTTC CAAGCGGTGC GGCACGTGTG 480  
 GTCCCGTGGG GCGGTGTTCG GCTTTTACCA GGGGCTGATT CCGTGGGCTT GGATTGAGGC 540  
 10 GTCCACCAAG GCGCGGGTGC TGCTGTTTGT TTCTGCCGAA GCGAGTACC AGTTTGGCG 600  
 GCTTGGTCTC AGCAACTTCG GTGCAGGCAT CCTGGGCGGG TGTCGCGCG CGTA 654

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1543RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGCATT GAGCTCTTAC GAACTGCACA 60  
 AACCTACTCG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTTCAACTGC TTTCGCATGA 120  
 40 AGTACCCCCC AGGCTATTTT TCTTACCCGC CTGGTGTGTTG TCTATATAAC CGGTTGTATT 180  
 TTTGATAAAA AACTCAGCTC TTCTCTTACG GCAGAAATAT ATATCCAGTC CTTAGGCCA 240  
 45 TCGGAAAATC TGCTTTTFTA CCGCTGTTTC TOCCAGTCTT AGCACTGGCA GAAAAAAGAT 300  
 GTATGGCGTA TAGCGCTGG CCGCGCGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA 360  
 50 AAAAGACGTG GCGCGCCCG CGGCAGACG AAGAAAAAT AGGCGCCAC CCCTCCAAGC 420  
 AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCAGCTC 480  
 55



EP 0 866 129 A2

COGGCCTCAT ACGCTGCCAT TCTGTTCAT CCGGCTTGCA AACCCAGTAG TGGCATGTCA 540  
 5 AAGCATTGCT CCGACGCTCC GCTGCCTTGC AGTCGACATC CTCTTCCTAA CCCCAGCCAG 600  
 ACTTCCATA CTTTGCACIT CACATAGCAT ATCACTTTTC AGATCACTAC GTGACATTGG 660  
 10 GTACGGAATG GCACTCCAAT GCGACAAAC CTCTTCCTAC CCGTGACTT ACCC 714

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1543UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GATCCGTAACT TCGGGATAA GGATTGGCTC TAAGGATCGG GTAGTGAGGG CCTTGCTCAG 60  
 35 ACGCGGCAAG TGTGCTTGTG GTCTGTCTC GGGGGCTTGC TCCTGGGGAC GGACTGCTTG 120  
 CGTGCTCTGT CGTAGACGGC CTGGGTAAAC CATCTCTGGT CGTCGCTTGC TACAATTAAC 180  
 40 GATCAACTTA GAACTGGTAC GGACAAGGGG AATCTGACTG TCTAATTAAA ACATAGCAAT 240  
 GCGATGGTCA GAAAGTGATG TTGACGCAAT GTGATTTC TG CCGAGTGCTC TGAATGTCAA 300  
 45 AGTGAAGAAA TTCAACCAAG CCGGGTAAA CCGCGGAGT AACTATGACT CTCTTAAGGT 360  
 AGCCAAATGC CTCGTCATCT AATTAGTGAC GCGCATGAAT GGATTAACGA GATTCCCACT 420  
 50 GTCCCTATCT ACTATCTAGC GAAACCACAG CCAAGGGAAC GGGCTTGCCA GAATCAGCGG 480  
 GGAAAGAAGA CCGTGTGAG CTTGACTCTA GTTTGACATT GTGAAGAGAC ATAGAAGGTG 540

TAGAATAAGT GGGAACTTCG GCGCCAGTGA AATACCACTA CCTTTATAGT TTCTTTACTT 600  
 5 ATTC AATTAA GCGGAGCTGG AATTCATTTT CCACCTTCTA GCATTTAAAG TCCTATAACG 660  
 GGCTGATCCG GGTGAAGAC 680

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1544RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GATCTCAACA AGATCAATAG GCATATCCTG CCGGCTAGGG ACACCACTGA ATTTTATGAC 60  
 GAGAAGGCGG AAGAGTTGGA CCGCAGTGTG AGAATGGAAG AAATGGCCAT TCGGATGGGC 120  
 AAACGGCGCA AGTGGCTGAT GAAGCACTGC GAGGGCGATG TGCTAGAAGT TGCATCTGGT 180  
 ACTGGTAGGA ATATAGATT A CTAGACTTG AGCAAAATCG ACACAATCAC CTTTCTGGAT 240  
 GCGTCTAAGA ATATGATGAA GATCGCCAAT AAGAAGTICA GAGAAAAATA CCCACACTTC 300  
 AAACAAGCTG CATTCTAGT TGGAAAAGCA GAAGATTTAG TGGACCTGGC GACTGGGCAT 360  
 TCGCCTCAGC AACAGAATCT GGAATTGGTC AACTCTCCTG AGCAGGTGAT CCCGGAGTCC 420  
 AAGCCCAAGG TTAAATACGA TACCATCATC GAAGCCTTCG GTCTGTGCTC TCACCATGAT 480  
 CCTGTACGGG CATTGAAAAA CTTTGCAGAA TTGCTAAAGC CTGGCGGAAG AATAGTTCTG 540  
 CTTGAGCATG GCAGAGGGAC CTATGACGTT GTGAACAAGA TTCTAGACAA GAGAGCCGAG 600

CACCGTCTCG AGACCTGGGG CTGCAGATGG AACTTGGATA TTGGCGAAAT TCTAGATGAC 660

5 TCTGATCTAG AATGTCACC GAAAAA 686

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1544UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GATCAAATTC CAATCTCCGT CAGCGTCAGG CAGCCGCGTT ATGTGTGAA CTCTTCGCTG 60

30 CTCTCTTCT CTTCGCTGAA CCCGCAAGAA AATTCACCT CACGCCGAAC CAGAGGCGAA 120

AAACTGAAAA TGAAATAAGG CGCCGGCTTC CGAGGACGTT GCGGGCTGGT GCAGCTCTAC 180

35 TTGCAATACC CGCAATAGGA CTACCAGACC TTATTAGACA CTGTAATATG TGGGCAGCAG 240

TAGGTGCAGT CTACAACTT TTATAGCGCA GCGGGCGTA TTAATCTTTT CTGCTCCCGC 300

40 GTCCGCGATA AGTGTGACT CACAGTCCCG CGGAACGAAC GTGCGACCGA GTGCGGCGAA 360

TAATGAGTAA TGTCTATGT ASTGGTGTCT AGGGGCTGA AGGCTATGCT CTGGGCTAGC 420

45 TGAATGTCA CGCAGACAT GGGCTTCGTA GGTGCCACTT TGCGCAGCAG GTGGAACGAC 480

AGCGCAGTCA TGGCAGGAT GTCTGCGCTG GTGTGCATTA TCTCGACAC ACGGCGGTGT 540

50 ATGCGGGCGT GCAGGTCTGC TGGCGCGGCG TCGGGCTGGT CCGGGCTGTA TTTCTCGAAA 600

CAGTGACAGT GGATGTAGG CAGCACCAAW TGCTGGGTGG GCAGCGCGGT OCTCCGAGAT 660

55

CCGTGGGCGG AGTACAGCCC GGC

683

## (2) INFORMATION FOR SEQ ID NO:867:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1545RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

25	GATCATTAAAT CAGCCATGCG ATACCCGGGC AAGATGACCA TTAGCTCCTG CTTTGGACAG	60
30	AAACAACGGA CTATGGGTAT AGAACTTGAT GATAGAACTT TGAGGCATTT AAAAAAGTGG	120
35	CTAGACCGGG CTTTAGATCC GCGTACGACA GACGAGAGCG TCACAGCCCT TGTAAGGAC	180
40	TATGTACTAC AGGTACTACT AGAGTGGGAC ATGCGAGCTG TGAAGGGCCG AAAGAACGAG	240
45	TTCTGGGAGC AGATGAGCCA GTACCTGGCA GGTATGGTCA AGGACCACAG CTGTCTAGAT	300
50	GGGTGTGTTT ATCAGCTAGT GGACTTAGGC GAGCCTCCCG CCGGGAATAG TTGCGGGCGA	360
55	CAGCTGCGTG TCCTGAAAAT CCCAGCGGAC CGGCTTGGCT GGGAAACCTT GCGTGGGAG	420
60	TTTGCGGCTT TTGGAGCGGT CACCAGGGCG AGGATTGATT ACGTGCATCG TGAGGCATTC	480
65	TTGGAGTATG CGGATGCGGC CAGCGTCGTC CGATGTTGTT CCGTCCGGA GGCATTCTTC	540
70	GGGAACCGST TCGTTGAGGT GCAGCCCTGC TCGGAGGGCG TGGGAATCAC TAAGCGGTGT	600
75	CGAAGTCTGG CCGCCGATC ACGAACAAC TGTGCCCGAG CATGGATCAT CTGGGGTGCC	660
80	TCCGGAAGT GGTGTGTCT TGGATCGTGG ACGTGGCCCT CCGCTGTCA TCCT	714

## (2) INFORMATION FOR SEQ ID NO:868:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1545UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GATCATCTTG CAGGGACCGC WCCACGTGGC GTAGAAGTCC ACGAACAAGA GCTTGTGGGA 60  
GCCACCGCG GACTCAAATT CAGAAAGGGA CTTGATTTTC GACACATTG CGTTCTGTGT 120  
GGCTGACTGT ACCTTGTTGA TACGCAGTAC CCAGGAAGCC GGGCGGAGCC CCGCCTTTTA 180  
TACCCGGCGC CTGCGGTCA CGTGTACCA CGTGGGGGT CTCCTCTTA TTTCGGCTCA 240  
GGAGATAAGG ATGACAAAG CGTCTCGCG CGTCCGCAT TGAAGTCTT GACAGCAATG 300  
GAACCTCTGC TATAAGCGT GTCTGGGCG CAGCCCTTCT CAATGGTCCG TCTCTCTGTT 360  
CGCTTTGTTG AGCCAGGCG CCGTTTGTG TACGTTTCG ACGGGGTTGG ATCTCCAACG 420  
CACGGTCGAA TAACGAACAT GAAAGCCAGT TGTACAGTAG CTACACCCCA GCAGACGAAG 480  
CATCAGCAGG CAGTTGAGAG CCGGTACGAG AAGTTCGGT ATAGAGCACA CTOGAGACCA 540  
TAGAGGTCAT CCGCTAGGCG GTACTTCAGG TCAGGC 576

## (2) INFORMATION FOR SEQ ID NO:869:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

EP 0 866 129 A2

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1546RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

15	GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GCCCCTTTTC	60
	CAATATTTTG AGCGTGTGTT CATAGCTGGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT	120
20	CTGTTTCATGT TCGCTCATGA AAGGTGTC TCATCAAATCT AGCTCCATCA TGCAGAGTA	180
	GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTCGTCAGGA TTACAGTAAA	240
25	ATAATGGTAG AACCGCGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCCGA	300
	AAAGATCGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TGGGAAAGTC TGTTCACGGG	360
30	GGACACCGTG CCCATAAGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
	CCGGCGGAGC TCAGTCTCAA GCTCGTGGAT CCGTCGCAGC AGCTCCACAT TGGGCGTGA	480
35	GCTGAACAGC TCCCGTGAGT TCACGTCTGT CGTAAACTCA GACAGGTACA CACACTGGG	540
	CAGGCCCTTC CCAATACATG TAGAGCACTT CGGCCGCGCC TTGTTGCACT TGACGCGCCG	600
40	CTTGCGGCAG AACACGCAAG ACTTGCTGAC CTTCCGCTG GTTTTCACAA TCTTGCCATC	660
	GGACTCTGCC ATCCCGGCAG CTTCAGCAA AATGAGTAGG TCATATTATT TACCTGCTGG	720
45	TAATCTTGAA TAATGCTCAC T	741

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1546UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GATCGCGGAC TGGAACACTG GCCGGAGATG CGCGCGGCCA TCCTGGTGGT TTCTGCGGAC	60
CGCAAGGACA CGCATCGAC GAGCGGTATG CAGCAGACGG TGCACACGTC GGACCTCTTC	120
AAGGAGCGCG TCGGAGCGGT GGTGCCGCGG CGGTACGGAG AGATGGCGGC GCGGATCGGC	180
GCGCGCGACT TCGGAGCGTT TCGCGCGCTG ACGATGCAGG ACTCGAACTC GTTTCAGGCC	240
ACCTGCCTGG ACTCATTTCC GCCGATCTTC TACATGAACG AACTTTOGG CGGATTTGTC	300
AAGCTGTGTC ATCTGATCAA CGAGTTCTAC AACGAGACCA TCGTGGGTA CACGTTTGAC	360
GCGGGTCCGA ACGGGTGTCT CTATTACTTG GCGGAGAACG AGGCGCGGCT CTGCGGCTTC	420
CTCTCTGCCG TCTTTGGCGC CAACGACGGC TGGGAGACCA CGTTCTCGAC GGAGCAGCGC	480
GCCACCTTCG CCGGCGAGTT CGACGAGTGC GTGCGCGGCA AGCTTGGAC GGACCTGGAC	540
GACGAGTTGC ACAGAAGAGT TGCCCGCTC ATCTTCAOGA AGGTGGGGC AGGGCCCCAA	600
GACACTAAAT CCTCGCTCAT CGACCGAGA CGGCGCTGOC CGCTGACGCT ATTCTCTGTC	660
TATTTTCTGC TCTGTATACC CTGCCAGACC GCGCTATATA TATAGAA	707

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1547RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GATCCTCCGC CTACACCAGA ATATTTCTGG CCAATTAGTT GTTCACCATC GCCCCGAACG	60
TTGGTGAAGC CAOGGCCATA CGCTGCCATG CCGAGTGCAA TTTTCTTGG GCTGACCTTA	120
AATTGTTGGG TCATCATGAG TATGCCATCA TGTGCATTCA ACTCATCAA GTTGTCATA	180
CCCATATCTT CATACCGAG CTATCTAGG TGGGATTGT ACGGCGAAT CGTAGCATTG	240
TACAAGTTGC TATGGTAGCC TGTTCGCTCT GACCATGCAC CGTGGTAGTC GTATGTCATC	300
ATATTCCACA TGCTGAGATA CTGTTCATC TOCTCAACG GGAAAATGCC AAGTGTCTGA	360
GGAAAGGCGG GTGCTGCCAT GCTTAAGTGG AAGGCGGTT CTGTAGTCCC GCGGGGCCCC	420
CAGATATTGT CTTCCAATTC GTCCATCTTG TGTGCAAGC GGCTACACAT TTCTAGATAC	480
ATCTGGGGTT CGTAGCCATC ATCCTTAGGG AACTCCAGT CAAGATCTAT CCCATCGAAG	540
CCGTACTCAA ACATTGCGTC GATGCGCGAG TCGATGAAGT TGTTAACTT CTCCTGTCA	600
CGCACAATTT TATGGAACGG CTCCCGATTG GAACAGCGC CAACGGGCAT CATGAGCTTG	660
AAATCGGTCC CTGGCGCGT CTTGAGGTAA TTAAGCTTCG CCTATTGCCC	710

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 608 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1547UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

10

GATCTCTGAG GGTTCOAAGG CAAGCCCGCC GGAGCTTGCC CAAATTGTGT CACCCGCTCT 60

CGAGTAGATG GTGGCCTTGT CGACCTTCCC GGTTCCTAAC AAGTGTTCAG TGTAGGCTAA 120

15

AGCTCTAGTT AGTACCCACG AACGGGCCAC GAGCAGAACA CGTAAAAACA CATACTTGC 180

CAAGACATGA TGGTTCCGG ATGAAATCTG AGTTAGTGCT AACACTCGCA GATGCTCTGG 240

20

TGAGTGAAT CTACGTATCA ATAGTATTGA TTTGTCAATA AATATACCTT GGCTTTTGT 300

AATCTTTTTA TATAAGGGGT TCCGATCTGC TGACATCATA GCACAAGAAT TAAGTATCCG 360

25

GGTAACGAAC TGCCCGGGTA ATGGGGGCA CAGGGCAAGT GCGGGTAAC GGCATOCACA 420

TACCGCAGAG ATGCACTGGC GGCTACATAC TGTACACAGG CTGCAGCTA CTCGTGCTCT 480

30

GAGTCGAGAA CAGCCACCTT GCGAGCTTG AGAGCGACCT CTTTCATCTGC GCGGGGGGCC 540

GGCGGGGCAG CAGCGTACTT GCGTGGGCC TCGGTGTICA GCTGCTGCAG ACGCGGGGCG 600

35

TTTAGGTC 608

(2) INFORMATION FOR SEQ ID NO:873:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 706 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1548RP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

```

5      GATCATCATT GCTCGGTTAG CGATTGCCGG CAATTTTACA GCTGGTTCAT CGCTAGGCGG      60
      TAAGGCGACC GCGGGTAGTT TCCGTCTCTA CCGGTCCGTC GTGTTTGSTT TTGCATCGGG      120
10     ATGGACAACA TATGCTGCAG ACTACACTGT CTACATGCCC AAAAATTTCTA ACAAATAACG      180
      CATCTTTTTC TTCATGATTG CCGGTCTTGC GACCCCGTTG CTGTTCAAGT TGATTCTTGG      240
15     AGCTGCTGCC GGGCGCTGTG TGCACACAAA TCCTACGTGG GCGAATATT ACAAAAAACA      300
      TTCCGTGGGA GGTCTGTGCT TTGCTATACT GGCTGAAAAC GCTCTGGGCG GGTITGGGCA      360
20     GTTCTGCTGC GTTGTAAGTG CCATGTCCAC AGTTGCAAAC AATATTCCAA ACATGTATTG      420
      CATCGCTCTC AGCAACCAGG CGCTGTGGAG TCGTTTCGGG CGTGTGCCAC GAGTGTCTTG      480
25     GACCCGTGGT GCACACGCAT GCAGCTTGGT CATTCGAATC GTTGGGTACT ACAAGTTTGA      540
      GACCTTCATG ACCAGCTTTA TGGATTCAAT TGCTACTAC CTCCTCATAT ACATGTAAAT      600
30     ATGTGTACTT GAGCACTTTC TCTTCCGCA GGGCTTCGGT GGTTCACAGT CAGCCACTGG      660
      GAACGTCCCG ATCTTCTCTC AGCTGGTTAC GCTGGCTGCG CTGCGC      706

```

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1548UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

EP 0 866 129 A2

GATCGACAGA TTACAGTTAC AAGCGAGAGT TCGGCTTATT TAAGGAACAG AACCTATAAC 60  
5 ACATTTGAAG CTOGAGTTTT GGCACGCCAA GACCGATTTG CGGATTAAAT ATCTTGAAGT 120  
TTGCACTCAG ACTCAAGAAC TACTATTACG ATACTATAAC AAAGACGATG ACTAGCACAG 180  
10 CCGACCACAA GCAGCCCAATT TCGTTGAAGG TTAACGGGGC TCTATTGAC GTCGACGGGA 240  
CCATCATCAT CTOGCAGCCC GCGCTAGCGG CCTTCTGGAG GGAGTTTGCC AAGGACAAGC 300  
15 CGTACTTGA TCGGAGCAT GTCATCAGTG CCACCCACCG CTGGAGAACC TACGACGCCA 360  
TCGTACCTT CGCGCCAGAC TATCTGAGTG AGGAGTACGT GACGAGACTG GAGGCGGAAA 420  
20 TCCAGACAA GTAAGGCAAG TTCTCCGTGG AGGTTCCCGG CGCTGTTACG CTCTGCAATT 480  
GCCTTGAACR AACTTCCGAA GGAAATTTGG GCGTTGGTA CTTCGGGCC CTTCAGATG 540  
25 GCACCAAGTG GTTCGATGTC CTCGGCATCA AGCGTCCTAG CACCTTCATT 590

(2) INFORMATION FOR SEQ ID NO:875:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 736 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1549RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

50 GATCTGCTTG GTCTGACCAC CGAAACCGA CTGCTTACGG TCATATCTTC TCTTACCCCTG 60  
AGCAAACAAG GAAGCCTTAC CGGCTTGTG CTGGGTCAAC TTGTGCTGGG TGTGCTTGCG 120  
55 GCAGGCTTGG CCCTTGCACT AAGTCTTTCT GTTCTTTGGA ACGTTAACTG CACAGTTAG 180

EP 0 866 129 A2

TATACGTCCT CTGGGAGT CCTTTTGA TGTGAGCG CGCGTCAGA AGGCGCTGCT 240  
 5 GTAGCGAGCC GTGGCCCCCT GCGGCGCTC CGCGCTTCC CTCGTCATA TTGAACATAC 300  
 CCATTGCGAG AAGTAGCTTC TGTGATGCTC TGTGCTTACT ATCAAGCAGG ATGACACCGG 360  
 10 GCGTTGAATC CTGAAATTTA CCATGTTTTT CGCTTCGGA GCTGGGCGG CGGGCGGGCC 420  
 GGCTGCGCG CCGGAAGGTC CAGTGTGCC CGCGCTCGT CGCCCGAGTT CACCGGGGCC 480  
 15 ACCACGCAGC GTGGTGATC ACGCATGTGC AGTATGTGTG GGTGTGAAT AAATAGATGT 540  
 ATGGGTGTAG TCACATGTTT GTCACAGGCA CTCTCGCG GCTAACGCT CGAGATTGGC 600  
 20 CAATGCGTGT GCGGCATAG GCGATGGCAG CCATGCGTTG AGCTCTGCGC GGGGTAGAG 660  
 CCCAGTCAT TAGACTGCG CACTGCAAGC GTCTGACCG CAGGTTTTAA GCTGGTGTGT 720  
 25 GGCGCTGCG TACGTT 736

(2) INFORMATION FOR SEQ ID NO:876:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 707 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1549UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GATCCATGTA TAATACCCCC ACAGCACTT TTGCAGGTTT TCGCGCTTGG CCCCCAGCTT 60  
 CTGCTCGTAG AACTTCGCAA ACAGACTGAC GTTGAACCCC CACCCATCTG CAGCAGAGGC 120  
 55 AAAAATCACA TTGTTCCGGG ACGGTCGAA GTATATGTCC GCATCATCCC GCTCCACATA 180

CTCGGCTTGG GGGTCTGTCT CCAGTTTCTC TCTCCACGAG AGGTTCATCCA GCAGCCGCTC 240

5 CCGGCCAAAG AAGGACCCCA GTACAGAGTT GACCTGTTC AATGTCCTTG ATAGATGCAC 300

GTAGGCTTCC TGTGGGTCA GCTGGAGCTC CGTGATCAGC CGATCGATCT TGTTCAGCAC 360

10 CAGGATTGGT CTCAGCTTCT CCGTCCAGCA CTGCCGAGC ACGTAATCG TCTGGGAACA 420

CACACCTCG ACCACGTCCA CCAGCACGAT CGGCCATCA CATAGCCGG AGCCCGGCT 480

15 AACCTCGCTG GAGAAGTCTA TGTGGCCCGG AGAGTCGATC AGGTGATTA AATGTTGTT 540

GACCAGGGC TGGCTGCTCC CTTCTGTTT GTGAAGCACT CCGAAGTTAC AGAGAAATCG 600

20 CACTGGACTC CATCGTGATG CTTCCAGCT GTCATCTGG CCGGAGTCT AGGAATCGCA 660

CTTTCCCGC TAACCGCTGT GAGATAATAC CGTTGGATGC GAGGAGG 707

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1550RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

GATCGAGTAC ACAAAGTACA TGGATGCTGC CAATAACTAT AGTCTGAAAT CAATGCGTTC 60

CITAGCGAAT GCAGATGAGT TGGCGCAGCT GGCATCATTT AACTCCATCA GCCATTATTT 120

ATTGGCTGAA TGGCCATCTG TCCAGACACT ACAATTTTTA TTAAGCTCAT CTAAATTGTA 180

CCCAAAATTA ACGAAGGAGA ATCAAGAATC TGCAATTATC GAAACACTGC TGTCTCTCAG 240

EP 0 866 129 A2

TGAATTTACG TTGCTGCACG ACTTCTCTCT CCAGGCAGGT TTCCAGGTGG AAAAATCGGT 300  
 5 CATTTTGAAG TACTTTTGGC GCTTTTTCAC CAGCGCACCA AATGGGTCCA GGGACCGGC 360  
 CAGAAATGAC AAAGGCGAGG AACAACTCTC GCTTACTGCC CAAAAGGAC TATTATTATC 420  
 10 TTGAGACTCT TCTTGATGTC GCAGACGCTT TGGCAAAGTA TTGCTAAGC TACTCAGTG 480  
 GACAACCCCTT CAGACCATCG CATATATTGG ATCTCAAAGA TGATCCATTC AGAATCATAA 540  
 15 GCAAACCTGCT AGAAACGAAT CCCAGTCTGT ACCGTGACGT TGAAACGACT TTGAAATCC 600  
 TCAAGCAATT ATATGAAGGA TTGCAACTGC AGCCTCATGA TCCAAAGTAC ACAAGTGAAT 660  
 20 ATACCCGTTT GCTAGTCTGT CACATTGATT GTGCATTGGC AAATAT 706

(2) INFORMATION FOR SEQ ID NO:878:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 736 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1550UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

45 GATCTCCTCC CGGATATCA TGCTAGCCA GGATTCCAGG TGTTCACTAT CGCTCATGTG 60  
 TGCCGGTTTA CTTGAATCCA TCCATTCTGC CGCAGCCATG ATATACTTGG CGCGATACCC 120  
 50 AAACCCCAAA TCCCGCAGTG CGTCTCGCT AGGCGCTTCC ATCAGCTGCT TGCTGGTGGG 180  
 GAATGAGTAG TATGGAGTAC CGTCGAGCTC GCGAGGAAG CTCCCGTACT GCGAACACAG 240  
 55 TGCATGGCAC ATCTTCGTGA TGCGCCCGAT ATTGTTGTTG CTAGAGCAA TAAACGAGCA 300

EP 0 866 129 A2

CAGTGTCTCC CAGGGTTCTT GTGCGAGTAT TCGCAGGCCA CGATGTGTTT TCCGATGAA 360  
 5 ACGTGTGTCT GCTTTCTGCC ATTCTGCTAA CAAAGCCTCT AGGTTACCTT CCATCCGTAG 420  
 GTAGCGCATC AGCCATTGTC GTGCGGCCCC GCTGCAGTCG TCATCTTTAT TCCAGCTAC 480  
 10 GCTGAATTCA ATACTGCACT GATCGGGCTG CTTCAATACA ATAATACGAT AGCCCAGCTT 540  
 GTCATTTAGT AGCATGCTCG CGAATAGTA CCTTTTCTCA TGATTCCAGA TCCACCTGAA 600  
 15 CGCTTGACCA CATTGCAATA CATGGTCCAG GACTATTTCT CCTTTGGGA ATATCAATCT 660  
 GTTAAACTTC ATAAGTGTG ATACAGCACT GACCTGGCTC TAATAATCAG CGTCAGGCG 720  
 20 CTGGCTCGAG CATGTT 736

(2) INFORMATION FOR SEQ ID NO:879:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 702 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1551RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

45 GATCTCAGT GAATGGATA TCTGCTCAAC GGCCAATTCT CGTATATTCT GACGAGATCT 60  
 TTGGGTCAAT TACGTGCACT TTGGCCGAAG CCTTCGCACG AGCTTCTACG ATACAGAATG 120  
 50 CTGCCAGGTG CATCTTAAAA AGCGGGTTTA CAGTACGCC TCCGTCTTTC AGGGCACCAG 180  
 CCCCTAACTG TACATAGTTT CTGTTATGTA GTTTCGCTTT CCTCGGATG CTGCTCTT 240  
 55 GTGGAACAAA AACAGGCGGT AGAAGGAAAT TCCGTGCGT CATCGGTATC GGACGGGCTC 300

EP 0 866 129 A2

TGCCTGGATC TGGGAGTAG CTTTATGAGC CATTAGTGAG GAACGCCAGT TTAGACGACA 360  
 5 GATTTAGTCT TTTCGTGTT OCTGCAACA GGCTTGAAT GTATCAGGC GCTGGCGCAG 420  
 CGACAGGCGA CACCGCTTCA CATAGGGAGA GGCCACCCAC TGAACACCGG GTGCACTGTC 480  
 10 AGGGGGGCGA GCGTACTGCC TACAATGGTA TCGTCCGCAA ACGGCAGGC AACCGGCAGA 540  
 GCGGGCATTT AGATCTAAAT TTATCAGCC ATGGACGGAT GGATTTACGG CAGGTGTTCG 600  
 15 CCGCAGCAG GGCACGCCA GACTGCGAGG TGGCAAATAA TTCACATAGC AACCTGCATT 660  
 ATAAACATCC CAAGTCATTA AACTTACTAA ATATTGTTGC GT 702

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1551UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GATCCCGGTG AAGCTGCGCA ACTGCACGGT GCGCTACGAG GACCCGGGCG GCGCAGTGA 60  
 GCTGGCGCAC TACGACTACT CGAGCGAGCT GGACCGGTAT CTGAAGGATA TCGAGGTGA 120  
 45 GTACGAGGTG CTGGCGTACA ACTGGCGGAC GTTCTGCGG TACGTGCAAG AGCTGGAGGA 180  
 GGGGAGTTT CCGAGTTCT TCTGCGAGCT GCTGCGGTAC GCGCGGAGA ACGAGGTGTA 240  
 50 CCGCGCGAAG CTGTGGGCGG GGCTCGTGAA GGAGCGCTCG ATGCAGGAGC TGATCAGCG 300  
 CAGAAAGCGC TCGTCACTCA CGCTTGTTCG CCGCGAGGA GGAGACGAG CGACGGCAGG 360  
 55



TGGAGGACGA CTGGCACAGC AAGCTCGACG AGCGCGACCG CTTCCTGCGG CTGCGGAGCA 420  
 5 AGCTCGTGGC CAAGCGTGCC AAGAAGACCA AGGACGGGCT GTGGACGGTG CTGTGGGAGC 480  
 GCTTCCAGAG CGACGCTAAG ATOGAGAAGA TGCGGCGCCG CAACGAGGCC GGCACGCCCC 540  
 10 AGGCGGGCGG CGACGAGCTC CTGACGCGCG CGGAGCGCTA CGCGCTGGAG CAGGGGCAGG 600  
 GCTTCCTTGG CGCTGTGCT CCTGTGCGG GAGCGGCGC CGGCCCTGGC CGTGCCCTGC 660  
 15 AACGAGCTTC CCGATGAATA CTGCATCACC AAGACTGACT TCGACGGCT CGCTAGCCAC 720  
 GGCATCCCGG TCGAG 735

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1552RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GATGTCGGC TCATGCCACC ACAACTTCCA CGTCCACTGC ATCTACCACT GGCTCAACAC 60  
 45 CTCACGTCC AAGGGCTCT GTCCGATGTG CAGGCAAGCG TTTTCACTCC GGGAGGGCAT 120  
 CCGCATTAAC GAGCCCCACC GCGACAAGTT CGAGAAGGTG TTGATGAAGG CGGCCAGCA 180  
 50 GAGCGTGGTG AGCGTCGCGG GCGCCAACCC GGTGGGGCGG GACCAGGACG ACGTCATCAT 240  
 CKACCAGGAG TTCATCCGCT GACACTAACT AGCCTGTGTA CCATGTAAA AATAATGCTT 300  
 55 CCAACCAGAT TCGAACTGAT GATCTCCACA TTAGTAGTGT GGCGCCTTAC CAACTTGGCC 360

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ATAGAAGCAA TACGAGCGTC TAGCGGACTG CGCCGGGCTA TATGCGCGG GCGTGACCGC 420  
 5 GACGAAACGC TGGCGCCCAA ATACCTGATC CCAGGTTTCC AACGCTGGTC ACGCAACTTC 480  
 TGCCACGTGC ACTGCACACC ACGCCAGCAC TATATAGCCC CGCACCGGC AGGCGTCTTT 540  
 10 GCCAGGTCAC CGCGTCCAGC TGTGCTGGCA GCATTCCACC TGAAAAAGTT TCACCAGCAG 600  
 AAAGACTTTT CCACTTCTCA ATAGCACTTC TATCCCTTAT TTCTCAGCA GTTTTGCAAT 660  
 15 GAGCTACACT ACCAGACAGA TTGGAGCTAA GAACACCTTG GACTACCGGG TGTTCATOGA 720  
 GAAGGCGGCA AGGTGCTCTC GCGTTCCAC GACATCCCAT TGTACGGGA NGAGAGAACC 780  
 20 AATCTTCNAC ATGGTGGTGG ANAT 804

(2) INFORMATION FOR SEQ ID NO:882:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 490 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1552UP

40  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

45 GATCTTGAG ACACGCTGC GCGGTAGTC CGTGGAGTG CAGACTGGT CGCGAATAA 60  
 ATAGCTTTGT GCCAGGCGGT CGCGAGGCG TTGCGGACT CACCGCATAA AAGAAACAG 120  
 50 CTGCGCGGC GCGGCGCAA AGCAGCCAGG CGCAACGGC GCGCGCAA AGCAACCGT 180  
 ACACAGATA TGGCAGATTC ACRTACATAT TATACATAGC CGGCGCGGC ACGCGGCTCA 240  
 55 GCGCGGAAG CCGTACAATG TGGGCGCTG GCGCTTGAGC GGTACACGA CGTCAGCGA 300

GGTGACGGTC TTGCGCTTGG CGTGCTCGGT GTAGGTGAAG GCGTGGGGA TGACCGACTC 360  
 5 CAGGAACGAC TTGAGCACCG CGCGCACGTC CTGCTAGATG AGGCGGAGA TCGCGTTGAC 420  
 GCGGCCACGG CGGGCCAGGC GCGCGATGGC GGGCTTGGTG ATGCCCTGGA TGTGTGTCGG 480  
 10 GAGGATCTTG 490

## (2) INFORMATION FOR SEQ ID NO:883:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1553RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

GATCCGAGG TGTACACGT TCACAACTG GTCCGGGTAC ATCATGTTGA ATGCTTGA 60  
 35 CTTCCTCCGC GTCACAGCG TGTGGTGGC GAAATCCATC GAGCTGACCA TGCAAGAGTG 120  
 CCCCAGAAC GTCTTACCA CCGTGTGCT GTTTGGGTCC AGCAGGTGA GCATCCGTT 180  
 40 CTGCCGGCA ACCGCCATCA GTGGTGTCT CCACTGCATC AGCTTCACCT TCGACGAGTA 240  
 CTGCACCGTG TTGCTCAACC GCGCCCTTAC CAGGTCCACC GCCACCAGC CACTGGCCAG 300  
 45 GTTCGTCCC CCGCAGTACA CCGTGTCTG CGAGTTGCTG CCGTAGCACA TCGCCCGCAT 360  
 GTGCATAGT TGTGGATGT CCGCCGAGT TACGTGAGT TTCGTACGC TCGCCCGTT 420  
 50 CGCGAAGTTC AATGACTGC CCGCCAGCGA CAAGACGCC TGCTTGTGGC TCAGCAACTC 480  
 CACCACCGC TCTGCCCCGA TGTGTGCGT GTGCCCGTG TATAGCGAGT ATGACGGGTC 540

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GTACGACGAC ACCCGTCCGT ATGIGTCCCC ACCCAGATCA GATTGACGTC CTGGTCAAAC 600  
 5 GCCATCTTGG TCGCGCTCTT CTCCTTGGCG TCGTAAGCCC AATACAACTT GCGCAGGTGC 660  
 TCGGTGAGCT CCACCGGCGA CTGGTATGAA A 691

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1553UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

GATCCGGCGT GTGTGCCCCC ACGCAATGCC TACCTGTTC A CTGTCTCCA GGCTCCACAC 60  
 CCGAATCGAG CGGTATCCG AGCATGATGC AACCAGTGGC CCGTCGTGGC TCACCAACGC 120  
 GCAGAAGATC GAGCCCTCGT GGGCTCCAG CCGCTGCACC ACCGCCCCCG TTGTGAGCTC 180  
 CCACACCACC ACCCGGCCCA TCACCGTCCC CGCGCACACA TACACCGCAT CGCCCAACCAC 240  
 CTCACCGAC CCGAGTACA GCAGGACCG CTCACCGCG TTGATGCTGC GCACCACAG 300  
 CATCTCCAGG TCCATCTCCA GCACGCTGTT GTAGCAGGTC AGCAGGTAAC ACGAGCGCCC 360  
 GTCCGGGCTG AACGCGGCCC CGAGCACCCA CTCGGGGTTC ATGTACTCGT GATACTTCAG 420  
 GTTCCGGCGC GTATCACGT CCTCCAATC CAAGATGCTC ACCGACCGGT CCCCATATGC 480  
 AATTACCCAC CGTCTCTCA CGCATATCCC GTGCACCTTG TTTGCTGGA AAACCCGGCA 540  
 GCGGTTCAGC AGCACTCCG CGGATACTC GTATACGTAG ATTTCCGGC CGCACCTGC 600

EP 0 866 129 A2

TAGGCACCTC CCGTCCCCGA GAATCOGCAC TGCAGTGCAT GGCGCAATGT CATTGACCTT 660

5 ATCCAGCGAC ATATTTCATCG TTTAATCGAC TATGATCCCG ATCTAATG 708

(2) INFORMATION FOR SEQ ID NO:885:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 705 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1554RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

30 GATCAAACTA GGAATTTTGT ATAATACTGA AGAAGGTCCC ATATTCAAGT CTCTATCCAG 60

CGATGATGAG GAAGTGGGTG AGATTGTGCT GCACGACCTG ATGAACAATC TOGATTTCAT 120

35 AACTATGGAT CATCTGACA GATCGAGAAA CCAAATCAT CAAGATAGAC CGATGATGAT 180

CAAGAACTAG TTTGAGATCC CTCTGCTACA AACACATACC TAGATTTCCTC ATATTTTATA 240

40 CTGAATACAT ATAATATATC ATTTAACTGT CTTCATTTCAT GAGACGTCTG CTAAGTTCTG 300

TGCTGCTCAA CTGTGTTTTT CACTGTGTCAG CCTCTTCGCC CCCCAGTACG TTCACCACAT 360

45 GCACGGCTAG CTTCCTCATT CCTTTGCTCT CACGGGTATC GTTGATTGTC TGGGCACCGG 420

CCACAGTTTC CTCACTCACT ACCAGGGCTT CGATAACCAGG TTCGCTACCC GTGGGCCCCG 480

50 ACACGTCTTG TAAAGCAAAT ATTTTGATTT CCAGCCCCGG TTTCAGCCTG TGAAGGAAGC 540

TGCACAGTT ATCGCATCGT TCGTCGAAGG ACTGAAGCTG CTCCTGTAT TTCTTGTTCC 600

55 GCAGCAGTTC TTCATCTGTA ATCCCCACGA TCAGCCGGGA AGCAGTCAG AGCGGGGCAA 660

CACTGAGCAA TATTTTATGT CCGTCGTGTA AGTGGTCGAA AGTGC

705

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1554UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GATCACTGAG GAAATCAAAA CCTGAGCAG CTTCCTGTG TTGGGTTGT ACGGTGTGGA	60
CTGTGCCCAA GTTGAGACTG TCTCCAGGC CAAGGCTCCA GGCCAAAAGC TCTTCCTAGG	120
TATCTTCTTC GTGACCAAA TTGAGGCGG CGTGAAGGCC ATCAAGGAGG CTGTTCAGAA	180
GCATGGATCC TGGGACGACA TCGACACCAT TTCTATCGGT AACGAAGTTG TGAACAACGG	240
CCAGGCGACC GTGGACCAGA TGGCTGGTTA CATGAAACT GGCCGCAAGT GCCTCGCTGA	300
GGCCGGCTAC AAGGGCCAG TTGTTTCGGT GGACACTTC ATCGCTGTAA TCAACAACCC	360
TGGTCTATGT GACCTATCAG ACTACATGGC TGTCACGCC CACCCATACT TCGACTTCCA	420
CACTTCTGCT GCTATGGCCG GGCCTGGGT TTGCAACAG ATCCAGAGAG TCTGGAGCGC	480
CTGCAACGGT AACAGAAAG TTGTATCAC CGAGACCGGC TGGCTACTC AGGGTCAGAC	540
TTACGGCAAG GCCATTCCAT CCAAAGCCAA CCAGAAGATG GCCTTGGAA CTATCAGGCG	600
CACTTGTGGT GATAGCGCTA TCCTATTTAC TGCTTTGAC GACTACTGA AGCCAGATGG	660
GCCTACGGT GTCGAGAAGT TCTGGGGTAT GCTATAAGTT GCGTGTGCT TCTTTATGAC	720

CTGTC TC

727

## (2) INFORMATION FOR SEQ ID NO:887:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1555RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:887

GATCATACAC GCATTGCAGG TATACATTAT AGTGCTCATA ATTATCGGAT TGCAAATAGA 60  
 ATGGGGCCCT TACCGTAGTA CTGTCCTGGT AATGCAGCGA CGCTCAGGCT TAAGAAGCTT 120  
 TTTGTCTTCC GGTATTACT AACAAATAA TTCTCTGAG CACAGGGAGT AGAGATGAAT 180  
 TACATAATCC ATATGGACAC CTGCTCAGCT TCCAGCGACA TTAACATTTC CTTATGAATG 240  
 CCCAATAATG GTGCTTAAAT GATGTGCTTG GTGTAATGCG CATTATAAAA TGTATGTGGA 300  
 TTATATATTG TTTGTAGCAT CTAGTAAAC CATGGTAGCG AGGTCTTTGG CCATACCTTT 360  
 CTGAAGAGAG ACATAGCAAC AGTGTCTTGT GCAGACAGTC TGGCGTCGAA TGTTCGCTTG 420  
 AAGTAACCAT GAGTACCAAG ACTCTCCTTA ATGAAGCCAG AGCGTCCAGA TTTCTGTAAT 480  
 AGTGGGATCG ACTTGAACCA CTCGACATCT TCTGGCCTAA AGAACATATA GCGCACTGTG 540  
 ACGACGCGCT TGTGGAACCT GAATGGATGG GCAGTTAATA TGATTCTCTT GGCCAATATC 600  
 CGTGTGTGGT CTGCGTTCAG GAACGTGCGG TGGCCACGTA ACGTCAGGCC CTTTGGATCA 660  
 GAAGGGTTTT CTTTGAAGTA GATGGCCGCT GACTGGGTCA GGTCCAAGGG AA 712

## (2) INFORMATION FOR SEQ ID NO:888:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1555UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GATCTGGGAA ACAAGCATT CCAACTAGTT GGAATGGCTG GCAAITAGCA GCTGGGGCAA	60
GGCAGATAAA GCTAACTGTG GCATAGTTTC CGTGAGTTTT GATTGGTTTT CTCAAGCAGG	120
AATACTTTGC TGGCCGCCAC GGNCGCGT TTTTACTGT CAGGCCAGOC CGCGGCTGC	180
CGGGTAATGC CTGGCAGACC CGCTCTAGGG CACGCGAAT CGCCCGTGAC AACGCCTGCC	240
GCCGCAAGAT GAGCACCTAA AGGGCCGGCA GCTCCGCTA GACAACCTGA TGGTAACGTC	300
GTATTGTAAT ACTTAACCTA TACAGGTTTT ATTGATTATA TTAATCAGAA ACTGCCGTGA	360
GACCCACAGC CGCCCCCGG AATTGTGTAC AGTAGGGGGC AGCGGGCCGC CGCGGCTCT	420
TAACGGTACT TGTGGAAACC AATGTGTTG GCCTTCTCTC TGAAGCACTG ACGGCAGATG	480
TTCAAGCGGT ACTTTCTGAT CAAACCAGAG TGCGAAGCGC ACACGGGGCA CTGGCGGGAG	540
CCCTTACCGT AGTTTCTTGG GTGGGAGAAC CAAACGTTTT CGTGAGCCAT CTTGTCTGCA	600
ATGGGTTAGT ACTCTGTCTG ACCGCTTGA AACGCTCCG CCTCGTTGA GCTGCCACAA	660
CGCTCGGCGT CTGCGGGCTC CTCATTGCC	689

## (2) INFORMATION FOR SEQ ID NO:889:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1556RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GATCAACCAG TCGGCGGAGT CCTATACGAC CGGCATCAGG CTGGTGTTCG AACTTCTCGG	60
TGACCCCTCG ACGTACCTGC CTAAGGATAG TTTGCCGCCA GAACACCTG ATGAGGGCTT	120
CACGAGTGCT TCTGGGTCCG AGCTGCAGCG CCGCTTTGCA TTCAAGTGTC AAAATCCAGG	180
AGTCACCTTC GTAAATGACT TCACGGTAGA CGTATACCCG GCCTCAACCT TCCAGCTGCT	240
CAATGATAAT ATCTGCTTGT GTTTTGATAT TCTGAGAAGG CAGAAGTGGT GGCACACCGT	300
CTTATATCCT ATTTCCCAAC TTTTGCTGCA TCAAGGCCAG GATTCTGCGG TAGGAGACGC	360
CCAGCACCC GCAGCCCAAC CCGGCTCCA CCGCCGCGA TCAAGCAACA AGGGCTGTGG	420
CCGAGCAAGT GCGGCGGAGT CAGCCACGCT AGGGGACGAA AATATGCACC AACTTACCTT	480
AACGGAAATT ATGAACAAGT CTGTGATTCC CGAAGATGAC CGATGATGGA TGACCGCATT	540
GAGCTCTATG TTAACGAGAA CTACGCTCTAT CTGGGGACCA GGAGGGTTC AGCTTCTATA	600
ACGATCOGAT TGAGAGGTGG GAGGCGTTTG TAGAGTCACT AAGACAGATG CTTACGTAGG	660
TATATAATTC TCATCTCAGC CTTGGTATGT ATGCGCTTGT	700

## (2) INFORMATION FOR SEQ ID NO:890:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1556UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

20	GATCCGATA ACGTCCACAT AAGGGAGAGA CTAGAGGCTT TGACTGCCCA GCTAGCCAAC	60
	CCAGGGCCCC AGCAGGCTCA GCAGCAGGCT CAACAGCAAC AGATGCAACA GCTAGAGGG	120
25	CCAGCACCCA TTATGTTGCA GCCAACATTG CAGCAGCAAG ACCAAACAAA TCGTTGAAT	180
	AACAAACCTG CGTTCCTACG GTCTCTCC CACGGAGTTG CGGTTGCCG AACAGAGTCC	240
30	GCAGGCCACA CACCAATGTC AGGACGGCCT CAGCCGTTGC AGCAGTTGAA CAATAACGGA	300
	AGTATCCTGG AACCGTCATT GTTGCCGCAA AAGAGGCTTA TGGAGGGTGG AATGGATACA	360
35	TTGGTAAATG CCATTTCGCA GCAGGAGTTG CAGCAACATC AGAAGAAACA TATGCTTCT	420
	CAGAACCATC CTAGTTTGGC CCTGGCTACA GGACAGCCGC AGCAGTTACC ACCCGATGCC	480
40	GCTCCCATAA TACCGCCCGA AAAGAAAGGT GCGCTCTCC CCCAGTTCA GAAAACTGAA	540
	CCAGAGCATG CGGCAAAAAG ACTGAAGCAC GAGCAGAATA ACGTTAAGA GCAACCGGTC	600
45	CGGTCTCGAA TATACCTTG ATTACGCACC CAGCTTCCAT GGAACATTCT GGTCCGGGAG	660
	ATCAGAATCA CATTCTATCT GGGCCTTCAG TCCAGCAAC CCAGTGTTA CTCGGTA	718

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1557RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GATCAGGCGA GACATTGCGT AGAAATATCA ATTGGTTCCA GAGGAGATCT GTCTCTGGT	60
CATTGTAGAG AAGCGGCCAG ATATAATTGT CCAAGTGAA CTGTCITTTT TGAGAAAACA	120
CGCTTTCATA CACAGCGTCC GACTTTTGGG CTAGACCATA AGCAAGGTCT ATAACTTCCG	180
TGGCAGTATA ATTCCAGACC GCGGTGGT GCGCGGGAC AAGGGACTCC CAGTACCCAA	240
GTAAATCCTT CGTCATTGAG CTTTMTTAAAC ACAGAGCCAA CTAAGATCGA CATGGTAAAC	300
GACGCGATTA MTTTGTACC ATTTTATAG GAGACCAGAT ACATTTCAG AAGCAACAAC	360
CGCAATCGTT TTAATGGTG CAATCAGTGC CATTCTGCA GCTGGGTCCA AACTCTAGAT	420
TTACAAACCC CGCAGCAATT AGCTAGTGTT GAACCAGCGA ACATGTAAGG AGTTTCATTT	480
CCCCACACTA TTGAAACTA CTGCGGTGAA GCGAGGTGGG GCGCATTAAC CGCCATATAA	540
CTGTGGGGTT TGATAACAAT TATCTCATAT TGTCTTTTTT ACGCACAAAT ACATCCACTC	600
ATAGAGAGCA TTACGCCAAT GCAGTCAAAT ATAACGGAGA ATTTGCATAT CAGTACGTGG	660
AATCGCAGCA GTTGCTGTGA TTTTACTATT GATAACGGGC GCAGCATAAG GGCTGTGTTT	720

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1557UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GATCCGCGGA TTTGGGCACC ACAGGGTAGT GTGGCCGCAT CAAATGATGG CACACAAGCG	60
ACGTGGGTAC TCAGCCCCCT TATTTGATTT GAAGAACAGA TTGATTAGGT CTGATCTAT	120
AGCTCTGGGC AAAGCGGGGC GCCTTGGGCG CTGTGTGGCC GCGAAGTATC GCTTAGGAAA	180
ATGCTGGTGA ATGTATATTA TACGCTGACG GGAGCATTGC AGTCAGGTGT CATGTATGGA	240
CTTGCTGCG ATTAAGTATC GCAGCAGCCA TCTGATGCTT ATGCACATCA ACTAGCACAG	300
CAGCCATATG ATGCTTATTC ATACCGGCGG CCTATCGCCA TCTTCTTCAT ATAAAGGCAG	360
TGTTGTACAG ATAGGTGCAT TGTCTCTGA ATTCCAAAAG CTCATCGCGA GTGCAGATGA	420
AAGATCTCGC TTCCTTGGTC CCGCGCGAGG CGGCACCATC GTGGAATTTC AGTCACAAG	480
ATGTTATTAG TCTTAGCCAT CAATTGATCA ACCAAACCGA GCGGGTTTAC CACAACGTGT	540
TACAAGAAAA GCCACCAACA ATTGACAATT ATATCATGCC TCTAATATAC CATGAGGAGG	600
AAACAGACCT GCTATGGAAC CAGTTGGTGT TTCTCCGCAA TGTTTCGCC GATCCGGAGA	660
TTGCTGAAGC GTGAAGAAC GCAACATCCA TGCTGGACGA CTGGATTATT GGCCTTACGT	720
CAAAGT	726

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1558RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

GATCTATTTT GCGACTTCC CTTATCTACA TTATTCTATC AACTAGAGGC TGTTCACCTT	60
GGAGACCTGC TGGGTTATC AGTACGACCT GGCATGAAA CTATTCCTTC CTGTGGATTT	120
TCAAGGGCCG TCGTAAGGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	180
ACCCCATCTC CGGATAAACC AATTCCGGGG TGATAAGCTG TTAAGAAGAA AAGATAACTC	240
CTCCAGGGC TCACGCCGAC GTCTCCACAC TCAGTTACGT TCCCGTGAAG AATCCATATC	300
CAGGTTCCGG AATATTAACC GGATTCCCTT TCGATGGTGG CCTGGAAAAT CAGGCCTTTG	360
AAACGGAGCT TCCCATCTC TTAGGATCGA CTAACCCACG TCCAACGCT GTTGACGTGG	420
AACCTTTCC CACTTCAGTC TTCAAAGTTC TCATTGAAT ATTTGCTACT ACCACCAAGA	480
TCTGCACTAG AGGCCGTTG ACCAGCTTT ACAGCCTAGG CTTCGTCACT GACCTCCAG	540
CCTGCCTACT CGTCAGGGG TCATATTTGC CCTGACGGTG GAGTATAGGT AACACGCTTG	600
AGGCCATCC ATTTCAGGG CTAGTTCATC GCGCGTGAG TTGTTACACA CTCCTTAGCG	660
GATTCCGACT TCCATGGCCA CGTCCGGCT GTCTAGATGA ACTAACAC	708

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1558UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GATCGGGTGG	TGTTTTCTTA	TGACCCACTC	GGCACCTTAC	GAGAAATCAA	AGTCTTTGGG	60
TTCTGGGGGG	AGTATGGTCG	CAAGGCTGAA	ACTTAAAGGA	ATTGACGGAA	GGCAACCACC	120
AGGAGTGGAG	CCTGCGGCTT	AATTTGACTC	AACACGGGGG	AAACTCACCA	GGTCCAGACA	180
CAATAAGGAT	TGACAGATTG	AGAGCTCTTT	CTTGATTTTG	TGGGTGGTGG	TGCATGGCOG	240
TTCTAGATTG	GTGGAGTGAT	TGTCTGCTT	AATTGCGATA	ACGAACGAGA	CCTTAACCTA	300
CTAAATAGTG	CTGCTAGCAT	TTGCTGGTTG	CGCACTTCTT	AGAGGGACTA	TCGGTTTCAA	360
GCGATGGAA	GTTTGAGGCA	ATAACAGGTC	TGTGATGCCC	TTAGACGTTT	TGGGCGGCAC	420
GCGCGCTACA	CTGACGGAGC	CAGCGAGTAT	AACCTTGGCC	GAGAGGTCTG	GGTAATCTTG	480
TGAAACTCCG	TCGTGCTGGG	GATAGAGCAT	TGCAATTATT	GCTCTTCAAC	GAGGAATTCC	540
TAGTAAGGCG	AAGTCATCAG	CTTGGGTTGA	TTAAGTCCCT	GOCCTTTGTA	CACACCGCCC	600
GTOGCTAGTA	CCGATTGAAT	GGCTTAATGA	GGGCTCAGG	ATCTGCTTAG	AGGAGGGGGC	660
AACTCCACCT	C					671

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1559RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GATCCAGAAT CCAAGTTGCG TGTTCGTAGC AACCGCCGCG TGCGCAGGTT ACGAAGCAGG 60  
CTAAGGAAAA GGGGCGCTGA TGCCGAGCAC ATCTCAGAAG TAGTACAACG CATAAAGGAG 120  
AAAAGCAAGC CAAGCGCTGA AAACAAGACC GTGGGTGAGC GGAATCCCTC ATCCGCTGCG 180  
GTTGCTGATC CTAAGAAGCG GGTAGTGAT GTCCCAAACA ACCCGCCAAA CAAAGTATTG 240  
CTGTACAGG ACCTGCCAAC AGACATTACC GAGCAAGAGC TGGTGGATAT ATTTGCAAAC 300  
GATAAGTTGC TCCAGGTAAG ACTAGTCCAA GTCCGGCAAC TGGCGTTTGT AGACTACGCC 360  
GATGTACAGA GCGCTACGGC GGTCAAGAAC AACTGGGTA CAAATTATGT GATCAAAAAT 420  
CAAACAACCA TCATAGGGTA TCGAAGTAC ATAGGGCGGT GGGGATATGG GTTCTTTACCA 480  
GTGGGTGGGA ACCCGACAGA TCATTAGGT AACTACATAA TGATAGTATT TACMAGACTC 540  
CTTAAGTGGC ACGTGCCTCG ATGTCATTTC CCAAAGAGGA CTGTTCTCAT AGCTGTGAGC 600  
AACGACTCTT TGCTGCGTCC TT 622

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1559UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

5	GATCGGATGA CCGTCATGTT CTTCTACAAG AACAAAGCACA TGCGATGCGA CTTGGGCGWG	60
	GGGGAACAAC AACAAAGATGA ACTTCGTGCT TGACAACAAG CAGGAGATGA TAGACATCAT	120
10	AGAGACGGTC TTCCGCGGGG CCAGGAGAAA CAAGGGGCTG GTGGTGTGCG CGTATGACTA	180
	CAACTACAAG CGGATACAAT AGAACATTTT TTGCAGCTAG TGTGTGCCA CGATAGAAAG	240
15	TTTATACGCA ACCCGGCACA GGCGCGGGT TGCTTGGCTC CACAGCTGGC GATGGAGCCT	300
	TGGGTAGGGC CCTGCTGGCC ATTATTCCTC TGACTCGACC TTACGCTAT AGATGGTGTG	360
20	TGGGCTGTTC TGGCGTGAT AGTGAAAATT TTTTGGCTTT ACGCTCCACC GGGTTCAGGG	420
	CTAGGCAGCA GGATAAGTAC WTAGGTCTTT CTGCTTCAGG CATTATATAA CCTCAAGGGA	480
25	GCTTTTCAGA CCTTTTAGGC CAATATATCT CCAAAGTGIG GGCATCTGGA CTATTAAGCA	540
	GGAGGTTCTA TTCCAGCGTC ATCAAGAAAT CTGTCAGAAT AAGAACCATG GCTCAGAGG	600
30	ATGTGCAACT GGCCAGGAAG GCTGTGAGT TTAACAGGGA GAA	643

(2) INFORMATION FOR SEQ ID NO:897:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 139 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1560RP

50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:	
55	GATCGCGCGG AGGTTCTGTG AAAACCTTCC ATGCACAAAC CCCACACCAT GCTCCCGCTC	60



GTCTCTTCA AACTCCTTCG CACTAATGGT GCGTCGTCC ACGACTTTAT CATTCOOGTC 120

5 AAACACTAAG TCAGGGATC 139

(2) INFORMATION FOR SEQ ID NO:898:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1560UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

30 GATCOCTGAC TTAGTGTITG ACGGGAATGA TAAAGTCGTG GACGACGGCA CCATTAGTGC 60

GAAGGAGTTT GAAGAGGACG AGCGGGAGCA TGGTGTGGGG TTGTGTCATG GAAGGTTTTT 120

35 ACAGAACCTC CGCGGATC 139

(2) INFORMATION FOR SEQ ID NO:899:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 688 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1561RP

55

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

5	GATCCAAATA AGCGTGGGT CCATACAAAT GAAOGGTGA GTGAAGCTAC TTCGCTCGGT	60
	CGCGTATGAT TACTGCGACC AGGCTCTGGA TGACGCGGG GGAGATGGCG CTGCTGCTAC	120
10	GGCAGCCAAT ATATACATCT TCTATAGGTC TAATTCATGT CCGCTTTTTA AAAAATGGCT	180
	TGGTCAATT TGTATGTAGT AGGCTATGTA ACGGCTCAGT CCGTGGACTC GCGAAGCGT	240
15	TCTGGATGG AAGCAAAGAG CTTTTCGAAC TCTGGGTGA CCTCGGCTC GCGCGGCTG	300
	GGCTCGAAGA ACTTGGAGGA CGAAACGGCG TGTTCACGT CGCGGTTC CTCCGACAGC	360
20	ACGGCCAGT TGGCGCGGT GGACAGCTC TTTTGTCCT CGTCGAAGTA GGACACAAAC	420
	GCTTTCATCA TATCGTAGGT CTTCAGATG GGCAGAAATG CGTCGTAGGT CGAGTAACCG	480
25	TTCTGCTGCA AGAAGTCTC TTTGATTAGC GTCCGACAT CCAGTACGAT CTTGTCTTTG	540
	TCAGAGAGCG CGACTTACC GACCAGCTGA ACAACTTGCT CCAATTCTC GCGTTGGAG	600
30	AGGATCTCTT TGATACGTC TCTCAGGACT GCGAACCGG GTAATTGCTA TCATAGTATT	660
	TGTTTAGGAC GTTGGTGTTC CTTCAGT	688

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1561UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

EP 0 866 129 A2

	GATCGCAGTC TGTAGTTGCT GGTACTGGAG TCTTGACTGC TCTATGCTC TTGCTGTGC	60
5	TAAAAGCGAA GGAGACTCGG TTACTTGTAT GTTTTGCTGA CCTTCTGGTG GCAAAAGGGG	120
	TGGGGCGCGG GGTCCGACAC TATTTTGGAG CGGAATCAGC CTGAGTGTTC TTTTGTTTT	180
10	CACCAAGGGC GGGTAACCTG GGGCCAGCGG CTGGCCGGCG AGGTGATGGG CCATGAGCAC	240
	AGCAGGTATC GGGGAATAT GGAGTGTCCG GGGCGCGCT TATGTAGACC CAGCAAGGTC	300
15	CCCAGCCATC GCGCGAATT GCGCTTTTG TAGAGTCCCG CTAGGCGGC TGCCGCGGC	360
	GTCAGCGCT GTGACACAGA CAAATAAAAT TGGGCAAGCG CGAGACACAA GTCCACAAG	420
20	CGGCACTGC ACGAAGCTAT GCACGCATTC AAGGAAGACT TACCCATAC CGTGGGTTTT	480
	GGCTCGACA ATGAGGAGAT CACATCCCC AACTACGTGC CCACGCATGT GCAATCGTTG	540
25	CCCCACAGT CCAACGGGAT CCGACAGCTA GTCATAGATA AGCAGAACCA GCGCGTCTC	600
	CCACATATA ACCGCTACT CGACCGCATG GAGGACGGC TCGTGGCTG GCGCGCGCC	660
30	GCCAGCTCC ACGTGGCTC CTGCTAGCA ATCCACGGCA CGCACCGTA C	711

(2) INFORMATION FOR SEQ ID NO:901:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1562RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:	
55	GATCATTTGA GTGCAAAGG AGAAGTAGCG CTTTGTACAG TACGTGGGT GTGTGGACAT	60

CCTAGGTA CT GTTGACATTC ATGTGGGTCA GTCAGATTAC AAGTACACAA AGTCGATATG 120  
 5 ACAAGCCACG TGACCATATA TCCAAGAGCG CCCCCAGCG ACGCTGCTC TGTGCATAGG 180  
 ACTGGCTACC TACCAGTTAC AATGGGGTTT GCAACTTAAC TGCTCTAATC CTCACACGCG 240  
 10 GAGTTATATA TGTGCTATAG GGCATGCTCC CGGGCGCAA TTCAGGGCCA ACGGCTGOC 300  
 ACCATGCCAG AGCAGCCATA CCAAGCGCTG CAACAGGATG CGATATCTCG TTCTATATAT 360  
 15 ATACAGATAT ATATATATAC TGTAAACAAA TCCTAGCGA TCTGCTGTG AAAGGCCGGT 420  
 ACTTAAATCA TATGTCGTC TTCTTCAGCC CGATCGACA AAGCCCCGCC ATCGTTCCGG 480  
 20 AAGCTTGAA GCTCGGGGCG AGAAGAGCTC AACTCGAGTG CGCGCATAT AAAGCCGGTC 540  
 ATGAAGAGCA TTGTAAATGC GCAAACTTGG AAAAAGCTG CTGGCAAAG CATCACTGCC 600  
 25 AGGAGGAGTT GTAGGAGGCG GCGACCATG TAACTATAGT AGAAGGAGCG GTATTGTGA 660  
 AGCAATGTA CTGGTCGAA TTGAGGTAT ACCAGCAGGA CGGAGAGTGG AAGGCCGAAA 720

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1562UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GATCTGGCGT GCATATATAA CGTATCTGCG CTCACGCGAC CTGGTGCGGA CTCTTTAGC 60  
 55 CGGCTACTAA CTCTGTAGCT GTTGGGGCTG CCTGCGGCGC CGCGGGGCGA GCTTGGCAGA 120

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ATCCGCGGTT GCGTCACGGC CAGTGCCAGC CGAACAGGAC GCGCTTTTCT AGCAGCAGCG 180  
 5 CTTCCGCAGC GGTTCCTTTT TTTCGCCAGC TAAGGTGCTG TATTTCTCG CAGAGGGTTA 240  
 GAAAAGTACA CTTTACATCT GAACACACCA CAAAGTCGTT CTGATTGGAG AGGCACGAAA 300  
 10 CCAAACAATT GAAAGGTATG TTGAGTGGTA AGCAGACGGT ACACTGAGCT GCGCGTCTTT 360  
 TAGCAGCTGG CGGCCACCG CACTTTCTCT TTTCGGCTC TGTTGCTTCT TGCGCGCCCC 420  
 15 CTTGGCCTGG ATCTCGAGAG CCGGGAGCT ACCGCGGTC CCGCGCCAGC CTGGGCTTCC 480  
 CAGGCGGCCA GTGGTCAGAG CCGGTGCGC ACCGCAGCG GCTTCATGG CCGCTGGGG 540  
 20 CTCTGTTTAC AGGATCGGT CAGTGGCGT GTGAGGCTAA GCGGTGGCG AG 592

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1563RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GATCCTGCT ACTTTGACAA CATCAGGAAG GCGCTTGCTG CAGGCTTTTT CATGCAGGTA 60  
 45 GCGAAGAAAC GCTCGGAGG GAAAGGCTAC ATTACTATCA AAGACAACA AGACGTGCTC 120  
 ATCCACCTTA GCACGGTCAT TGGCCAGAT GCAGAGTGGG TAATCTACAA TGAATTCGTG 180  
 50 CTGACTACTC AAAACTACAT ACGGACGATC ACCTCGTCC GTCTGAGTG GTTGATTGAA 240  
 CTCGCACCTG CGTACTATGA CTTTGATAAC TTCAAAAAG GTGATATCAA GCTCAGTCTG 300  
 55

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GAACGGATTAA AACAAAAGAT GGATGCAATC GAAGAGCTAA GTAAAGAGCA ATCCAAGAAG 360  
 5 CATAGACAGA GCCGCGGTA NITCGTGAGC TTGTTGTAGC TAAATATCTC TCTGATATAG 420  
 CATGTACACA ATAATAGGAC TTTTGAGCTG TCCTTCGTTA CTTCGGATTA GCAAATTATC 480  
 10 GCAGAAGTTA GCAGGCACCG CCGCCCTTGT TGGTGGCCTT GCACGAAAGC AGCTGGTGAT 540  
 GTTCGGGGTC GCTAAAAACC CTCATTTGTG CCTATCATAT GCCCAGCGCT ACAGAGTCTT 600  
 15 CGCATCATCA TGTTTGAGAA GGACGAGATA CTCCACTTG ATGAGGCCAG GTCCCAAAG 660  
 ATAAAGGAGT TCCTGAGCCT CTCCCTCGG CTGATCACCG AATCCATCGA AAAGAAAGAA 720  
 20 TATGACTCCA TA 732

(2) INFORMATION FOR SEQ ID NO:904:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 717 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1563UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GATCGGTTGT CTTCGACGC TGGTACAGGG CTGGATGCG CGTCTGGGC TGGCGGTGCA 60  
 45 TATCGGAGAT ATGGCGCGT GCCCGTACGG CAAAGAATCA GCAAGACACT AGCGTCTGGC 120  
 50 ATTCTTTTTC AATGCATTAT TTAGCTTTT TTTTTTTTTT TTTTITAGTA TAGACACAAT 180  
 ATAAAGTAGA GTTCGTCATC AGTAGCGCTC GTAAGGTTAG GGGCGGCTT CAGGCCATAG 240  
 55 TAGCATCTCC GTCAGACTCC TGGATTGGCG CTTCCTCTAT GCCGCGGAT TCCGCAACTG 300

CGTAGGGTCT TTCGTTAGCG GACTGGTTCC CACCGGGGCC ATGGGCAGGC CACGAGGGAG 360  
 5 CTCCGGTAGC AGCCTGTGAC TTGTCTGGCA GCGAGCGGCC TGGTGGGTGC TGAAGAAGC 420  
 AGTGGGCGTT GCGACATTGG GCGCCGAATT TGCAGGGCTC GTTGATGGGG TGGCCGAAAA 480  
 10 AGCAATCTAT GCGCGTGCAC GCAGCGCCCT CGCGGCACAT AATGTGTGAA CGCGCATGGC 540  
 GGTACTTACA CCGTTTGTTC GTGCACTTGA CGCCGAACCTT ACACTGCTGG AGCGAACGCT 600  
 15 CCGCTGGTGC AAACGCACCG GCTTGAAGG ACGTGGCGCA GCAGCAATAG GCTGAACATC 660  
 TCGTATCTTG GACAAGGAAG ATGCGCCTTG TCGCAGTCCT CTGTGCACAG GTTAGGT 717

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1565RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GATCACATGT TTTCCTCCAGA GAGGGACCTG GCGTTGAGAG AGCGATGGGC CGTTATACCA 60  
 45 CTGAGCCCTA TTAGTGTCTG GATTTGTGTT TCCAGCAGCT GCGCATGGGG CCGGATTCCG 120  
 TCAAGTGTGA TTCCGCAGAT GTTGGTTTGT GCTCGATAAG TCATAAGGA AGCTGCTCTG 180  
 50 TTAGTACATG TCACATAGGA GGCTTCCGCA TTGGGOCATG GCATCCAGTG GCGGGCTTGT 240  
 GCGCGACCG GTATTCCAGT AGCCGTCTGC GAACGTATT CAATCATCTT TGGCCAGCG 300  
 55 GTATATAAAG CGGCTGATGA GCTTGGATGC AATGGGTGT AGCTGGGAG ACTGCACCGA 360

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AGATGTCTAG CAAAGTTTCA TTCTATTGA ATTGGCAGCC TGCGCCATAC CACATTGCGA 420  
 5 TTTTCTTAGC CCAGTCCAAG GGCTACTTTC AGCAGGAGGG TGTGGACATT GCGCTGCTCG 480  
 AGCCACGAA CCGTCCGAC GTGACGGAGT TGATCGGTGC GGGCAAGGTT GACATGGGCC 540  
 10 TAAAGGCGAT GATCCATAAG CTGGCCGCTA AGGCACGTGG TTTCGCCGTC ACTTCTGTTG 600  
 CATGCTGCT GGATGAGCCG TTCACCGGG TTCTGTACCT GCGTGGCAAC GGAGTCACAG 660  
 15 ATACTTTCAG CTCTCTTCAG GGAAGCG 688

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 558 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1565UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

40 GATCCCTTTC ATACAGGTCA ATATTTTATG CAGAGACAGG GGCTGGACGT TGTAAAGGTC 60  
 TTTCATCCAG ATATGCTAAG AGGCGAAATT TCATGCACGA GTATGATCAC AAAAAATGAC 120  
 45 ACAGCCAAAC AAATTGCCAT TATTTTTAGA GGATCTACAG TGATACAGGA TTGGATTATC 180  
 GATGTTCTAT CCACCCCTAT TCCATTCATT CTCGCTCTTA CCCCCTATCA GCGGTCAGT 240  
 50 GGAGCTGCAA AGTGCCAGG GAACTGTCTC ACGCACACTG GCGTCTACGA TCAATTTAAA 300  
 AAAGCATTTA AGGATATTTA TGCTGTTTTT AAGCCGCTAA AAGACACACA TCCGGATTAT 360  
 55 GAGGTGATAG TTA CTGGTCT TTCTTAAAGT GCGGCTATG CTCACTTTAT GGGTATTGAA 420



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TTGCAACTTC TGGGCTACAA GCGTCATGTT TGGCGCTTTG GATCATTGCG TATAGGCMAT 480  
 5 AAGGACTTTA ACGATTGGGT GGATGATATA TTTCGGTGG AAGACGTTTC GAGAAGAATC 540  
 CCAAATAATG AGATGCCC 558

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1566RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GATGCGAAA CACAACGGC GCGGCGGGT AGCGCGCGG GCGCTGCTGC AGGACGTGCG 60  
 CGACGCGCTC GCGGCGCACT ACGGGGTAGG AGTACATCAA CCGTACGTG GAGGACGAGT 120  
 GGGTGTCAA CAACGCGGGC GCGCTATGG GGCAGATGCT GATTCTGCAC GCGTCTGTGA 180  
 GCGAGTACCT GATTCTGTTC GGCACGGCG TGGCACCGA GGGCACACG GCGTGCCT 240  
 TTGCGGATGA CTACTTCACG ATCCTGCACG GGGAGCAGAG CGCGGCACTG CCACACGGCG 300  
 TGGAGCGCGA GGTGTACACG CCGGGTATGA CGCATCACT GCGCATGGG CACGGAAGC 360  
 AGTACGGAT GCGGTGGGC TCTTTTGCGC TGGAGCTGC ACAGGGGTG ATCCGTGCA 420  
 TGCTGCGTT CGGTTTTCTG GACACGTTCA ACAGCACACT CGACGTGTAC ACTCTGGCG 480  
 GCACCGTGCA GCTGACAGCG CCGACATGT TCAAGAACTT GGTGTACAAT TTCAAGTTTT 540  
 AGCCTAGATA CATAACCACC ACCAATGTCT GCGCAGGCGT CGCCCGGAC AGAGCTGCCA 600

GAACCCGACG CTGGGCGAG TGTACGCCAC GCTGACGGC CACTC

645

## (2) INFORMATION FOR SEQ ID NO:908:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 701 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1566UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GATCCTCAAG TCTACGAAC CCTCGAAGGT GTTTACGACG GCGTTTITGG CTGATGTCAT 60  
CACAGCTGAG GCTAAGGGTG ATTTTGAAGC GAAGTCTGCT GTCCAGGTC ACGTGCAACA 120  
GGGCGGGCTA CCATGGCCAA TCGACAGAAC CAGAGGAAC CTCTCGCGG TCGTGCGAT 180  
CGGCTTCATC GAGGCTAAGC AGGACGTCAT TCGGAAGCC AGGGGAAAT GAGGAGGCT 240  
TTGACTGGC CGACAAGCC GTCTCTACA CCGCGCGCT CCTCGGCATC ACGGCTCC 300  
AACTGAAGTT CACCTCCATC AGGCAACTCT ACGACCTGGA AACAGAGTTC TOCAAGCGTA 360  
TGCCAAAGGT TATCCACTGG GAGCCTAACC GCGGATTC GGACCATTTA GAAGGCCGCA 420  
AGAGGGTAAC AGTTTAGTGT CTCTGTTTCG CCGCTGCCC CACTATATGT ACCACTAGAT 480  
ACCAAGATTA TGGATAAACT TAACATGGCA GAGTACACTC TCATCCACCT GCCATGTATA 540  
TAATGTGATT TTAGTGACGA AACTGTTTT AAAGCCGTT GCAGGGTCGG TCGCAGCTCG 600  
TATAAATATC TTGACGCCAC CTCGATCTCC ATTGGTGAGG AAGTACCCGT CGAGATACAA 660  
TAGTGCCAGC TTGCTAAGG GTAAGCTGAC CACTCTACAC A 701

## (2) INFORMATION FOR SEQ ID NO:909:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1567RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

GATCAAAATGC CCTTCCCTTT CAACAATTTC ACGTACTTTT TCACCTCTCTT TTCAAAGTTC	60
TTTTCATCTT TOCATCACTG TACTTGTTGG CTATGGGCTT CTGCGCAATA TTTAGCTTTA	120
GATGGAATTT ACCACCCACT TAGAGCTGCA TTCCCAAACA ACTCGACTCG TCGAAAGAAC	180
CTTAGATGGC ACTAGCACCC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCCTGTTCC	240
AAGGAACATA GACAGGGACT AGCAACCAAG GTACTTTTCTT CAAATTACAA CTCGGAGGCC	300
GAAGGCGCCA GATTTCAAAT TTGAGCTTTT GCGCTTCAC TCGCGTTAC TAAGGCAATC	360
CCGGTTGGTT TCTTTTCCTC CGCTTATIGA TATGCTTAAG TTCAGGGGT AATCCTACCT	420
GATTTGAGGT CAACTTTGG GAATACTATT CGCTTGAAG GCCTTGTTTG TGTACGTTT	480
TTCAAGCGCC AGCTCCACTC CACGATCTGG TCGAAACCTA ATAGCAGTG TAGAACTAG	540
CTCAGACCGC AGTCCGCGCA AGTTCCGCCC ATGGCCAGCA TTTTCAAGTT AACCTGTCT	600
TACGACCGAG TATCACTCAT TACCAAACCC GAGGGTTTGA GAAAGGAAAT GACGCTCAA	660
CAGGCATGCC CCTTGGAAAT ACCAGAGGAC GCAATGT	697

## (2) INFORMATION FOR SEQ ID NO:910:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1567UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

GATCGTCAGA TACCTTAGTC TCTATACAGC GCAAGACATG GGTGATGGCG GGTTTGTTCT	60
ATGCAAAGTC ATTGGGTTTC CCTCTGCGCG CGCATACAAC ACCTGCTTAA CCTGAACAGT	120
CTCATCCTGG GCATCTAGCG ATCCCATGGG TGAGCAGCGG AGGATTTGGT GGATTACTAG	180
CCAATGGCAA TCCAAACCAA AGAAACGAC TTGGGGGAAT GCCTCATTGA ATAGCCGGTG	240
TTTCGACACT GTGATCTCTT GAGTGTAAAC TCCTCTTTGG TTGCGGATAT TAAACCTGTT	300
CTGTGAAACA TCGGAGCGGT GTTTAGTGGG AAGCAACTAG AGGAACTCAA AGAGTGCTAT	360
GGCATGGGGG CAGCTGTTCG GAAAGTGTA AAACCCGAGC TCCGGTTCCG TTGACACAGA	420
AGTTACTTTC TGTATCTCTA TCAGTCTATC ACCGAAGGAC CGTGGTGTGC TTTGCGCAIT	480
TTGGGGTTGT TCTTTAAGAT AGTTATCTGG TTGATCCTGC CAGTAATCAT ATGCTTGTCT	540
CAAAGATTAA GCCATGCATG TCTAAGTATA AGCAATTTAT ACAGTGAAC TGCGAATGGC	600
TCATTAAATC AGTTATCGTT TATTTGATAG TTCCTTTACT ACATGGATAT CTGTGGTAAT	660
TCTAGAGCTA ATACATGCTT AAAATCTCGA CCTTTTGGAA GAGATGTATT AT	712

## (2) INFORMATION FOR SEQ ID NO:911:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1568RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

20	GATCAGGAAA CGGTGCTAT TAGGTTCCCA TGCAAAGCGC ATGCAGCGGT CCTTAATCTC	60
	CACCTTCTCA AATGGAAACT CTCTGGCAGT CAAAGAGCAA ATCTCCATGT TGGTGAAGAT	120
25	GGTCTTCTTA GACTTGTGT GACGGTCCAC CTGTACACAG AGGAACTCTG CCTGGTTCTG	180
	CCAATGGAAG GAGACATCAG TAACCTCCAC CAAGTTGATG GTACGCAGAA CACGGCGGTT	240
30	CGGTAGCTCA ATCAGGACAG CTTTACACGA CTGGTTGTTC GACTCTGGAG TCCAGTATAC	300
	CATGACAGTA GATGGTGGGT CGTTGGGTCT GTTGAAGCC AACTTGATGC CCTTAGGAGC	360
35	AAAGGAGAAG TCCTGAACAT CCTCGATCTT CATCACTTA CCGCCCAACA GCTGGAAGTT	420
	CTTCTCGGTC TCGTACACAG CAATTGCGCC AGGCGCAAGA CGAGCGCAGA ACTTGTGTTC	480
40	AAAGGACCAC TTGACCATAG GCCATTGCAG CTGCTGCTGA GCGGCGAGCG CAAAGGTCTT	540
	CACGAGACA CCTGTTGCCA CATCCCATAT ACATAGCTGG TGGCCCCGCG ACTCGGGGCC	600
45	GAATGGACAA GCGTCGTTAG GTTCATCCGA GACTTCTAGA GGTTCGAGC AAAAGGTAAC	660
	CAGGTACTTC TCGGTGAGG ACATGGAGAT CGCCTT	696

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 697 base pairs  
(B) TYPE: nucleic acid

EP 0 866 129 A2

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1568UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

GATCATCTAC GTGGCCCATG AGGATAATAA GGAGAAAGAA TTCGAAATTG AGCTGAGCTG	60
GTGCTCCGCT TCGGAGACGG ATGGCTTGCA CAAGGGAGGT ACCAAAAGAG CTATTTGATG	120
CAGCGATTGA GTTTGCGAAG AAGGAGACCG GTCAGGAGAG TGATGATGAT TCAAGCGATG	180
ACAACGCATC TCGAGGTGAA GAGTCTCTAA CAAAGAAGGA TGCTGACGGT GATGTCCAGC	240
TTTCATGATA ACAGCCCCGC ATTATGTGGA GGTTCATTTT ATGACAATTG ACGGATGTTA	300
CTAAGTGTAT ATTAAGTTAA TCCACCTATA TAAATTAAATA ACATGCAAAG CAATTTAGAA	360
TTTGTCGGAA AGCAGGTTAA AGCATGTCTA CTCTCCTTAA TCTTTCCOGA AGCTGTACAT	420
TTTCTTCTTC AAGTGAACGA ATTCTATCCA CGGCTGGGTC TGATTCTAAT TTCCTACGTT	480
CGCGTTCGTG GTACCATTTT CGGTCAGCT CTTCTATCAT TAATTTTGAA TGCTGATCAA	540
ATGTATCTGA TTCATCCGAG CCTGCGACA CCTGGGATAG ACGTTTGATT CTTCTGTCTT	600
TTTCCTTTAA CAGCAGCTTT ACATGTTCTT CCACTATTGA TGATGTGGCA TTTTGGGATG	660
AACATATAAA TAGAATCCCA TTTCAGCTGG TTTCTTTC	697

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1569RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

GATCCGATAT ACGCTGAGTG CTATATTACA AACCATCAAT TTGATGTTAT CTTGGACGTA 60  
TTGTTGGTTA ACCAGACGAA AGAAACTTTG AAAAAGTTGC ATGCGCAGTT TGCAACCCCTG 120  
GGCGACCTGA AGATTATATG CAACCCCTCA AGCACCATC TAGTTCTCTA TGGTTTCCAC 180  
AGATTTAGCG TTACAGTGAA GGTTCAGT GCCGATACTG GTATAATCTT TGGGAATATA 240  
GTTTATGACG GTGGACACGG CGAAGATGCA CGCTATGTGA TCTTAAATGA TGTCATGTT 300  
GCTACAATGG ACTACATTAA GCCTGCAGTT TGTGATGAAG CTTCCTTCCG CAAGATGTGG 360  
AATGCATTTG AATGGGAGAA CAAAATGGTT GTCAAATCTA AGCTACCGAC TCTGCATGAC 420  
TACTTGAATA AGCTGATTGA GGTCACCCAT ATGAATGTCC TGACTCTCTA AGAATCATTT 480  
GCCGACCCCG AATGTGTTT CTTAAGCTGC AACTTATACT CGAAGTCCAC CTTCCGCGAG 540  
GATGCTCTGG CTAATTGTG TATCGAGAGA GACCCCTACTA GTGGTTCCAT CATCGGAGAA 600  
GTTCGCATCC GCTCGAAGAC GCAGGGCCTT GCTTTGACCC ACGGAGACAG TATTGCGCMC 660  
ATGGAAAGGT CC 672

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1569UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GATCTGCAAT GCTCTTCAAC AATTGCTGC AAGCTATTCT CCTGATGACC TTGOCATCTT	60
GAGTGAGCTT TTTGATTCCA ACAGCAAATC TGAATAGGCC TCTATCTCCT TTAAAAGCAG	120
CGTCGTGCAT GGGGCTTTGG GTTTACATTG GAAAAAGCCC CAAAGAACAA GGTAAATGCAT	180
GCCAAAAGTA GOCITTAATC CACTTCACAT TTAGATATTG TTACGCAGTG TATCTATACA	240
AAAAATAACG ACAAATAATA TCTTTTAGAG CTGGTCTCTT AGACTAAAAT AGGGCTCGGT	300
ATGCAATACC TCAGATGCTA TCTTGATATC CGTGTGGATA TCCTCGATTA AAGCCTCTTT	360
CGTGGGTAG TTTAATTGG GCGGATGTA GCCAAGGAAG CTGAACCTAA TTTTGGGGCC	420
ATAGAAGTCT TCTTCAAAGT CGTTTAAAT GTGCAACTCA ACCGTCTTCT TACTGTGTGT	480
ATAGAACGGG TTCCATCTTA CGATAACAC GATTGGAAAG ACTCCAGCT CTGTTTCCGA	540
CAGCTTGGAG CCAAAGTTGT ATATGACCTC GCTCCCATCA TTTCTGTGAT GGGACCTGGC	600
CTTCTTGGTC CATATTAGCC TTAACGGGC CCAGCCAAA TATACTCTG TGGCCATTTC	660
GTAACTTCC CTAGGCAATT GTTCTATTGG GAACATTC	698

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:



(A) ORGANISM: PAG1570RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

10 GATCCACAAC ACACACAGCT TGCGACTCT TTTTCTCAA GACAGTTCAC CAGTCCAACA 60  
 CTGTGAAAAC CATCTGCTAA CGTTTCAACG ATTGCGCAGC AGCAAACCCA GCCAACCGCT 120  
 15 CTCTCTCAAT CTCATCTCTA GCAACAACAA GGTTCACAAG CTCAGCAGCA GCTACTTCAA 180  
 CAACAACAAG GTTTCACAAGC TCAGCAGCAG CTACTTCAAC AACAACAACA GCAACCAACA 240  
 20 CCACCACCAC CACAACCACA GCAACAAACA CAACAACCAC AACAACCACA ACAGCAGCAG 300  
 CAGCCCCAAC CTCAACCGCA ACTACAACAA CAACAACAGC TTGGTTTACA GCTCATCAG 360  
 25 CCACAACCTG CGCAGGCGCA GCGCAACAA CCACAACCGC AGCAGCAGAC GCAGCAGCAG 420  
 ACGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGACACA GCAGCAGACA 480  
 30 CAACACCAAC CACAACCACA ATTGAAACCA CAATCAGAGC AACCACAACC GGTTCACAG 540  
 CAAGTCCAGT CTCACAACCC ACAGCAAGTC CAGTCTCAAC AACAACCACA GCTTCAGCAA 600  
 35 CTTTCACAGC CTGCCAACA ACAATCGCAA CAACAACAGC AGCAGCAGCA GCAGTCTCAG 660  
 CAGCAGAAGC TTGCCAAGT GCAGCTGC 688

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(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1570UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

5 GATCTTGGG COCGGGGGC CGCTGGGCTA CGTGCTGACG CTGTATGGA ACGGCAGTT 60  
CTTCACAACC ATGATCGTGA ACTCGCACCT GGGAGCGCG CTGTTGGACT ACACCATTC 120  
10 GTCGCTGATG GGTATCCATA TTGAGTACAA GGGCCATAAC CCTGAATTGG TGGAGCCGGA 180  
GGCGTTCAGC GCATACGATG TGCTGACGGT GCTGGGCTG GTCATGAGOG TTGCGGTGAT 240  
15 GGTGGTTCTG GTGACCATCC CGATTCTGGG ACCTGTTCTA CTGATGTTTG TGATGAATGT 300  
AAAGTTTTC TACGACTTCT ACGAGCGGTT CTTAATTCTA CGGGGACTAA ACCAGGTGCA 360  
20 GGGCGGTGAC GTGTTCTACC AGCATATCTT ACAGTTTGCA TACTTGGGG GGTGCTACAC 420  
GGTTTAAAT TTCGTGCTC TATTCTCAGT CTGGGGCTTT GTGTCTATC CGTTGGCAAT 480  
25 CAAAATGTGG GCGACTTCCA ACATCATCCA CTTTACAGOG GAAGAAGTGG AGTCCATCAC 540  
TGAATGAAAT CATTCAITTA ACATGTCCAT CTATACATAA AGATAGATAT AGCCAGAATC 600  
30 AATACCCCTG CCATTAGTAA AGTACCATGC TGTCGACACA GCGGAATCCC GCGCAACACC 660  
GCCCTGTTG GACGAAGGCA ACTTGAACG CAGCAGCCAT CCCAGGTAG TGGT 714  
35

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 658 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: PAG1571RP

55

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

5	CGCAGGCGGT AGGCAACACC GTTGGATATC TGCACTGGC AAAGGTCTG ACCCGGCAGC	60
	AGAAGCTGCG GCGAACGGT AGTCCACGCA TACAAGTGGC CGCGGGGGTC GATTGCCAAG	120
10	TTGCAACCCCT CCTCTGCCAG CGCCACATCC CGCAGCCGCT CGCCTCAAA CCCCGGCAAC	180
	CGCAACGGGA ACCGGGTGGA GCCAGCGTCC TGGCCAGCC GCGCGCCCCA GTAGTAGAGC	240
15	CCGGCTCTC CTGGCTGGG CGCGTCACC GGGATCTGG GGATCCCGG CAGCTCTTC	300
	TTGCGTTGA TCTCTTCAG CCGTCAAGC GTGTGTGGT CCAACCGCG GTGCGCGCT	360
20	AGAATCCAGC CCTTGATCTG CGGCCATTGA AGATACCGG TGCTGCTAC TCCGATCCG	420
	ACGACCACCG CCAGGCGCTG GAACACCGCC ATCAGCTTCT GCATCTTCTC CACCTTGTC	480
25	GCATACTCT GCTCCAGTGG GCGCGCGAT TTGTCACTCC ACTGGTAGTC CAGCTTGCTG	540
	CGCTTGGCT TGTATGTGCC ATGGTTCAGC TGCTCTTGG ATCATCTGG GCTCATCAA	600
30	ACGCTGCCCC TTGGGCAAG CCTTGCTTC CATAGCGAGC GCTGCGCAC TCGCAGCC	658

(2) INFORMATION FOR SEQ ID NO:918:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 657 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1571UP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:	
55	GATCAGTGA TGGGATGAAA ACTCTGACAA ATGCACCGG AATATATAAG GCATGGAGCT	60

5 GGGGACTCGG CCAGACAGTG CGAGCAGOGA AACAAACAAC TCATCCAAAA TGGCCAGAAG 120  
 ACCAGCTAGA TGCTACCGTT ACCAGAAGAA CAAGCCTTAC CCAAAGTCTA GGTACAACAG 180  
 AGCTGTGCCA GACTCCAAGA TCAGAATCTA CGACTTGGGT AAGAAGAAGG CCACCGTTGA 240  
 10 TGAGTTCOCCT CTATGTGTGC ACCTAGTGTG CAACGAGTTG GAGCAGTTGT CCTCCGAGGC 300  
 TTTGGAAGCC GCGGTATCT GTGCCAACAA GTACATCACC AAGATGACCG GTAGAGACTC 360  
 15 GTTCCACTTG AGAGTCAGAG TGCACCCATT CCACGTCCTG AGAATCAACA AGATGTTGTC 420  
 GTGTGCAGGT GCAGACAGAC TGCAGCAGGG TATGAGAGGT GCGTGGGGTA AGCTCAAGG 480  
 20 TTTGGCTGCC CGTGTGACA TGGGCCAGAT CATCTCTCC GTCAGAACCA AGGACAACAA 540  
 CAAGGACATC GTTGTGAGG CTTTGAGAAG ACCAGATACA AGTTCOCAGS TCAGCAGAAG 600  
 25 ATCATCATGT CCAAGAAGTG GGGTTTCACC AACTTGGACC GTGCCGAGTA CGTCAGA 657

## (2) INFORMATION FOR SEQ ID NO:919:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1572RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

50 GATCTATTAT TAGAGGTAAT ACATTTAAAC TATTATCTAA ATTCTTCTTC TTCTTAATTA 60  
 TTCTTAACIT TATCTTATTA GGTAAATTAG GTGAATGICA TGTGAAGTA CCATTTATTT 120  
 55 TAATAGGTCA AATTGTACA TTTATTTATT TTGCTTATTT CTTAATCTTA GTACCTATTA 180

TTTCTATAAT TGAAAATATT TTATTTTATT TACTAAATAA AAAATAATAA TTAAATAAAT 240

5 AATAATAATA TTCATTAAAT ACTTTAATAT TAATATTAT ATATTATACT TCTTTATCAT 300

TTAGGAGGGT ACCTCATATT GCTGACTAAC AATAGGGGGG TGAACCTAC GCACCTAAAT 360

10 GATAAGAGTT TATCATTAAT TTATATACTA TATATTATAA GTAAATTATC AAACCATATA 420

TAAGGTATAT ATATTAAGAA AGTTTGACTG AGTGGTTTAA AGTGTAATAT TTGAGCTATT 480

15 ATAAATCTTT ATGATTTCCT AGSTTCGAAT CCTATAACTT TCGTATTAAA TAATTATTTA 540

AAATAATTAA AAATAGTTAA TAATAATGAG AACATGATGT TGGTTCAGAT TAAGCGCTAA 600

20 CTAAGGGACA TTACACATGC CAATC 625

## (2) INFORMATION FOR SEQ ID NO:920:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 677 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1572UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

45 GATCCGTGTA TTTTATTATT ACATTATTTA ATTAAAAATA ATGATTTAAA TAAATATTTT 60

TTATAAAAAA TAATTAGTGC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAAACC 120

50 ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTTCRC TTAATTAAGA ATTAGGAAC 180

TTATCTATTA GTCTGGGCTG TTCCCTTTT GATTATTAAAC CTTATCGCTA ATAATCTGAA 240

55 ATATTTAATT TTAGATTAAAT AATATATTCT GAGATTTAAT ATTTTAAATA AAATAAATAA 300

TTATTCCTTA AATAATATTA ATAACATATC CATATATATC TAATATTTAA ATAATCATAC 360  
5 TAACATATGT TTCGTAGAAA ACCAGCTATT TGCAAATCAG ATTTGACTTT CTCTACTTAC 420  
CATTATTCAT CAGATAATAT TGCTACATTA ACCIGTTCAA TCGTTTTTAT ATTTTATTAT 480  
10 ATTTTAAATA TAATAAATAT ATATTTTAAAT CATTGATAA TAGTAAGATC ATCTGCTTTC 540  
GGGTAAATTA ATATTAACTA AATTTAATTT ATTTTAATTA ATTTTAACAT TGTAAATAT 600  
15 TTATATTATT TTTAATATCA TTTTTATTT TAATATTATG CTAATATTAA TTACTTGCTG 660  
ACCCATTATA CAAAAGG 677

20 (2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 623 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: PAG1573RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GATCCGTATG GAAATTATTT TTTTATTGA ATTATCTTTC TCCAGAACAT CCAAGAAGAG 60  
45 TGTCAGAGTG GTGGGCAGAT ATGGCTTAAA CTCCTCTCC AAAGATTTAG AAATAGATTG 120  
GATAACAGAA ATGATTGTAA TTTGCAGTTT AATAAATGGG AAGAACTCTT TAATGACTTC 180  
50 AAATATTTTC TCAACATATG GCCTGATATG TTGCTTCACA ATTGATACCA TAACACCTAA 240  
TTGTTGAAAA TAAAACTCAA GTATTGATGG AGGACAGCTA CGCATCACAT TAATCATTC 300  
55 TCGAATAATT TGCTTTAGGA AGGAGACGCA GCGGAGTCCC AATGTTTGA AGATGTGCAT 360

CACTGCCCTGT ATGACAGCAG TGTGATGAGA AGATAAAGAA GGATCCTTCA AAATTTTCAT 420  
 5 TAGAGTATTG ATCAAGACGG TTGGATAATA TTCTTCATTG GAGGGTGACA TACCTTGCAT 480  
 TAACAAAGCA ACATCTATGG ATGGGGCATT TTGTTGACG GATATAGGCG TCCTGGATGT 540  
 10 TCTTTCAACT TCTCTATGTT TATAAGGGTC CAGAGCTCC AGAATCCCTA TTAGTCTAAC 600  
 TGTTCCTTC CTTATGCTTT GGG 623

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1573UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GATCSGATAG GACAGCGAGT ACGACGGCCC CTGTGCGGCT GCCAGGGGCT CGTTGCCAAT 60  
 GTAAAAGTCG AGGTCTCTCG TCCCGGCTT CCCAGCCAGG TTGTTGACA TCAAAGAAGA 120  
 TGACGTAAAG CCCGTGAACG ACGTCGCGA CGTGTGTGTG CCAAAGAATG CAGACCGGCC 180  
 AGCGCCATA CCGCTCCGC TCTGGCCAT ACGCTCATA CTGCTACTCT TGGCGTCTT 240  
 GGAAGGCTGC GCAGTCGAA TTGCCGTTGG GAACACCCAT GAGGGCGAGT CGTTACCTGC 300  
 AAATCCAAT TTGGTCAATC CTGTACCATT GTCCATGACA ACAGCAGGAT TATTGAGGTA 360  
 TGACATGCTG TATTCTGGT CTCAAATGCT TCTGGTAGAC TTGTGTGAGC CTTTGGCTTC 420  
 55 GGATGGCTTG TCACTTACTG GCTTAAGAGT GCTGCCAGTG GAAAAGGGGT CTAATGGGCC 480

TTTCGTTTTTA GGTGATCACC ATCACCAACC ACGGTACACC TGACGAAAGG CAACGCCGTC 540  
 5 GCTTGTGAAG CCAGGAGAGC CCTCGTAGGT ATTCCGCGGA GCCAATTGGT GGCCCTCTGC 600  
 GTTCCTCGAG CGCTCCTGCT CCATCTGCCC TCTTGAAGTC TTTATGAACC TTGAAACAGG 660  
 10 GCATATAGCG ACACGGACTT TCTGCAGGTC TGTAGAGTAG CCCACATCCG GCGAA 715

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1574RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

GATCCCGAAG CTGGTCTGTT TCGAATTCGG GATATTTTTA GGAAGTACGT TTGTTCCAAC 60  
 35 GACGTTGCTT CCATGCATCT TGCGGGGTG TTGACGCAAC ATTTTCAGTC TCACATTCCG 120  
 TGAACAGCTT TGCTATCTAC TAGGAGTTAC TGAAGCTTTT AATGTCGTGT AATAAATCTT 180  
 40 TTGAGTTAGA TAATTCGCTG CGCTACAGTC TCCATGGGTT TTCATTGGCC AATCCATCTG 240  
 TAACTCTAAT TGAAAGGGAG AAGATCCTAT ACAGGAAATT AACAAAGGAG TCTGTGGCAC 300  
 45 TAGTTTGGG TGGGGGGTGC GGACATGAGC CTGCGCACAG CGGTATGTT GGGGAGGGCA 360  
 TGTTAACCGC GGCTGTGCA GGAGACATTT TTGGGTGCCC GTGACGGCT CAGATTTTGA 420  
 50 CTGCAATAAG GATTGCTACA AAGCAAGCAG CTGGAGCATT GCTGATCGTG AAGAACTATA 480  
 CTGGCGACGT TCTTCACTTT GGCTGGCAA CTGAGCGTGC TCGGTCTATG GGCATTGATT 540  
 55



GCCGCGTGGT TATTGTTGGT GATGACGTAC TGTTGGTCTT ACCAAGGGTG CAGGAATTGG 600

5 AC 602

(2) INFORMATION FOR SEQ ID NO:924:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1574UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

30 GATCAAAAGC GTGAAGCTGG AGCGTAATGA GGAGCAGCCA GTTGTTTTGA TGGACTGGGA 60  
 CCAGCTGTAC GACGTGTCTT CGAACATAAT GGAAGAATTT ACAAGGAAA TGGACGAAAT 120  
 35 AGTGGCAGAG CTCAACCACT CGTTCAAGGT ATGTAGCAGC ATGAACAGC AGGGCGGGCG 180  
 GGTTACTAAC GCGATGGGTG CAGAAGCAAT TGCTTTGGCA GGAGGGGGG TTTACCGTGG 240  
 40 ACTCGCACAG AGGCGCCACC CGGTTCGGCG CTGCGGAAAG CTGGATGAAG AGCAAAGAGA 300  
 CGCACTGGA ACAGAAGCG CGGGAGCTCA ATGCATCGGC GGCATCATC AAGAGCAGC 360  
 45 TCGAAAATTT GACGCAGGA TAGTCCCGGC CGGCATCGT CATGCAATGC CTTGCTCAAC 420  
 ATTACATGGA TGGGATTTT TGCTATGTA CAAACATAAT TTACGCGAAT TTAGCTTTCT 480  
 50 TCCAAGGCCT GTCTCGGTG TCTGCGCCAT CGGCGGCTT AGTTTCACT TCCGAGACAC 540  
 CGGCGTCTGA GTCAAACTC TCCGCGAGT CATGCTCTT CCACTCCGC TGGAAATCT 600  
 55 CGTCCACAGA CTCATCGTCC TCTGCAGCAG AACCATGTTA ACGTCTCAT CTGCTGTCA 660

GAACCAAGGG CTGTTTGTAG GCGCTGCTGA ATCTCTTTCT CTTCGTTTTT GACGCGGACG 720

5 TT 722

(2) INFORMATION FOR SEQ ID NO:925:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1575RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

30 GATCCAGTAA ACTTCAGCTC ATCGTGAGCA ACCGACGTCA CCCCACCAAG CGCAGGCGAT 60  
 ACTCCGGTGG AAATCACCTG AGTATATGCA GTACTCTTGG AACCATCGTG AGCAACCGAC 120  
 35 TCACCTCAC CACGCGCAGG TGAAAGTCCG GTGGATATCA CCTGAGTACG TGCAGGCGAA 180  
 CTGCCTGCGG AAATCACATC ACTATCAGCA GGTGAAACTC CAGTGGAAAT CGCCTGAGTA 240  
 40 CGTCAGTAG GCCTGACTC ATTGTGGGCG ACCGATGTCA CCTCACCCCG CGCAGGCGAA 300  
 CTGCCTGCTG AAATGCGATC ACCACGCGCA GGCGAGACTC CAGTGGAAAT CACCTGAGTA 360  
 45 CGTCAGGCG AACTGCCTGC GGAAATGCA TCACCACGCG CAGGCGAGAC TCCGGTGGAT 420  
 ATCAGCTGAG TCGGTGCAGT AGGCTGAGC TCATTGTGGG CGACCGATGT CACCTCACCC 480  
 50 CGGCGAGGCG AGCTTCCAGT GGAAATCACA TCACCACGCG CAGGCGAACT GCCTGTGGAA 540  
 ATCACCTGAG TACTTGAGT AGGCCACGAC CCACGTGGG CAACTGACT 589

55 (2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1575UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GATCAAATAT CAACTAAGGC ACTAGTTTTT GGTGTAGCTG CTCAAGCATC ACCGGATGCT	60
CAGAAGCGTG TAATTAACTT ACAATCTCGG ACTTCACCAC CCAAATCTGA AACACATTCT	120
CATATAAGGC ACAACGCTTC TAGCGTGTAT CAGTCGGAAA CAACAKATAA TATAACTAAA	180
GATACCGGGA TGTTTTCTGC AGTGAAGTCA GGCTTTCCOC ATATACAACA GAAAACCATA	240
TCAGCAGGCT CTGAACTTGA TGACACTGAC TTTCAGAGAA CACAACTAC CAGCACAGGC	300
CCACTTCCAA CTTCAAGCGA ATATGACTCT GCGCTGTGTA CAGTTCATGG AGGACTTGAT	360
ATTTCTCCAA GACCACCTTC CTCTAGCTCC ACAGATTTCT ACGAGTATCC AACTGGTACA	420
ATAACAGAGT CACACAGAGC GCCTTATAAC GTTAGCCAAC TTCCCGAAAA TAATGGGAAC	480
TCAGCTGCCA CTCGTGTGAT TAAGAGAAAC AGTTCTGTTC TCAGCTGGCC TGGAAAGCGTG	540
ACCAACACCC CAATGGTTAA TCRAGCTACA GTACTCAGCG CCTCGCCGGG AGCGGTTAAA	600
TTAACCGAGA AACAGCATAG TCCGGCATCA TCTTCAGATA TTTCACAGC CAATAAAACA	660
CATTGGAATT CTATTGATCT AAAC	684

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1576RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

GATCTTGTTG AGAACACTCA ACATCGGCGT AATTGCAGAG CCCCCTGTGA CCATACCGAT	60
TTTCTGTGAC GCATTGCTCA CATAGCTGAA CCGTCTTACA GGACCTTTGA ATTCCACAGT	120
TTGGCCTGGC TGTAGCCAG CAAACCATTT GGATACCTTA CCGTCGACAT AAGATTTGAC	180
AATGATATCG AAATGGCCCT CGGCAAAATTT GTTGGAGATA GCGGTGTAGT AACGCACATC	240
TTCTACACCA TOCAGCATCA CCTTCGCAGC TAAATGAAAG CCAGTAGGTA TATCAAGAGT	300
TTCCACGCTT GAACGGAGCT TGAATCTGTA TATCGCAGCA TTTTGTCTTA GAAAGATCCG	360
TTCTTCCAAT TCTAATGGCG TCCACTCATT TGGAAGAATT GAAGTCTGC TTCTGTATGC	420
TAGTAGCAGG CGTGCACCTA CAAACATTGC CAAAGCTAGA ATGCCTAGAA GGTACCATGC	480
GTTCCTCGCT GACCAGGCGA TAACAAGAAC GCCCAATGTA AAGATGCGCG TGGGGATGAA	540
GATCCCATGA ATGGGATCAT CCAATATCTC CATACCTCTG CGTTCGGTCA TACTAATATT	600
TTGAAAGCTC GTCGTAGCTA TCGTCTAGTA AGGATGAGAC CCGTTAATAT ATGCTTCCTC	660
CTAGTTCTAT AAGCAGGAC TCTTTGCAAC TGGTGAAGTA TCGTCTAAGC GTCATCATGC	720
ATCTGCCGAA AA	732

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1576UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

GATCAGGCGG GACGGGTACT TGCAGGAAGG CCTCAGGAAA CCCAAGGGGG GCGAGGAGGG	60
CTTCTOGACG TTTTCAACG AGACGGGCTC GGGCAAGTTC GTGCGGCGCG CCGTGTACGT	120
GGACTTGGAG CCGAACGTGA TGCAGGAGGT GCGCACGGGC GCGTACCGCG AGTGTGTCCA	180
CCCGAGCAG TTGATCAGCG GAAAGGAGGA CCGGCGGAAC AACTACGGCG GTGGGCACTA	240
CACGGTGGGG CGGAGCTCT TGAAGATAT CCTAGACCGC ATCCGCAAGA TCTGGACCA	300
GTGCGACGGG CTCAGGGCT TCTCTTCAC GCACTGGCTT GGCGGTGGTA CCGGCTOOGG	360
CTTGGGGTCG CTGCTTTTGG AGCAGCTTTC TATGACTAC GGCAAGAAAT CGAAATTGGA	420
GTTTGCCGTG TATCCGCGC CACAGGTGTC CACCTGGTTC GTGGAGCCAT ACAACACCGT	480
GTTGACCACC CACACCACAT TGGAGCATGC CGACTGTACG TTCATGGTCG ACAACGAGGC	540
CATCTACGAG ATGTGCAAGA AGAACTTGA CATCTGAGA CCTAGCTTTG CGAACTTGAA	600
CAACTTGATC GCCAGGTG TCTCTGGT GACCGCGTCA TTGCGTTTGG ACGGCTCCTT	660
GACGTGGAC TTGAACGAGT CCAGACCAAC TTGGTGCCAT ATCCAAGAAT CCACTTCCCA	720
TTGG	724

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1577RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

20	GATCCGTTTA GAGAAAAACG GTAGCCCGGT GAAATACGCA TTTGAGTGGC CAGAGGGCG	60
	CGAGCGGTCC GAAAGGTAGA TTTGTCCAG TGGGAAGTTG ACTCGTTTGC TTATTTCGAC	120
25	AATCGACGTC TTCAGCTCCC CGTCTTCCAA CGGGGTGAGC TTGTGAATA AAGCTGTAAA	180
	AACGGCTGA AGAGCAGTCA GCACCAGATA GAAGAACAGC ATCAGGATAG AGACGTAGCT	240
30	GACGAAGCCA GTCCGAACT TTTCAATTAC CTTCAACAGC GCATAGGCTG CAGGAGTGGT	300
	AATCATGGAG GAGATCATAA ACACCTTTAG CTGGTCCGTT AGCCATAGCT TGACCGTGA	360
35	CTTGTGAAC CGAATTTTT CCTCGAGCAC AAAGTTGTAG TAATAGCTCC CAAACAACCC	420
	CTGCCACCAG TTCAGCTGTA GGTAGACGAT CAAAAGTAC AGCGACTGCG AGATGGTGA	480
40	TACTGGCACC AGCATGGCGG GCATGCGCTG ACCTACCGCC ACTCTAGGT TCACATCCG	540
	TGGCAGCCAG TCGTACTTAA TCATTACCAG ATTTAGTCCC AGGAACACCA GATCTCTAAC	600
45	CATACGGTAG CGTTACTTGG CCGCTCGTA CGCTCGCTC TTTGCAATTG TTTCTTTATC	660
	AATAACGCC TCAGTTCGC TGGTA	686

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1577UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

GATCTTCGAC ACTATGTAGG CCGGTAGAT GAGCAACATT ACCACGAGT CCAGGAAGGA 60  
CACAGCGTTC ATCAGGCATA CGTAGCGAT AATGCAGAG GCCAGCATCG CAAACAGTAG 120  
GTCCACGATG ATCGAATGCC GCTCCGCGC GCTAAGATT ACCACGAGT ACCTCATCAC 180  
CATAAATATC GCGCCCTGTA CCACACAGAT GATAAGCGC CAGGCGCCA GCACCTCAC 240  
CACAGACAAG GCGCGGCAT TGTGCGCGC GTTCCAGAC ATCAGACTGG AGAACAAGTC 300  
GGCGACGAA TTGCACCATG CCAGTAGGAT GGCTGCCAGA ATGCCCTTGT GCGCGCGTT 360  
CGGTGGCTC GTCAGGTCA CCACTATGG ACATAAATAA TCAGAAGGG AAACGCCAG 420  
CAACACAAA CACACGCTCA GATGTAGAAC CGTCAGCACC ACGAACCCAG GGATAGCTTG 480  
TTGCTCTGAT ATAGATACAC TGGATGTGTG ATCCGTGCC ATGTACTTGG TGCATGGTCC 540  
ATCCTTGCAC TCTGCCTTTC CAGGTACTTG GTAATAGTAG TGGTAGCCAC CGCAACACTG 600  
GTCAAAAAGC ACACCTRAAA CCTCAATATG TAAGGCGTGC GAATGGTAGA TCGTTATTT 660  
AAAATGCAGT GCTTGAGATG AACAGATAGA CTGGTGCC 699

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1578RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

5	GATCATCCTG CTGGAGTTG AAGTCATCTT GCGATTCCCT CATGCATAGG AGTTGGTTAG	60
15	CACCAAACAT AGGATTCATT CTCAAGTCCA CCTGCGTTAA CCGTCTGTG CTATACTTTA	120
20	AGTAGTCGAT GAACTGTCTT GTAGAGTGAG CCAGGTTATT AAAATTAAAC CTGTGGGAAC	180
25	TATCCCGGTC TAGTOGGATG AGATTATCGG TAATCTTATT CACGACACC CAGTCTCTGT	240
30	TCGATAGACG CTGGCTACCC GCAGCCTCAT TCCGCAACTC CTTATCGATA TCTATTCCAA	300
35	GGATCTGTG CAGGAGAATG CTACCATTTT TATCGTTCTG AATGAACTTG CCTCTACATC	360
40	GAGCAAAGCA TAGGTGTTTA ATGTGGATAT CCGCTAGATC GAACCCAGAC TCATCGCCGA	420
45	CTTCTCTGT ATCTAGCCCA AAACCATGCA TTAGCAGCTT CAAGACAATC GCCACAAGCT	480
50	GCGATTGTTT CCAATGCTTG CAAGGAAGCT TTACGACATA TGGGATTGG TCATCGCGGC	540
55	CATGTTCAAA GTTTTGCAGC ATTAGCAGC AGCTAGTGA TGGGGTGAAC ACGATCCTAG	600
60	TAAGGACCGC GACGAAGTCA ACCTTCTGTG CTAAATATC ATTACTTGA AAAAAGCTC	660
65	GAAGTTCCGC GG	672

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 737 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1578UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

10	GATCTTTTTC TGGTCTTTT CCTTTAAACA GAATAATAAT TGAACAGGTA CCGTATTATC	60
	GCGCATGCT AAGTGCACCT TTGACCGAGA CACTTTAGTG ATATTTATTT TGGTAGTGTG	120
15	CTCGTATACG TGGGCCACGA CTTCCTTGCC ATTAATCTCG TCCTTGGCGA AGCGTCTCTG	180
	GTAGCATCTT AACGCACTCA TTAATGCCAA TGATCGGGG TTGATCGCTT CACGCCCATC	240
20	CGAAACAACA CAGACACATA TCGTTTCCA GGCATCGGGG CCCAAATAT CAGAACGCTT	300
	CCGTGAGTG AAATATTTTA TGTTGTCCAT GACGCTTTT AATGTCCGTG CCAATAATAT	360
25	GTGTTTTTGG TTGTACATCG TTATCACGAT CATGATTTCT GTCTACGGG GTACAGCGTA	420
	TTTAAATTGT CTCACGGTAA AGTCTTTTAG CTGAAACTCA GCTGGCTCAC AGGTGACAGC	480
30	CTGATATCGC ATGAATTTGT ATTGGTTTGT GAAGTAATCT TCTCTCATGC CAGTGGCGTA	540
	CTGGGACACT AGCTGTTTAC TGA CTG GACA ATCAAAGATA AAGTTTCTCT GATATAGCTT	600
35	GAAGTTTCTG AATACAATGC GATTTTTAGG CTGTTTGGAC TCGGTAAAC CACTCAGAAG	660
	CGTTCTGAG CTGAGATCGC TGCAGTCGCC AGAACCTTGG GAACCGGAGT ATGCCGATTA	720
40	GGGCTACGC GAGAGAT	737

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1579RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

10

GATCGAAATA CCACTGATCG ACCGCGGTGC CTCGCTTTGC AGCTGCTCG AGAGCCGCTC 60

TCGGAGATAC CCGCAGAGC ATGCCTTTTC CAACACCATC TTCTGTAAC GTTCGGGAG 120

15

TGACCCCTACT ATACTTATGA TAATGACCTT CTGTGCTTC AGAGTCCCT CTGTTTCTTT 180

CTTCAGGTAA AGGTGCGATT CTCGGCCAGG CTGTTAGTAG CCACGGACCG CAGACGCAAT 240

20

CCGCGTGTTC CACGGCATGG GATGGAAGTA CTCACCCGA GAGTGGCCCG GCAGAAGCAC 300

CGAGTTGTTC ACGCCGACCA CGTACTCCGA CTGGTGCTCC AGCGGACACA CCTCGAGCGG 360

25

ATACTCCTTC AGCGGCAACT GGCAGTTCTG TGACCCGGTG TTGCAAGGC TCAGCTCGCC 420

CTGACCAGC CCCCAGACC CCGCCATGTC TCCATGTCC GGCAGTACT CCGTGTGCCA 480

30

GCACCAGGAG TCATTTCGCC GCGCTACCGC CTGCAGCGCC TCTGTCTCA GGTATGCAC 540

CTGCTTCGA GTCACTGAT GGTACTCCGT GCTCTGGTGG ATCAGCAGCC CGTCTCGGG 600

35

GGTCTGCCAG AACGGCATCC ATCCCACCAC GCTTTGTAGA AACGAGGTGG TGGGGCGCCT 660

GCA 663

40

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1579UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

5	GATCGCACGG ACCGCGAGAC GAGTTCCTCT GGTTCGTGTCG ATTGGCGATG GTAGGCCGCC	60
	CTGTTGCACG TGACCTGGGG ACAGCAGACT TCGCGTCAA AATCAACCTTA GCTCAGCTG	120
10	TGATGACATC AGCCAAAACG GCGTCGGTA AACACCTTC GAGGCGTTCG TCGACTTGAG	180
	GATCAGTTTA CCGTGCTTAC CCTTCCCGTG CGCCTTTTCG AAGGACTGCG GGAGCGTCTC	240
15	AATATCTTGT GAGAGCTGTT CCAGCGAGAT ACCCTCTTCT GGAACGTAGG AAACCTGTGC	300
	GCCCACCGCC AAGGCAGCAT GCGTTGCCAG ATAGCCTGAG TTACCACCTT GGACATGAC	360
20	GACAAAGACC CGCGCTCTTG TGGAGGCTGC CGACTGCTTC ACAACATCAC AGTACTCCAT	420
	TAGGCATTC AGAGCTGTGT CTGAACCGAG CGAATACTCA CTGCCCGGGA CGTTATTGGA	480
25	AAGTGTGCTT GGAATGAGTA CCATTGGTAT TCTGAAAGCT GGTAGTTCTT CAAGGGCCCC	540
	CTCCAATTGA TGCAAGGAGA CGAAGGCTCG AACCACCAA CAATAACCA GCGTCAAAC	600
30	TTGTAATTTT GGAAGTAGTA GGCAATCATG CCAATGTCTG CATCTTCTGG GACAGTTCTG	660
	TTGGTTCCCA ACTCGGAACA CCGCGAGATT GCCAGCCAAG CATATCTTTC CAGTTCAACG	720
35		

(2) INFORMATION FOR SEQ ID NO:935:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 718 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
45	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1580RP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

5	GATCCGTGTC GACAAGTTGG TCAAGTATAT ATGGGCGGTG TTGAGGCGG TCTGGGTGTA	60
	CCCGCCGAAC CAGCAGCGCT GCCATCTCGA AGACATCATG CTCTTGGGTG TGTACTGCGG	120
10	CGAGGCGCGG GGGCAGCCGC TCTTGCTCAT GCGATCGTT CAGGCGGTGG CGGCACGCTA	180
	CGGGGTGCAG ACGCTCCTCT GCGAGCAGGT ATTGATCATC ATTGACCGCA AGTTGCGCGG	240
15	CGGACAGTCA TACTTGATGA TCCGCTGCG AGGGAACGCA AAGCGCGCA TCTTCACGG	300
	GCGGCGCTTG CTGACACTA TGCGGCACAC AATACCCAAC ATTGCGGACC CGCGGAGCCT	360
20	GGCGCTGGCC CGGTTCCTCA CTCGCTCAC GAAGCGCGG GGTGCTGAGA AAATCTTCAA	420
	AGACTGGTCC ATCTACTGCG ACAAATCCAT ATGGCGGACG ATCCCTGATC ACTGCCCCAA	480
25	TGGCATTCTG CGCTACCTCC CGCACTCTG CAGCGCGATG GACGAATCCA TCTTTGAGTA	540
	TTTCATGTC TATTGGAAAA CCGCAACAGC AAACCACTCC ACGACAACA TTTCCACAC	600
30	CGTCTTCTC AAGCAATTG AAACGATCTT GTCAAGAGT ATCCCGGCGA CGCATCCACT	660
	TTGTGATTG CCGGGAGCAG CTCATGGACT CCATTATCGA GATGTCTTTC GCGAGTCC	718

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1580UP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

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5      GATCCTTTTC ACCAACAGCT GTCTGGGCCA GCTGCGGCTT GGGATGAACT ACAACGAGGC      60
      AGTGAAAGCG CTGACGAACC TGGGCTTGA CAGCTTTACA CTGCGGGGGG ACGGTGGGGT      120
10     TTCGCTGAA CAACGTGTAC TCTGTCCCG TAGAAGACGG TGCTCAGATG GAGCTGCTGA      180
      AGGGGTACCT GCAGCAGTTG CGGCAGGAGC TGGCCACGGG GCTGCTGGAC CGTGTGTATG      240
15     GGGCGGAAAA GGCACAGCCC TCGAAGTTCT GGCTGGCCTT CACAAGGGCC AAGTTTATGA      300
      ACAAGGCGCT GTAAGGCGAA ATAGGTACGT AGCTGGCGGC GCCAGGAAGT ATTTACAAAG      360
20     TTGGCTGTAT CGCTACGAGG TTTTGGTGGC GTGTGCCTTG TTGGAGCGCA CGAGGAGTTC      420
      AACGGCGGAA GCTCGGAGCT GTTCCCGGTC TTTCACGATC GCGTTCAGT CAATGCTGAG      480
25     GTGGTGTTT TTGGCGCGGA AGCCTTGGAT CCGCGCCTGC AGGTCTGTCA GCGCCTGGAG      540
      GACAGCTCA TAGTCTGCAT CTTCTTTCAC GCGCTCTTTC TATGTTTGA AGGACTGAAC      600
30     GATGTCTTTC ATACCGGGCT CGACTCTGCT GATCATCTCG ATGCGCTGGC GCAACAAC TG      660
      ATGCGGGTGC CTGTGGGGT CCGGTCCCTA ATCATCTGCT GGATT      705

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(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1581RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

EP 0 866 129 A2

GATCTTAATT TAAAATTTTA ATTAACATAATT TATAATTTAG AAATATATAA TCTAGAGATA 60  
5 TATAATCTTA AAATCATAGG TAAAAAATACT TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTTG TGGCATCTTA 180  
10 ATTTTATTA TTAAATGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAATATT 300  
15 AAATATACCA TTTTATTTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GTGATATATA 360  
ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
20 TTTCATAATA TTTATTTTAA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCCCTTAA 480  
TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540  
25 TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTATTAT TATTCTAAAT 600  
TATTATTAAAT TAGTAAATTA TATTTATTTA TTTTATTAAC ATAATTTTIG ATAATAATAT 660  
30 ATCAT 665

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1581UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA 60

EP 0 866 129 A2

	CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
5	ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCAATTCAT TTAATACTOC TCTAATTCAA	180
	TCCTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG	240
10	GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAA ACTGAATATC TACATATTAT	300
	ATCATTAATA TAATAACTCT TTAATTAGAG TGGTAOCACA AGAATGCTGA AAGCATTAGG	360
15	GGTGTGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACTAAT AAAAATAATT	420
	AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT	480
20	GTTATATTTA AATAGATCAA AATTCAACA ATTCCATTT CATTTAGTAC TACCATCACC	540
	ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACCTTAG CTTTACTAT	600
25	ACATGGTATT ATTGGTAATA TTTATCCTTT ATTATTATCT TTATTAGTAG TTTTATTACT	660
	AATAACTTTA TGATTTAGAG ATATTGTAGC TGAACCTACT TATTAGGTG ATCATACTTT	720
30	AACTGTAAGA AA	732

(2) INFORMATION FOR SEQ ID NO:939:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 694 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1582RP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:
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55	GATCTCAACA CGGTGGTTGG AGAAGTGTGC AACACACGAG TAGGTAGTAC CCAATCAAT	60
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ACCGACTGAT TTAGACATGA TCACIGATTA GAAAACGAAA TCTCTGGTTT TCGGATAACC 120  
 5 GGGAGAAATA CCAATGGTGA TAACCGTACG TAAGGCCAGA GGTACAAAGC TACTCCAATC 180  
 TGAAGCTACA CACGCCCAAC CCTTTTATAC AATTTC AATT TTTTCTCTCC CAAACGAACA 240  
 10 TGGCAGATAG TAAGAGTCTT CGAGCCCAAT GCCTGTTCGG TTTTITTTTG TTCTGGAAAA 300  
 TTCTACCATA ACGTATGTGG CCGTTGAAAA CTGATCAAAC GGGTCTCGAA GATCTTAGAA 360  
 15 TAGAGGCTCC GACAGAAAGG GGGAGGCCGA TTCAAAAAAG ACCGCATGAG CCTCACTCGT 420  
 GCTTCGAGGC GGGAGAGCCC ATAGGCTTCT TTCCAGGGC CACCGACGGT TTCTGGAAAG 480  
 20 GAGCGAAAAC AGAGAATGAA CCGAGGCGGT TGATCTGCAT CTTCGACTTG GCGTAGGCCC 540  
 GTTTCAACTG AGCGGGAATG CGTGGATGCG AAACCTACGC GTCCGCACGC AACTCCACT 600  
 25 TCCGTACCAC CGCAGCATG TTGGCGATT TTGCTAGGC GCCTTGATGA AAAGCGAGTA 660  
 TAGAGCCAGC ACAATCCAG AGCGCGCGC ACAA 694

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1582UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GATCTTGTC TCCGATCCA GATACTGGTC GAAGCGGAG TTCATCTCGT CTACAATCGG 60  
 55 CTTCACGAG TCGGTGTAT CTATCGGTC CCCGAAGCCC GCGTGTCCA CCACGTCAA 120



EP 0 866 129 A2

CTTCAACACC ACGCGTTTCT CCTCGATCTC CGTCGTGACG GTCTCAATCT TCAOCTTGTT 180

5 CTGCGCGTCC TTGGCCCGCG ACTCGTCGCC GTCTTCACCG TCCTCAAGCT TCAACGGGTT 240

GAACTGCTCC GCGGTGTGCT CCTTCGCGGT GTATAGCTCC TTGTTGAACA ACGTGTGAT 300

10 CAAGGTCGAC TTCCCCAACC CCTTGGCGCC CACGCAGAGC AAATTGAGGT TGAACCCGCG 360

CCGATCGAC TTGCGATGCC ACTGCTTGGG AAGGTTTGCG AACCCACGT ACCCGAGAT 420

15 CTTGCGGTGG ATGATCCCA GGTCGGCTG GTCTGCAGC ACCTGGCCCG CCGCGAGCTC 480

GCCACCCAGT GCGTCGCCA CATCTCCTT GTCTCCGGA AGGTCCAACC CCATCTCTC 540

20 CTCCTTCACG TTCATGTCC AGCTTGTGTC CTTCGGCTC GCGTCCCGT TGCTCATTAG 600

TGGCCCCCG TGCTGGTGT CAGCCTCC GCGTGTGG CACTGTTGT GTTTGCGAA 660

25 TCCTCTGCG AGCCTGTAGG TAACATGCTT GTTCTGATTT GGTAGTC 707

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1583RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

GATCAATTAC CCTGGGCCA ACCATATTTG GATGAATATT TGCATTGTTG CGGATAGGGG 60

TTCCCTCATC GTGTATGTTA TAGACCTTCA CGTCTTCATT AAAAGGGCAT GTGATGACTT 120

55 TCTTGCTGTC GGCAGAGAAG GTCAAACAAA TTACAGATTG TTCTGTACCG GCCAAACTT 180

TATAAACCCCT GAAGTTGTTT AACACGTCAT ATATGAATAC CTTACGATCG CTGGAAGGGT 240  
 5 CAGTGGATGC ACTGGCCAAA TACCGACCAT CTGGTGAGAA TTGGAGGTAC CAGATTTCAT 300  
 CTTTATTTTC CGAAAGAGTC TTCACATGAC TGAAATTGAA CATGCACATA GAGCCAACGT 360  
 10 TATCTTGAAG CAAGTTATAA GTGGTTTTCT CTCCAGAAGC GTTTCCTTCG TGGTTGTGAG 420  
 GATCGTCGCT GAAGCTTAAC AGGTCGCTGG ACCGCTGGAA CTGTATAGCC TGTTTTAACA 480  
 15 ACGTAATGAG CCTGCCCCGT GGAACCAAAT CATTGGGGTT GATATATTGT GAAATCTGAT 540  
 CAAGCGCCAA TTGCGCGAG GCTGCCAGAG ACCCTCCCA TATTTTGTGT GCTCTGCGG 600  
 20 ATTCCGCAGG ACACGTCAA ATAGTGTCA CTGCAGAAGA GCTGTGTGG GAGTCATAGC 660  
 CCACTCTCCC TGGGCTCCT CCACCATAGA TATGGTCTGT ACAGCCACAG CGAGTCC 717

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1583UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GATCGACTGG AAGTACACGT CCAGCGACCG GTCAAGGCC ATGTCTGGA CGGACTGCTC 60  
 50 GAAGGTCTTC ACGAGTTTCT TGGCGATGCG GAGCAITGGT GTGCGGTCTG GGGCGGGCGA 120  
 CGCTGCGGAG GGCTACCGA ATTTGCTTGT GCGTGTGGTC ACGTGACACT TGGCGCGCTG 180  
 55 GCGCGCGCGG GCGCGCTGG CCGGAATGG CTGCCCCGCC CTGGCACGCC GTTCTTGCAA 240

TCACATGATT CATGATTCCG CTTTTGGGGG GGATCACTGC GCAGCCGTTT TTGCTGCTTT 300  
 5 TAGCCTCCCT GACACCTCG GCTGGGTCTG GAGCAGGTC CCGGCGGCT GTCCGCTGG 360  
 TGGCTGTACG TGTGGGTGA CGCCATTTTG TGGGACAGCG GCGAOGCATG ACGACGAGCT 420  
 10 CCGAGGGTCC GCGGTGACG ACAGCCCCCT AAAGGAGTTT CTTTATTG ACGGGCCCC 480  
 TCAAACACTA TATATGAGCA AAGGCAGGAT GGAAGGTAGG CTAAAGCAAG AAAAGACCTC 540  
 15 GACCAACGGT ATCGAGTCT AAAATCTTAG CAGGTACCAG GATGCTTTT GAAGATTTC 600  
 ACAAGGCGCA ACGGGGAAA GTGAGGAGG CAGTGGACGA AATATGTAAG GATTGAGG 660  
 20 TGACGGAGGA CAACTCCG CAGTTGACCG CGTACTTCAT CGAATGTTTG GAACAG 716

## (2) INFORMATION FOR SEQ ID NO:943:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 677 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1584RP

40  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

45 GATCCAAAA GCCTCCGGG CGCGGCACA TTATCACAC CCGTGTGCT TGACGGCCTC 60  
 GACAATACAT CCTATGACAT GCGTAATCC TCCTATGTTG TTCCGACGG GCGCAAACGT 120  
 50 GCCAGCGTCT CGAAGGCTTC GCGCGGAGC AAGAGTTCTT CCCCCCTGA AGAGGAGGAG 180  
 AAGCCATTTA AATGCCAAGA ATGCACCAAG GCCTTCCGC GCAGGAGCA CTTGAAGGC 240  
 55 CATATACGCT CTGTGCACTC ATCGGATAGG CCGTTCCGT GCACCTATTG TGATAAGAAG 300

TTCAGCCGCA GCGACAATCT GTCGCAGCAT CTCAAGACAC ATCGCAAGCA TGGCGATATA 360  
 5 AAAGACACGC CACCAACCAC CAAGAAAGGC TGACTTTCAC ACATCTATGC GAATACCCGA 420  
 TGTTCATTTA AGAGATACAT ACAGCGCATA CAAGCTGACA CAACGTCCCG TACGCCAACA 480  
 10 GAGGAGATGA TAAATACTAC ATACTCAATA TATCAATACC TCCTACTTTT GGTAATCATA 540  
 TATAACTGTT TTCTTTCCGA CTGTCTGGT AACGTGTGCA TAGGTTTCCG TGTGCTGCT 600  
 15 AGCTGCCAG GATTCCCTTA ATGGATGAGG TCCGGCGGC AACCAGACAA AAGTTGGCA 660  
 GCTTAAGATA GTTGGAC 677

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1584UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GATCCCATTT TGTCCTCTTC GGCTACCGGG ACGGCCAGTA GAGCATCCAG AATAGATGTT 60  
 45 CACCAGTAGG CTTGCCCAAGT GCTCATTAGT TCGCGTCACA TGGCTGCCCG TGTACATGAC 120  
 AGTGACACAC CATGTTGTAT TCATATCGAA GGTGGAAGGC CCTCGATGC GCCCAACGCT 180  
 50 CAATCCAATG GACGGAGTTG CATCGGACTG GGTTTTGGTG TGAAGCTTG GAAAGACTAA 240  
 TATTGGGAAC CTGAATCATG GGGACGTGGT GATCTTCCGC TCACCCATGA ACCCCAAGAA 300  
 55 AGTATACTGC AAGCGCATCC AGGTAAGCA GTATGATACG GTGGCAACG GGTATCCTTA 360

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TOCGAAGAGT ACCTGCGAAG TGCCAAAGTC GCACATATGG GTGAGGGGG ACAATGTCAC 420  
 5 GCAGTCGGTG GACTCGAATC ACTTCGGGOC GATTTCGACG GGGCTTGTGG TAAGCGAGGT 480  
 GACACGGGTC ATATGGCCGC CATCGAGATG GGGGCGAGAC CTGCAAGAGG GCATGGGTGG 540  
 10 ACGGCGAGTT GTTGCTTCAT GATTGCGGGA GCCGGGGTAG GCGAACTAC CGCTAAGTGT 600  
 ACATAGCTGA AAGACTAGAT ATTATATAAT GTCGAACAAC GTGCTGCACT GCGGCAGAAG 660  
 15 GATGGCTTAA GAATCGTTGT CCTCTCTCTT GAGGATCTCT GGGAAA 706

(2) INFORMATION FOR SEQ ID NO:945:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 716 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1585RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

40 GATCCCCGTT GTTGTGCAAG TGTGATTCAA TATATACATA CTGCAAGTCT GTACATGTGC 60  
 TCTATTATAT ATGGTGCTCA TGTTCGGCTT ACATTCTTTC TTTATACAGT TCATGTCTTT 120  
 45 CCGTGTGGC ATACCCAGTG ATGCCCGTCA TACCTGGTAA CCACAGTTTC TATAATCATT 180  
 CAGGCTGAAC TGATCAATGG AGCTGCGTTT GCCGAATTTG ACGCAGAGGT TTGTATACAC 240  
 50 ATTGATGTCC GCCCTGTAA AGCCCTTGCT AAACGTGCAG AAGCAATTCT TCGTTTGGG 300  
 ACACGAAGTG CAAGGCTTGA ATGCTATCAA CTTATCCACA TGCTTCAGCA GCGTCAGTTC 360  
 55 CTTTGTGAGC AGCGGCTGCC TCACCTGCTC TGAATCTGG CTAAGCCACT CGTTTGCCAG 420

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CTCAGACACA TTACCGGTG CGTGAAGCAT CTCGTTGAAC GAGCCTGTGA CCGAGGCGTC 480

5 CTGGAACAGT ATCGTGATCG TGGCGTCACA CTTAATCTTC TTGGAGGGC AGATGTGCA 540

GCTGGGGGCC GTCCGCTGAC GCTTGACTT CGACGCGTG ATAAAGGTG GCTCCTGTAG 600

10 CAGGAGTTC GGTGGGAAC AGTGGCTGC AGTCCCCG TTGGAAGCC GAAGCAGATT 660

CCGACATCAG CCGGACATC GACACGCGC GCGCGGACTC TGGCGAGGC GCGTGT 716

15 (2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 740 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1585UP

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

35

GATCACTCTA CCGGGGACAG TTGATTGAGT CCAGTGAGT GAATGTCAGA GAGTCACCAT 60

TTTTCAACCT ATGACCTCA TGGCCAGCA TGAGTCAAC CTTCAGCCT TTAAATTTT 120

40 CTACATTTG CCGCAGAGTC TCATAGGAAA TAATCAATAC AGGCTTGACT ACATTACGGC 180

CCTGGGCAAT CGCCACTGC CTGACGACT GTGCAACCGA GCGTTGAA AGGGAACTTT 240

45 TACGTCCATC GATAGCCAGT GCGAAAGG CATCGGTCC CAACCACTTC ACAATCTCAT 300

TAGCCAGTT ATTAACCAGG GACGAAGGC AGACAATGAT GCACTTTTCA ATTGTAGGAC 360

50 GACCTTGGGA GCGTGGCT AGTAGGTCC ACATTACGC TATACATTGC AGCGTTTAC 420

CTAGACCCAT TTCATCAGC ATAATACACC CATAAGCCC OCTATTTGAT TCTGAGTCA 480

55

TAGCTGCATT GGCATCCAAG ATCTCAGGCG AAGGGGTCCG CGTCGGGGTA AGAATGGGCG 540  
 5 TCGGGGTCTC CTCAAGCACC TCACAACTA TTGGCTCACT ATCTTTACTA CCGGATCCT 600  
 TACCAGTGCC ATCGTCTTGC ACCTGGCCGG CTGCCAAGAG AGCCTGTGTA TCACAAAAAT 660  
 10 CCTTCATGCG CAGACCACTC ACACAGCGGT ACAGGAATCT TACCCCTTCC ACTTGATGAG 720  
 GGGTTAAAT CCGCGCCAGA 740

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1586RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GATCAGGCGT AAGGGCAGGA TATGAAGTAT GGAGAGCTCT ATTTTAAACT CAATGGCATA 60  
 40 TAAACACCGC ATATTTCTTG TGGTTATGAT AACTTCAATT ATCGAATCAG TCGCAGGGTA 120  
 GAGGGTGGT GAGAGTTTAC CACGATATCC AGTTGTGCT GGGCCCGCAG CACCAAATAT 180  
 45 AACTGAGAAT TTAAGTTTCT CGAAGAGAGT ATGCAACGGG GGCTTGTCCT CTACGATTAA 240  
 AAGAGCACCA GCTTTCTCAT GCCTTCAACT ATGTCAATAT AAATATATTG CAAAAGGCTT 300  
 50 AAGCTCTGTA TTGAGCCCCG GAAATGTTTC TAGCAATGTA GCTCTCTCAT CTTACATTAA 360  
 GGCTGGAAT GTGCTGACCA ACTGCAAAAA CCCAGTCATA TCGTAAATAG TGATGATAGT 420  
 55 CAGCGGATA TTTAACCGCG GGTGCAAAAA ATTGATTTTG CCCAGGATCG AACTGGGGAC 480

GTTCTGCGTG TTAAGCAGAT GCCATAACCG ACTAGACCAC GAAACCAACC TTGAAGAAOG 540  
 5 CACGCGCGGA AACCGACCAA CACAACCGGT GCAAACCAAG TGCGTGAAGA CTCCTTAGGC 600  
 GTGTGCTAGG GGGGCGCCCA CTCGTACTTA TTTTATAAAC CTGGATCCA GGTGCGTCCA 660  
 10 TATACAGGGC GATCGCGGOC ATCTGCAGCA GCCAGGAACG CA 702

## (2) INFORMATION FOR SEQ ID NO:948:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1586UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GATCAACAAA GTCAAAATCCA AAATGTGTCT GGGAGAGAAA AAGATTCGC CATCATTTGGG 60  
 35 CCTTTTCTAT AGCCATCAAT TCAACAATCG GTTAAGCGAT TTGAAGCCTT CAGCCCTTTA 120  
 TGAGGGTGAT CCTGAGAAAC AAGATGGGAC TGCTACCGAT GGAAGCAGCG GTAGTGTCCA 180  
 40 TGGGTATGCC ACTGATGATG ATATCATTGT CACAGGCGAG AACACCGTTT ACAGCCTAAG 240  
 CCAAGGGATT GCATATCATA TAGATGAGGA AGGAACTAT TATTATGCTG GTATCGATCC 300  
 45 GTTTACTGAT GCATTGGAAC AAGAGGCAGA TTGCTTATAT CATGAAAGTG AGGTAGAAAG 360  
 CGTAAATGTC AACAACTTGG ACCATCTTTC TTCCGATATC AAGGAAGAAA ACATAGACCT 420  
 50 CGATGGTAAC ATAGAATTGT ACGATTCTGA CTTTGACCAC ACTTCCCTCG ACCAGGTCCC 480  
 GAAGGCTACA GAAACAATCG AAAAATACAA TAATAACCAA TACTACAAGA TGAACACGCT 540  
 55



AATCACTGAC TCATCAAATT GGCAGGGCAA CACTGTAGCG CTCTCATCTG ATTATGGAAC 600  
AACTTCCGTG CATGTTGAAA ATGTCTCTAA TGAGAATTCC TTGGGGTCAT CAGGCTACAA 660  
GGAGATATTC CTGAAACTA TGATGACTAC CTTTACGAAG GGGACGAAGA TGATTTOGAT 720

## (2) INFORMATION FOR SEQ ID NO:949:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1587RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

GATCATCGAG AAGGAGCTGG AGGGCGTGGG CATCCGGCTG AACAAAGTGC CTCGGGACAT 60  
CATTGTGAAG AAGAAGGAGA AGGGCGGTTT ATCGATCAG AACACAGTGC CGCTGACACA 120  
TTTGACCAC GACGGGATCC GCGCGGTGAT GAGTGAGTAC CGCATCAACA GCGCGGAGAT 180  
TGCGTTCGG TGCGACGCGA CAGTTGACGA OCTGATGAC GTCTCGAGG CTCCAGCAG 240  
GCGTTACATG CCGGCTATCT ACGTGCTGAA CAAGATGAC TCGCTGTCAG TGAAGAGTT 300  
GGAGCTGCTG TACCGGATTC CGAATGCTGT GCCTATATCT AGTGGACGG AGTGGAACT 360  
AGATGAGCTG CTCGAGGTCA TGTGGGATCG OCTGAACTTG GTGAGAGTTT ACACCAAGCC 420  
CAAGGGGACC ATGCCCGACT TCAATGACCC GGTGTGTGTG CGGTCAGACC GTTGACAGT 480  
GCGGGATTTC TGTAACCAA TCCACAAGTC TCTGSTMAG GAGTTCCGA ATGCTTTGGT 540  
TTACGGTAGC AGTGTGAAAC ACCAGCCTCA GTACGTGGGT CTTGCACACA CTCTAGAGGA 600

TGAAGACGTT GTGACAATTC TGAAGAAGTA ATGTCTTGGC ATTTATGCAT GGTTCATG 660

5 CACACGTTCT CGCGCTGC 678

(2) INFORMATION FOR SEQ ID NO:950:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 702 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1587UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

30 GATCCTAATA AAAGCTTTTC TGCAATGCT CTACCTAGC CTGGAAGTC GGTAGGGCA 60  
CACGTTTCAA ATAGATGTC AGGAGATACG ACCTGGTAT CACCCCCCTT AATTGATTCT 120  
35 TTAGTGCAA CCAGATAGC ATCAGGTTTC GCACGTTGA AAGCCAACCG GGCTAGAACT 180  
AAGGACGGTG CGCACCCAC GCTTACCGAA CAGCGGCTG TCGCTCTGC TACTTCTGAT 240  
40 CGGATGCGTA TACACAAGTT TTGACAACTA AGTGATCGA GGGCATGTC AATAACACAG 300  
ACAGCCTCAT CCACCGAAAT TCGATACT GGTGAAAG CCTTTAAAC CTCCAATACC 360  
45 TGTAGAAGG CATTOGAAAT CGTTCTGAT TCATCGTAGG TATAGGGAG GCAAACCACT 420  
TGGGGGCACA AGTCTTGGC TTGGAGACC CACATGCCAT TTTGTATTCC ACATTCCGA 480  
50 GCAGCATAAT TACAGGAGG AACGTCGAA GATGAACCC CATGACACAC TGCCAACGGT 540  
ACTTCGGCT TGTCTGGATA GCGCGCTTG ATGCTGAAA TAGTCGAAA AAAGCAATCA 600  
55 AAATCCACGT GGAAGACGTG TGCTGGTGA GCGCGAAAT CATTTAGGC ACCTTCATTC 660

ATCCGGAGAT GCCTGTCGAG AAACCTCTCGC GTAGAGCCGC CT

702

5 (2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 685 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1588RP

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

25

GATCCTTTAG TTCTCGGAG TTTCAGGCTA GAGGTGCCAG AAAAGTTACC ACAGGGATAA 60

CTGGCTTGTG GCAGTCAAGC GTTCATAGCG ACATTGCTTT TTGATTCTTC GATGTGGGCT 120

30

CTTCCTATCA TACCGAAGCA GAATTCGGTA AGCGTTGGAT TGTTACCCA CTAATAGGGA 180

ACGTGAGCTG GGTTCAGACC GTCGTGAGAC AGGTTAGTTT TACCTACTG ATGAATGTTA 240

35

TCGCAATAGT AATTGAACCT AGTACGAGAG GAACAGTTCA TTCCGATAAT TGGTTTTTGC 300

GGCTGTCCGA CCGGGCATTG CCGCGAAGCT ACCATCCGCT GGATTATGGC TGAACGCCCTC 360

40

TAAGTCAGAA TOCATGCTAG AACGCGATGA TTCTTTTTCT CGCACATTAT AGATGGATAC 420

GAATAAGGTG CTTTTAGCAT CGCTGAACCA TAGCAGGCCG GCAACTGGTG TTCAGACGGA 480

45

AAGGTCGGG CGCGTGCCCG CGGATTGCAA TGTCATACTG CGCGAGAGTA AATCATTTGT 540

ACACGACTTA GATGTACAAC AGGGTATTGT AAGCAGTAGA GTAGCCTTGT TGTTACGATC 600

50

TGCTGAGATT AAGCCTTGGT TGTCGTATTT GTTTTCTATT TCGAAGTCTG CAGGAGCAGG 660

CTTTGAAATA GAGTCTTATG TTATT 685

55

## (2) INFORMATION FOR SEQ ID NO:952:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1588UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

GATCCCGTAC	ACGAAGAAAA	TCGGACGGGC	CAACCAAACC	CAAAGTTCAA	CTACGAACTT	60
TTTAACTGCA	ACAACITTA	TATACGCTAT	TGGAGCTGGA	ATTACCGGG	CTGCTGGCAC	120
CAGACTTGCC	CTCCAATTGT	TCTCGTTAA	GGTATTTACA	TTGTACTCAT	TCCAATTACA	180
AGACCCGTAT	GGGCCCTGTA	TGCTTATTTA	TTGTCACTAC	CTCCCTGAAT	TAGGATTGGG	240
TAATTTGCGC	GCCTGCTGCC	TTCTTGGAT	GTGGTAGCGG	TTTCTCAGGC	TCCCTCTCCG	300
GAATCGAACC	CTTATTCCCC	GTTACCGGTT	GAAACCATGG	TAGGCCACTA	TCTTACCATC	360
GAAAGTTGAT	AGGGCAGAAA	TTTGAATGAA	CCATCGCCAG	CACAAGGCGA	TGCGATTGGA	420
AAAGTTATTA	TGAATCATCA	AAGAGTCCGA	AGACATIGAT	TTTTTATCTA	ATAAATACAT	480
CTCTTCCAAA	AGGTCGAGAT	TTTAAGCATG	TATTAGCTCT	AGAATTACCA	CAGATATCCA	540
TGTAGTAAAG	GAACTATCAA	ATAAACGATA	ACTGATTTAA	TGAGCCATTC	GCAGTTTCAC	600
TGTATAAATT	GCTTATACTT	AGACATGCAT	GGCTTAATCT	TTGAGACAAC	ATATGACTAC	660
TGGCAGGATC	AACCAGATAC	TATCTTAAAG	AACAACCGAA	AATGCGCAAG	CACACCACGG	720
GTC						723

## (2) INFORMATION FOR SEQ ID NO:953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1589RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

```

GATCATTCAA GCATATTTAT TAATTAGATG ACATTAAACT ATTAGACCTT GGTITGGGTT      60
GCTGGACTTA GGGTGTGGT AGTCGGTGGG TTATATATTT TTTGTAGACA GTCACCAACA      120
CACTTGATGT ATTCTTTTGA GCTGTGTGCG ATAGGCTCCG ATTGGATGCG GCACTGCTCA      180
TTGGCATCCT GCCCCTCAGC AATAACCATA GGGGGCCCG CTAGAAGACC GAAAAAGTAG      240
GTTAGCTTCA TCTGTGATA TTATCTGTG TTTAATTAAA TGGAACTTTA GTGCTCTGGT      300
TCTCTGCCAT AGAGATCAGG ACCTTGGTTA GATATCGGIG CCCTTATATA CACTGCTGCC      360
AAGGATCGAT GGA CTGTAGC CGAGCACTT CCAACTCAA AGATCCGACA TCAATGTATT      420
ACTGAGAGCC AGTATACTTA CCGCTTATCA CACTAAACC CATAGCCATG GTTACGAAGA      480
TGCTGATCTA TCATCCACA CAGCTCGCCA CTGTAAACGG ACTTGAGGTG GGCGACAGAA      540
GGCCACTACA GGATGAGCGT AAATCTCCAA CAGCTAGCAA CACATGCCAT TATTCTATAC      600
GAACAGTAAC GTGCTTGATA TTACAGAATA CCGATTAGGT TTTTTCCTGC CAGACCAAAAT      660
GCTATTGGTC AAAC TCAAAT TTAGTCAGGC TTACATTACC TGCGTACCTC GAAGGTAGCA      720
ATGTTAGGCA CTCTGCCAGT A                                                  741

```

## (2) INFORMATION FOR SEQ ID NO:954:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1589UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

25	GATCTTCTTG GCCATTATTG CAGTAGCGGT AGGCGGGCAT ATGAAATGAG ATCGCGGACG	60
	TCCTGCGCTT GAGCACCTGA AAAATGGCAG TAAAAGAAA CGATCCCCGC AACATTTGTT	120
30	CGAGTGACTT TTGAGGCAGA AGTACAGGCT TCAGCCCCGC GCTGCTTTGC TGTGGATTCA	180
	GACCACCGGT GGTGAAGGTG GTGGTACACT GGGTTCAGCT ATGCTCTCAC GCTGCAGTCC	240
35	AGGACAGACA TACCGCCAC TATAGCAGGC CGATCACATA CATAAGTAAG AAAATTAGCC	300
	CCAGTAGATT ATTGTGGGG TCATGCAGTG CTGCACCAAT GGTGATGTG GTGTTGCCCG	360
40	GTAGTCTGCC ACCATGTGA TACCGGAGC CGCCAGATCC AACCGGAGGT ATAAAACTG	420
	GTAATGGGAC AAATCGGGG CCGCCCCGC CGCGCCTCC GCCCCGTAA GAAGGCAACC	480
45	CGGCGCTTTG CGCTCCTCCA TTGAGTCTT TTGGGCTGTT CGGTGGCGGC TGTGCTCCGC	540
	CGTTTGGGCC TTTAGGGCTG TACGGGGGCG GCTGTGCCCG CCGTTCGGGT CTTTCGGCT	600
50	GTACGGAGGC GGTGCGCCTT TCGGATCCTT CCGGCTGTAC GGAGGCGGTG CTCCTTTCCG	660
	ATCCTTCGGG CTGTATGCCG GAAGAACACC CTTGGG	696

## (2) INFORMATION FOR SEQ ID NO:955:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1590RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GATCATAATG ATTTGTCCTA ATTCTTTTCT TAATTATTCA TTAAATAATT AATTAAATATT 60  
 TTATTAATAA AAAATATTKA KAKKKATGTT CGTTTATGAT AAATTCTAAA ACTTIGSARC 120  
 ACGAACTGAA GACAACTATG TAACGCTGT AATTAAATTAT AAATTATTAT AATTAAATAT 180  
 TCAAAAAATG GTAAGATTTA TCGAGGATTA TCGAATTAAA TAACATGTC CACTGCTTAA 240  
 GTCTGTAACC GTCTATTGTT TTGATTTTAA TTATTGCTAA CGTAGTCATC AGGCGGAATA 300  
 CTTTAATTTT CATTTAATTT ATTCTTTAAT TAATAAAAAA TAAATAGGTA TTCATTGTTT 360  
 ACTGCTAAAA CTACTCGGGT ATCGAATCOG ATTTGCTACT TTAGCCTTCG TTCTCAATG 420  
 TCAATTAATA TATAATTAA ATTTTCACTT TATAAGTCTT ATTCATATAA TTATTATTTC 480  
 ATCTTTACTT GAATAATTCT TAAATTATTT TTATTAATTC TAATTATTAT TTTAAATAAT 540  
 CATCTACGA ACCCTTTAAG CCATTACGAT TAACGCTAAC CCCCTTGTG TTACCGCAGC 600  
 TCGTGGCACA AATTTTGGTT GGGATTATTT AATTATATAT 640

## (2) INFORMATION FOR SEQ ID NO:956:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: PAG1590UP

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

GATCTATTAT TAGAGGTAAT ACATTTAAAC TATTATCTAA ATTCTTCTTC TTCTTATTTA	60
TTCTTAACTT TATCTTATTA GGTAAATTAG GTGAATGTCA TGTGAAGTA CCATTTATTT	120
TAATAGGTCA AATTGTACA TTTATTTATT TTGCTTATTT CTTAATCTTA GTACCTATTA	180
TTTCTATAAT TGAAAATATT TTATTTTATT TACTAAATAA AAAATAATAA TTAAATAAAT	240
AATAATAATA TICATTAAAT ACTTTAATAT TAATATTTAT ATATTATACT TCITTATCAT	300
TTATGAGGGT ACCTCATATT GCTGACTAGC AATAGGGGGG TGAACCTAC GCACCTAAAT	360
GATAAGAGTT TATCATTAAG TTATATACTA TATATTATAA GTAAATTATC AAACCATATA	420
TAAGGTATAT ATATTAAGAA AGTTTGACTG AGTGGTTTAA AGTGTAAATAT TTGAGCTATT	480
ATAAATCTTT ATGATTTTCAT AGGTTGAAT CCTATAACTT TCGTATTAAA TAATTATTTA	540
AAATAATTAA AATAGTTTAA TAATAATGAG AACATGATGT TGGTTCAGAT TAAGGCTAA	600
CTAAGGACAT TACACATGCG AATCAAACGT TAATATTATT AATTAATAGT ATTAATAAGT	660
GGTGTAATCG TGAGTAAAAA TTAAGATTA TGAACCTAAA TTAACTAAA TAT	713

(2) INFORMATION FOR SEQ ID NO:957:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear



EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1591RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

GATCATAAGC ATCTTTAGCT CCACTATCCA TGTCGAAAT TTGCAGCTGA TAATAAAGTG	60
GTGTGTGGC CGAGCGGTCT AAGGCGCTG ATTCAAGTGT ATGCTTACAG CTGTTACAGT	120
TGGACACTCA GGTATCGTAA GATGCAGGAG TTGGAATCTC CTGCAACCA ATTATTTTTT	180
TTTTTTGGAG TTCCAATGCA ATATCAATTC TACTGCTGCG AAAAGGTCTC GTCAGCAGAT	240
AAAAGAATAT AGAATATGTA TATTTATATA CAAGAAGCGT TAACTGACTT TTTATTTGTTA	300
TAATGCCATT CGAAGAGATA TCGCTTATTA ACAGCAATAC CCGCTGCAG GTCCCCGCCA	360
ACCGTTGTCC AGTGATGCAA AATATATACC TCGCATGATA AAGAAGGCC TTCAATATCAA	420
ATGGCCCAGG CATTAAATATC ACCGTTGCG CGGCTTCAA CCAAGTAGCC ATCTTTATAT	480
CTGACATATT CCACGGCATT CTCACTATGC TCATCACCGC CGCAAAACCA ATGCTTCTTC	540
TCTTGCCGGT TGTAAACCTT CACTGTACCT TCCTGGTTAG CGCAACTAT CTTATTCAAG	600
TCAAACGCA AACATGTCAC CGGGTGTTC TACGAAAATG TATCAGCCAA TGTACCGGTA	660
CGTAGATCC AGATCTAATG CTGTTATCCA AGGAACCACT CACAAGGTTT AGAGAATCAA	720

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1591UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

GATCCCCAAT GATCCCTCTC CGGGCTACAA CATCGAGCAG CTGCTAAAC AGTGCAAGAA	60
CAAGGACAGG CTGGTGAAC TGCCCTATAC TGTGAAGGG ATGGACCTCT CCATGAGCGG	120
TATTCTGGCC CACATCGACT CGCTCGGAA GGACCTATTT CGTCGAAACA CGAAGAACTA	180
CAAGCTCTTC GACCGCGAGA CCGCAAGCA GCTCGTCACC GTAGAGGACC TGTGCTACTC	240
CCTACAGGAG CACCTGTTTG CCATGCTCGT GGAGATTACC GAGCGTCCA TGGCACATGT	300
GAAGCTTAAC CAGGTGTTGA TTGTGGGGG TGTGGGCTGC AATGTCCGAC TGCAGCAGAT	360
GATGGCGAGT ATGTGCCAGA GCAGGGCGGA CGGCCAAGTT CATGGGACGG ACGAGCGCTT	420
CTGTATTGAC AACGGTGTC TGAATTGCACA GGCTGGTCTA CTTCAATATC GCATGGGCGA	480
TATAGTAAAA GACTTCTCAG AGACCGTTGT CACGCAGAGG TTCGGACTG ATGAGGTTTA	540
CGTATCGTGG CGGACTAAG TGTGTACCAA GTTTAATAGA AGTTTACCG CCCTAATATA	600
GCTGTTAACC ATCAGTGGCC TCGATCAGC TGGTCCAGAA CAGTAGTGG CCGTGGCTGT	660
CACCAAGCTA CGGGCCAGC GGCAGGTATC CTGTTTG	697

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 669 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1592RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

10 GATCAGGAAC TOGCAGACCT TGGCTCTCTG GTGGCCCTGC AACTGGATGA TCTGGCCCAT 60  
 CTOGTGCTCC TTGAACCATGT TGCCGTTGCA GCGAAGTCC TTCCGCAAGA CCTTCAAGA 120  
 15 TGGCTTGAG GTGCTACTCC TGGGGGATGC CCTGCAAGGT GGTCACGTT TTCTGCCGT 180  
 TTCTCTGCTG GATACGGATG TGGATGTAGT TGGAGGAGGA GGCTTGCTCG TGCCCGGTGT 240  
 20 CAGCAAAGGG GTCGAACGAC TTGAGGTTTT CGATAGACAT GGTGGCGGTG GGGTGTGAGG 300  
 TACAAGGTAA GCAGAGAAA TTTTCAGCTG TCCTTTTAAA AGCGCGCACC TOGGTCTTG 360  
 25 GAACGCATTC GCTTATTTGT GAACCATATT CTTATCTGTA TAGGTGTAA CCGGCATTC 420  
 TCTGCAATG CCGTCTTTC TTGGCGGTG GGACAACGCT TCCTTTCAA CACACTTTCC 480  
 30 AGGAACTCCT TTGTTTCTT GGTAACTACT GTCTTCTTC GCTGTTTATC TCCTGTTAGT 540  
 AAGGCAGAGG CTGGGATTAC AATGAGACTC GTCACACATA CTTACCTAG CAGAACACTG 600  
 35 CAAATGGCTT GGATTGCTTG AGCTGTTTCT TCAATACYTG ACATTTGAGT TGTGGGGAGC 660  
 GAGGAAAGA 669

## (2) INFORMATION FOR SEQ ID NO:960:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 588 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1592UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

5 GATCCACTTG TTAACGTGG CGCCGCCAAT CCTCATCCCT CCATATGTAA CCACAAGTGG 60  
TTTGTATCCC AACAAATTGCA GCTCAATTGC CATCAAGTAC GCGTATCCCC CGCCTAGAGA 120  
10 ATGGCCAGTT ATAATTACCT CATAGTCTGG ATGAGCATCA TGTACTGGCT TAAACGGGA 180  
ATAGATATCG TTGTACGCCA ACTTAAATG CTCATATACG CCCGAGTGTA CAAAGCAATC 240  
15 TCCCGTACAC TTTCAGGCG CACTAAGTGG CTGGTATGGA ACCCCAGGAA AAATGAAATC 300  
CACAAATCCAA TCTTGAATTG TTACCGACCC TCTAAATATG ATCGAAATCT GCTTAGCCGT 360  
20 GTCATTTATT GCTATCATGC TATAACAGGA AAACTGCCCG CGGTCATGT CCGGATCAAA 420  
GTCATTTATT GCTATCATGC TATAACAGGA AAACTGCCCG CGGTCATGT CCGGATCAAA 480  
25 AACTTTAACT ACTTGAGTCC CTGTTGTTC ATGTACCACT TACCGTCATG AAAAGGGTCA 540  
GTGAGTATTA AAGTATTCAC GCAGTAAACG CTGTTAGTGA GATATGACAC ATATTTCAAT 580  
30 GTATCAAACA TCTCATCAGA GAAAGAATGG ACATGAAGGA AAAAAGGC 588

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 718 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1593RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

55 GATCGAAATA GACAACTCTG CAACGGTGTG CAAATGGCCC AGCAACTTCC AGGAATAAAC 60

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ACAAGTAGAC CATAGCATCC AAGTACCTAT GCTOCTOGCC TTACTATGTC TTTGGAATGC 120

5 AAAGGACCAA ACGTGCTGCA AGACGGAGGG AGAATTCCTC AGAAGAATTA CATTATACAG 180

GCTOGAAGGT GTGACAGOGA ACCTATCATG GTCTCTCTTT GTGGTTCTG CCAAAAGAGA 240

10 AGACCAGACC TCTTCAAGGG TGA CTGCAAT TCGTTGTCTA AGGTGCGCAG TGACAOGAAC 300

AACCGCTTTT CTGGGCAAGT CAGOGAGTTT TATOGTACTA GTAACCGGT TATTTCCAC 360

15 TAGGAGCAAT GCATTCAAAT AAGCAGCCCA CAGTTCCAA TCAAATTCAC TGGCATTCOC 420

ATCTGGAGGA ACATTATATT GGATTAAACAG ACTTTTGTAC ATTTCCAATA TAGTAAAGCA 480

20 TGTOCTCAA AATAGGGCAT GTAGTGAAAT CCACTTAAGG GAGGGCATGT ATCCATCTTT 540

GGTCAATATT GTTACAGTAT TAACGGCACT TATAATATCT TCCTTGGTAA ACOGGTAAT 600

25 GTTAAATACA GATGTTAAAA TAGGATCATT GGCGCAATCT TCACAACTT GTATAAATGA 660

GCTGCCATGT CCATATATTT CTCTCTACAA TTTGGGCTAA AGTTGCCAAT ATAGTACC 718

## (2) INFORMATION FOR SEQ ID NO:962:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1593UP

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GATCGATCTG TTGTAATTTG GACACGGGGA GCTGCAAGCA GGGTAACGTA TGAGGGGTGC 60

TGTGGGGCCT GCGATGGCT ATAGATAGGG TCATAACCACA TCATCGTTT GCGGGGTGG 120

TATAGCATTT GGAGGACAGG TTAGCCCGGA GCCACAGCAT AGACAGGTTT ACGAGGCTTG 180  
 5 CAGCAGAGGA AAAGATGGGC AAGCGATTTG ACTGGCAGCC GACGGGGAGG CTGGTGCGCG 240  
 GCGCGATTAT CCGGGCGTTT TTGCCCTTGA AGCGGCACCC GCAGCAGCTG CTGGACAACC 300  
 10 CGAACTACAC GAACCTGTAC CCGGGGGATG AGGTGTACAG CTTTGAGGAG ACGGCGGACG 360  
 GGCGATGGTG TCGCGTGTAC CAGGTGGTCC AACCGCTGCC GGAGGACTTT ATCTCGACCA 420  
 15 TGAAGCGGTT CTGGACAAG CTGCCGGAGG AGCAGCACCG CGTGGTGGTG TGCCCGAAGG 480  
 CGTTTGTGCA CTGGTATGAC GACGAAGTGG TGACCTTTCC GTTCTGGAC CTGCCCGACG 540  
 20 AGCGGGAGGT GAAGCGGGAG GTGGCGGAGA CGGACGTGCC GAGCTGCAC GACCTCTGCG 600  
 ATAGGGAAGA CTGGGGGAC CTGGAGCTAT TCCGCAGCT GCGGCGGACG CG 652

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1594RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GATCAAGACT GCCGAAGTGC TAGTTTCTTG CTTATGAGG TTTGGAATCT TGTCACGAT 60  
 50 GCGGGCGTTC ACCAGGCGGT TACGCAACTC AAAGTGTCA TTAAAGTGC GAGCAAACCA 120  
 GTAGGAGGAT TCTAGAAGAC TGTAAGCCG GATGCGTTT TTGAAGGGTA TTGCGTTTGC 180  
 55 GAAGTTCTCA TCCGCAAAGA GCTCGCTAAG CGACTCTATC ATAAGCAGCT GCAGGACACA 240

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TTTACCACG ATGGTATTCT TAATACTTAC ACGTGCCCA ATCTCTCGC TGCTTTTGGT 300  
5 GCGCAGAGT CCGCTCATAG GCTTATCTC TTCAGTACTG GCGTTGCCA CATCTCGCC 360  
CTTCTCTCG CGTTGGGCAC GCTCGACTC CCGATCAACA TCACTGGCAC ATGATTGGGT 420  
10 TTCAGCAGTA CCGTTGGTGT TGATTGTGGC TACTGATGGC TTTCTTCAC GCTTCAATGG 480  
ATCTGACTCA AAAAGTCTG TGGCAGTGGT AAGCTCAAAT AACCGGCCA ACGAGTTGGT 540  
15 AACCTGCTCC CAATGCGTTG TCCCGAACTT GTTGGTGTTC TGGATAATCA ATTGCTGCAG 600  
ACAAGACCTA CCAATCTCG CAATGGTGTG ATTTTCTGA CAGATGCAAG AGACTAACAA 660  
20 AACCAGGAAG CCATCCAACA TTTCGTTGAG TGAATCAAAG TAATGCGTAA CAGGGC 716

(2) INFORMATION FOR SEQ ID NO:964:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 695 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1594UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

45 GATCTGAATT TAAACGTGAG ATACCCGTTT TTCTGACAGA GATATATTTT CCTATATCTC 60  
ACATGAAATC TTCTACTCCA CATCAGAAGA GGTATTTTTT GAGTGTATC CAACGACTAT 120  
50 GCAATGACCC GAGAACCTTA ATTGAATTCT ACCTAAATTA TGAATGGAC AGTAGTATGC 180  
CTAATATTGT CGAGACTGTT GTGGATTATT TGACGGACT GGCGTAACA CGTGTGATA 240  
55 TCACCGCATC ACAGCGTGG TACTATGATG AACAAATGAA CAAACCCCTT GCAACGTWTA 300

ACCTATCGCA GTTGCCCTTA TTATCCATAT CTAATGTTAG CAGTATGTCT GTTGCTCCAC 360  
 5 AGCAACTCCA ATTCCCGGTG GAATTTCGCG TTAAAATGAC CTGTTGAAA TGTATGTTGG 420  
 CCGTGCTAAG ATCACTAAAT TCTTGGGCG ACAAGGCGAC GGCTCCAAAT GGCACATTAA 480  
 10 ACCACAATAG GGCATCTGTT GGCTCCAGTA CGATTGAAAG GAAGCACTCT TCGGCTTTTA 540  
 GCTCTTTCAG TCACACTATG AACACAACAC CTGTAGGAGA CCAGAATAGT GTCCAACAAT 600  
 15 CGGAAGCGAG TGAGGATATT GATGATCCCA CACAGTTTGA AAATTGAG TTAAGGAAAA 660  
 CAGAACTGCA AAAATGTATT CGGTATTCA ACTTC 695

(2) INFORMATION FOR SEQ ID NO:965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1595RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

GATCTTGCTG CTATCCAGAA ATGGGAAGTT CTTAGACAAC GGGGAATTAA GGGCTTTTC 60  
 CAATATTTTG AGCGTCGTTT CATAGCTCGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT 120  
 CTGTTTCATGT TCGTTCATGA AAGGTGTCTC TATCAAATCT AGCTCCATCA TCGCAGAGTA 180  
 GTTATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTGTCAGGA TTACAGTAAA 240  
 ATAATGGTAG AACCGCGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCCGTA 300  
 55 GAAGATCGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TCGGAAAGTC TGTTCACGGG 360



GGACACGGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT 420  
5 CCGCGCGAGC TCAGTCTCAA GCTGCTGGAT CCGTGCAGC AGCTCCACAT TGGGGTGA 480  
GCTGAACAGC TCCCGTGAGT TCACGTCTGT CGTAAACTCA GACAGGTACA CACTCTGGG 540  
10 CAGGCTTCC CAATACATGT AGAGCACTTC GCGCGCGCT TGTTCACCTT GACGCGCGC 600  
TTGCGGCAGA ACACGCACGA CTGCTGACC TTCCGCTGG TTTTACAAT CTGCCATCG 660  
15 GACTCTGCCA TCCCGCCAGC TTCAAGCAAA ATGAGTAGGC TATATTATT 709

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1595UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GATCGCGAC GTGGAGCACT GCGCGGAGAT GCGCGGGCC ATCCTGGTGG TTCTGCGGA 60  
40 CCGCAAGGA CAGCCATCG ACGAGCGTA TGACGAGAC GGTGCACAG TGGAACTCT 120  
TCAAGGAGCG CGTCGCAAG GTGGTGCCG GCGGTACGG AGAGATGGG GCGGCGATCC 180  
45 GCGCGCGGA CTTCGCAAG TTTGCGCGC TGACGATCA GACTCGAAC TGTTTCAAG 240  
CCACTGCTT GACTCATTT CCGCGATCT TCTACATGAA CGACTTTCG CGCGGATTG 300  
50 TCAAGCTGTG TCATCTGATC AACGAGTTCT ACAACGAGAC CATCGTGGG TACACGTTG 360  
ACGCGGTTCC GAACGGGTG CTCTATTACT TGGCGGAGAA CGAGGCGGG CTCTGCGCT 420  
55

1 TCCTCTCTGC CGTCTTTTGGC GCCAACGACG GCTGGGAGAC CACGTTCTCG ACCGAGCAGC 480  
 5 GGGCCACCTT CGCCGCGCAG TTGACGAGT GGTGCGCGG CAAGCTTGGG ACCGACCTGG 540  
 ACGACGAATT GCACAGAAGA ATTGCCCCGC TCATCTTCAC GAAGGTGGG CCAGGGGCCA 600  
 10 GGACACTAAA TCCTCGCTCA TCGACCGAG ACCGGCTGC CCGCTGAGG CTATTCTCT 660  
 GCTATTTTCT GCTCTGTATA CCCTGCCAGA CGCGCTATAT ATATAGAATA TGCATTGCGA 720  
 15 CGCTTACGCT T 731

## (2) INFORMATION FOR SEQ ID NO:967:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 672 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1596RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

40 GATCGACAAT CTGAGCGAAA TATTTAGCAC GACATGCTAC ATGGGCTCTA CGGTGATAGT 60  
 ATGGGAGTGG AGCAACCGGC TGTCATACT GGAGGCCAGG CGCCAGGCGC AGAGCATTTCT 120  
 45 GGGGCGGCGG GTGTATGAGG ACGAGGAGCA GGGGTACAAC TTGCGCGAT ATCGCTGAA 180  
 GATTGAGACC GCATTGACCA GCAAGTCAGA TGAAGGCGAC ACCACATCAG CGACTACCTT 240  
 50 TGCTGCACCG AGATCTGGC GCTTCGAAGG GAAAGGCGG CCCCATTCC CAGTCTATGT 300  
 TCAAGAGGCG GAACAGCAGG CCGTCATGGC ATTCAATAAG CGAATGGCA CTCGAGCGTT 360  
 55 GGCACATCAT GTGCTGGATA GCATCATATA CTACACAGC AAGGTGGTGG TGAAGGGCT 420

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TGGAAATTG TCCGCGAGCT TACCTTCCAA GACCTCTCTG GCGACAAGCG TCAGGGGTG 480  
 5 TGTAAGGAAA CGCATTGGTC TCGAAGGCGC AAATGATGTC TTTGTATACC GCACAAAAGA 540  
 CCTGGTATTC GATAGTGATG AAGATATACC CAGAACCTAA CTACTGTGTG OGATATTCT 600  
 10 CACACCGCCT GGTGCGGAAC CGGGGCGATA CATTGTTTTT ACACAAGAGG GGTTGATGCA 660  
 TAAACGCGC TT 672

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1596UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GATCTTCGTA TCCATGTGCG AAAGCTCTCT CAAAATCTTT TCGTCTOCAT CATGAGAGGC 60  
 40 TGCTACAGCT TTTGAGCCGA TAGAATTGGA AATACCATTG GAGATTGCTA TTAGTAGGAA 120  
 GACAATATAA GTACCATCTG TCGATGGGGC AGAGGCTTTA TCAAGAAGGT CCATCAGCTT 180  
 45 GTTCTTGGAT ACAGCAGTCT CATTTAATAA TAATGCCTGC TCACCACTGG GCAAAAATTC 240  
 AGAAACATTG AGCAGTTCAG AGAGTGAGTT CGACTCAAAG TTTTCGGTCA TTGTCTCTAA 300  
 50 CAAGACAAAA ACAACGTCTT TCCTGCTCTC ATGAACATCA TAAGCCTTGA AAACCTOGAG 360  
 CAAAATAGTA TTGTCTGGA TCACGTTCAA AAATACCTCT AGAATTAATG CCTTCTCCA 420  
 55 CAATAAAGTG TCAGATTTAG GAGACAGAGT GTGGATTAAAT AATGATAAAA TAACTTCCAA 480

TTCCAATTCC AGCAATGTCA AATACTGAAC CTTTATGAGA ATGTAATACA TCTGGGCGTA 540  
 5 CGAACCACAA TTGCAAAATT TTTGGATGAG GAAATGTACC TCAATAGCAG CGGCACGGCC 600  
 TTTGTTGCA ACAGAAATAA CAGATCTCGG TGTGTCAAAA ATAATAATTC ATAGTTCAAT 660  
 10 AAAACCAGTT CTAGGAGCTC TAATCATACT TCCTCATTTA TGCAATTGCT ATCCAGCAAT 720  
 GT 722

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1597RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GATCCATCAG CGGGCTACG GAAATCCTGC CCATAGAATG ACTCTCCAAA CCCCTCTGAA 60  
 CTATCAGCAA AAGCTCAACA GCATRCACGG GTGGCATGCC CAGCAAAAAC AGATCCAGCG 120  
 TCAGATAAGC GCTGCCARCG CACTCGATGA CGGAATACC ATCACCGCAA TGGTCCAGCA 180  
 TTTGATGCCC AAGAAGAAAG ACCAGCCACC GCAGCAACAG GGACCTATG GCTCTCCGGC 240  
 AAATCTGGC AACAGCTCCA CGTACGGCGG CAGCCCTGCT GCCACCGGC CGTCTGCATC 300  
 CGTAAATGCT CCCGCGCCCG ATGACGCCCA AAACGCTGTG CCACAGCGGC ACAGCGCCCC 360  
 TGGCTATCC GCTAACGGTA ACACAGCCCC TATGTGGGA AACTCGGTTA GCCTTAGTAA 420  
 TGGCTCATCA GCAGGGCCCG GTTTGTACA ACAGTCAAAC TCTCTGGAAT GGAAGCAGAC 480

ACCGCCAAGC AGTGGCGGAA GCGTAACCGA AAGAAAGCCA AAGCTGCTC TATTOGCTAA 540  
 5 GAAAAAATAA TATCATGCGA CCTATCATTT ACACATATTC TAACGTTCCA CCTGTGTTAG 600  
 TGTACTCATT TAATTAATTC ATTAGTGCTG CCACTGCTGC AGACATGTGG CAAGAGGCAA 660  
 10 AAATGGTTCC TAGCGGGATC GAACCGCT 688

## (2) INFORMATION FOR SEQ ID NO:970:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1597UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GATOGAGGCA GCGGTACOGT CTTTGTGTAC GCATGCGCAG AGTACTGCGG GATACAGGCG 60  
 AACATCTTAC GCTGACTACA GTTCTGGAC ACACCACCTT ACAGCTTTGG GCGTGGGTTA 120  
 40 TTGGTGCTCG AAGATATGAT GTTCGGAATT TTTCACCTCG CGTCCGGCCT GATGAAACTG 180  
 GAAGACAAGA CCTACAGTCA TCTAGCCAAC ATAACGCCCT GTAGTCGGGC TCTOGAAOOG 240  
 45 AGOGTAGAGC GTAGGAGATG CTCCACGCGC CCGGTGCGT ACAGAGAAGA ACAAGACGCG 300  
 CGGCATTCTT TTTATTTACT TGATTAAACT CTTGGCCAGT CTGGTTTCCA CTGACAAAGT 360  
 50 GCGCACAGA TGGATCGCGG GCGCGGTGAT CCTGCCCCGG CGATAGCGGG CGACCGGAGC 420  
 TTGCGTGGGT TTCACCTGCA TCTGCACAAG ATGTTGCTAC GCGGTAGAAG CAGCGCGTGG 480  
 55 GAGGCGCAGC GCGCGCAAAC AGGAGGTCAG TCTGACGCGC TACTTCGCCC GCGCTGCTGC 540

ACCGGCTGAA TTGGGCTCCC GGCAAGTCTT GATTGCTACG TTGAGTCATA GTCTCAGTAA 600  
5 TTATCGCATG GTGTTACTGG CGTTGCACGT GACCACACTG TGGGTCCTT TTGGCCCACA 660  
GATGAACCTG CCATCAGCTC TCGCCAGGA CGGTCACAAC AGGCAGCAGT AC 712

10 (2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1598RP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

GATCCTCATA ATCATAGTAC AATATCATTT CCAATAAATG GAATAGCACT AAATAAATTA 60  
35 GTAATAACAG TAGCACTCA ATGTGACATT TGTCATATA CTAAACAATA ACCTAAGAAA 120  
GCTGCTGCTA TAGTTAAAT AAAGATAATA ACACCAACTG TTCATACAAT AACTCTAGGT 180  
40 GATTTATAAG AACCATAATA TAAACCTTTA CCAATATGAA TATACATACA AATAAAGAAG 240  
AATGAAGCAC CATTAGATG CATATATCTA ATTAATCAAC CTAGTTGTAC ATCTCTCATA 300  
45 ATATGTTCTA CTGATGAGAA AGCTAATTCA ATATTAGATG AATAATGCAT AGCTAAAAAA 360  
ATACCAGTAA GAATTTGAAT AACTAAACAT AAACCTAATA AAGAACCTAA ATTTTCATCA 420  
50 TAATTAATTG ATGATGGITG AGGTGAATCA ATAACATAAC TATTAACTAA ATTTAAATAT 480  
AAATTTGATT TTCTATATGC CATATATTTT ATTATTAAAA TATTATTAAA TTATTATTTA 540  
55 ATAAATATTA GATTATAATA TAATTCITTA TAATAAATTA TATTATTTAA TTAATATATT 600

EP 0 866 129 A2

AATTTATTAT TTATTATTTA TTAATATTTA TATAATCTTT ATAGGGAATT GAACCTAATA 660  
 5 AACCATTAAAG ATTAAATTAT TTAATTATTT AATTATTTTA ATTATTTAAT TTATAAATTA 720  
 TTAATTAGAG AGATAAGGGT 740

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1598UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GATCTTATCG TCTAATGGTT ACGACATCAT CTCTTCATGT TGAAAATATC GGTTCATTC 60  
 35 CGATTAGAT TATTAAATATA TTTTAATAAT TATTATAATT AACAAATATTA ATTAGAGGGG 120  
 TACCAACATA TTGCTAACTA GCAATAGGGG TGTGTACCTT ATCTCTCTAA TTAATAATTT 180  
 40 ATAAATTAAA TAATTAAATA AATTAAATAA TTAAATAATT AAATCTTAAT GGTTTATTAG 240  
 GTTCAATTCC TATAAAGATT ATATAAATAT TAATAAATAA TAAATAATAA ATTAAATATAT 300  
 45 TAATTAAATA ATATAATTTA TTATAAAGAA TTATATTATA ATCTAATATT TATTAAATAA 360  
 TAATTTAATA ATATTTTAAAT AATAAAATAT ATGGCATATA GAAAATCAAA TTTATATTTA 420  
 50 AATTTAGTTA ATAGTTATGT TATTGATTCA CCTCAACCAT CATCAATTAA TTATTGATGA 480  
 AATTTAGGTT CTTTATTAGG TTTATGTTTA GTTATTCAAA TTCTTACTGG TATTTTTTTA 540  
 55 GCTATGCATT ATTCATCTAA TATTGAATTA GCTTTCTCAT CAGTAGAACA TATTATGAGA 600

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GATGTTCAAC TAGGTTGATT AATTAGATAT ATGCATCTTA ATGGTGCTTC ATTCTTCTTT 660

5 ATTTGTATGT ATATTCAATAT TGGGTAAA 688

(2) INFORMATION FOR SEQ ID NO:973:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 625 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1600RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

30 GATCTAAAAG AATCCATGTA TGTACACATA TTACGGAGGG TTAAGGTGAC GAACGGTAGC 60  
 TACAGGCTTA TAAATCTGGG TTCTTTTGCA AAAGTTCATG CAACTCATCT GGGACGTTGC 120  
 35 GCCAGTCTTC GGCAATCCAT TTCTTTATCC TATCTCATC GGCTGTGCT AGTATATCTA 180  
 CTTCAGAGA GCTCTGGCA CATGTAAAT TGCCAGCGG AGAGAGGAGA GGCGAAGATT 240  
 40 CTTGAGTGGG GTAAGAACT TGTTTGTATG GTATGCTGCT AGCATCTTC TTCTGTCTGT 300  
 GTTCTTACC GTTGTTAAT GATACTCCGA TATAATGTTT TATTAACCTC TCCTGGTATG 360  
 45 GGGCAAGTT TTTGGGCTG TAGTGGCCA CATATTTGCA CTTCCAGTAT ACAGACCAAT 420  
 GTAGTTCACC ATATGCGGG ATGTTCTTAT GTCTACCAAG GTTAGGCACA TAAACGTTTT 480  
 50 TCCATTGGCA ATTTTATCT TCAATCTTA TGCCGATGAA CATCATTTCC ACTATCCACC 540  
 AGGCAATGAA CTGAAATATA CTCTTTGTTT CATGTCCATC GTTCTTTGCT GGCCGGATTA 600  
 55 TACATCTCCG GAAGGAAGGC CTGGG 625



## (2) INFORMATION FOR SEQ ID NO:974:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1600UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

```

25  GATCAAGCAG CTACTGCTCA OCTGGAAGAA GCAGGGCCAC AAGGCCCTGC TCTTCAOCCA      60
    GTCCAGGCAG ATGCTCGACA TCCTGGAGGC CTACATCTCG CACAAAGATC CCGAGCTGGC      120
30  AGGCCTACAG TACCTCCGGA TGGACGGAAC CACAAACATC GCACACCGGC AGGCCCTCGT      180
    GGACCGTTTC AACAAACGGC CGTACCACCT CTTTCTTCTG ACCACCCGCG TGGGGGGCCT      240
35  CGCGGTCAAC CTCACGGGCG CGAACAGAAT CATCATCTTC GACCCCGACT GGAACCCCTC      300
    CACGGAACCTG CAGGCCCGCG AGCGCGCCTG GCGCATAGGC CAGAAGCGCG ACGTGACTAT      360
40  CTACCTGCTC ATGGTCGCGG GCTCCATCGA GGAGAAGATA TACCACCGCC AGATCTTCAA      420
    GCAGTTTCTC ACCAACAAGG TCCTCAGCGA CCCCAAGCAG AAGCGCTTCT TCAAGATGAA      480
45  CGAGCTGCAC GACCTCTTCT CCTTCGGCCC GGGCGCGGCG AGCGACTCCT TTGCTCTGA      540
    GATCGAGCAG CAGACCGCCT CCTTCGCGCG CCAGCCGGGC GCCCAGGCA CCGACGACTA      600
50  CGACTCCGTC CAGCGTTTCG AGGGCGTCTC CAAGCTGGAG GGCTTCTTCA AGGCCA      656

```

## (2) INFORMATION FOR SEQ ID NO:975:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1601RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

20	GATCTTTTTC CCCGCAAAC CGCACACTC GTTCCAGGGG TACTTGGGCA AAAAAAGGC	60
	GACGAGAGC AAGGTTCTAC GCGATGTTTT CAGGAAGGA GATGCATGGT ACCGGTCAGG	120
25	CGATCTCTTG AAATCCGACA AGTACGGGCA ATGGTACTTC GTGGACCGGA TGGGTGATAC	180
	GTACCGGTGG AAATCCGAAA ATGTCTCGAC TACCGAGGTG GAGAATCAGT TGCTCTCGTT	240
30	CAACAAGGAC CTCCTTGACT GTTGGTTGT AGTGGGCTG AAGATTCAA GCTACGAGGG	300
	TAGAGCCGGG TTGCTGTGA TCCAACGAA TCCAGCGGC CGGGACTGG ACCATGCCAG	360
35	TTTGTTAGAC GACCTTGTCG AGTATTGAA ACATGCTCTT CCTGGTACG CCTTGCCGCT	420
	GTTCATCAAG TTCACAAAC AGCTGGAAAC AACCGATAAC TATAAGTTG CCAAGAAACA	480
40	GTACAAAAC CAGCAGTGC CTCATGGTGC GGATGGGAC GAGACAATTT ACTGGTTAAA	540
	AGACTACTCC CAGTACAAAG TCTTGACCGA CGAGGACTGG GAGCAGATAT CAACCGGAAA	600
45	GGCAAAGCTT TAGACCAGAC AATGCCGGGA TTGACACCGG TAGGGAGTTC AAAATAAAAA	660
	AAATACCTGG GAAGCCATCC ATAAAAGCCA TTATCAACTA TAGAAATAGA AAAGT	715

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1601UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GATGGCCCTG TCCCGGGACG GAGAGCGGGC GCTGGGCTAG CATAAAAGCA CGCAGGTCAC	60
TGTGCATGAA ACTCGAATCG AACGCCGTAC TCGATGGTAG AACTAAACGG GCTCCGCTTC	120
GAAGTACGCA CAGTTGAGTG AAATGTCAGT GTGGGCGCAA CGGCCCCAAG AGCAGAATAG	180
CATGGACATC GAACAGAGGT CATGCGAGCC GAGTGAAGC AACAGCCATG CAGGATGCCC	240
GGGTACGAA AAAGTGCAGC CGCTGTATGC CGCAGAGAAC GGTTCCACGG AGACTGCCCC	300
GACAGCCACC GGGCTGTTTG ATAGCTGCA CGTTGTACCG GTGTGCAAC GCGGGGACT	360
GCTGAGTAGG CTGGCGCTTG TGCCCGAATT CCGGAGCGCA CGTCTCTATC CCCCAGGGT	420
CAAAAAGCTG ATCTGGTCA TGTGCGCTT TGCATGTATT CTGGGTCCA TGGGGACCAA	480
CATCATCTAT CCTGCGATCG GGACTATCAT GCAGGATTTT GGCACCTGCG GGTTTCTGGT	540
CAGTGTGTCT GTAGGCACCT AACTGCTGC GCTGGGCATC TTCCCCATCT GGTGCTGTC	600
GCTGGCGGAC AAAAACGGCC GCGAACAGT GTACGTGCTG TCGTTGCGC TGCTGGTGGT	660
GTTCAGCGTT GGGCAGGCT TCTCGCGCAA CATGAGAC	699

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1602RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

15	GATCCAAGCG CCGCACAAAC CAGCGATGTT TGCAACATAT TCGGCTAGTA TTCTCCGTTT	60
	GACTTTTACCC CTGCGTAGCG TTGGCGTCAG ACTGCTGAGC CAGGAACTC GGCGGGCCAT	120
20	TGAGGGCGCC ATTTCTCTCTG CCCCAGTGGT TCTGTTTATG AAGGGCACCC CAGAGTTCCC	180
	TCAATGTGGC TTTTGAAGG CCGCCATTGA GATCTTGGC AGACAGGGCG TGGATCTGCG	240
25	GAAGTTTGGC GCGTTCAACG TGCTGGAGGA TTCTGAGCTG CCGAGCGGGA TAAAGGAATA	300
	TTCCGAGTGG CCTACAATTC CACAGCTCTA CGTCAACAAG GAATTTGTGTG GGGGGTGGCA	360
30	CATCTCACC AACATGGGCG AATCCGGCGA GCTAACTACT ATGCTGAGG AGGCATCCGT	420
	TCTGTGCGG GATACTGAGT GATGCGCGT ACGGCTCCCG ACTATATTTA TAGGAATACA	480
35	GCTTGTAATT TAAGACTTGT ATTCTCATGC CTTTAGACTT GTAAATCATG GTTGTTTAAT	540
	TCACAACTC CGTTCTTTCA GTTGAAAGAA GTGAGAACAG CTTGCTTTCC GTCATGTGTG	600
40	AAAGAGGCTT CTGATGGAGG AGGCGTGAC ACGCAGCAG AGAAAGTCTC TCAAAAAATG	660
	ACGTTCTAGT GGAAGGGCGG ACGCAATCAC CCTTGAATGC GCGA	704

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1602UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GATCGTGCCC GGGCTTGTC TTGTGCCAG AGTTGTGCTT GTGCCAGGC TTTTGCTGGC 60  
TGCTCGGTC GCTGCCCGG GGTAGTACA CGCCGAAGTG CTTGAGCGC AGCGGGCGGC 120  
GGAAGTGCAC CGTCAGCTC TGTCCAGCG GAGAGAGACT GCGGAGAAC TCCAATTTTC 180  
TCTGCTTACA CTTGAGCTC TTCTGTCCA TGCTGGTAC GTCCAGGTAC GTGCCGCTGT 240  
AGCCACATT GGCATACCG ATATTTTCTG CCTTCGAGCA GTAGTAATTC CCTCCGATGA 300  
AATCACAATC GCCAGCACC TGCTGGCAG CGAGCAGGC AACTGCAAG ACTGTGACA 360  
GCTTCATAAT TTGTAAACG TTGTAAAGA ATGACTAGTA GTTAGAACAG ATAAAAGAGT 420  
GCTTGCTGT GTGCGCTGC GCGGTCCAC GCTTCGAG CTCACCGCC TTCTTA 476

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1603RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

GATCGGCAA GATCGTGTT CAGTTGACG GCAGATTGAA CAAGTGCGT GTCATCTCTC 60

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CAAGATTCAA CGTCAAGATC AACGACGTCG AGAAGTGGAC TGCCAAACCTA TTGCCAGCCA 120  
5 GACAGTTCGG CTACGTCATC TTGACCACTT COGCGGCAT TATGGACCAC GAGGAGGCCC 180  
ACAGAAAGCA CGTTGCTGGT AAGATTTTGG GTTTTGTCTA CTAAGCGGCT GCTATATAGC 240  
10 GTATCTAGCT CTAATGTACG ATACTCAGTG TCTATTACCA CGCGCGGAG CTCCACGGGC 300  
CACATAAGAG GCCAGCGGCG GACGGCAAGC GGGAAATTCAG ATGGGTAAAT TAGCAGTAGA 360  
15 TTAGTAGTAT ATATGTACAA ACAGCATACA CATGAAAGGC GTGCGGATC ATAATCTTCT 420  
AOCCTTTCTA CCACCTTCTT TTCTGGTAGA GTGGGATGGG ATAGGAGTGA CGTCTCGAT 480  
20 ACGCGCGATT CTCAAGCGG ATCTGGCCAA AGCTCTCAA GCAGCTGAC CACCTGGACC 540  
TGGGGTCTTG GTCTGGTAC CACCGTAGC TCTGATCTTG ACGTGCACAG CAGTATGCC 600  
25 GACCTCTTIA CACTTGGCAG CGACGTCTG AGCAGCCAAC ATGCCAGGT ATGGAGAGGA 660  
CTGCTCTTG TGGGCTTGA ACTTCATACC ACGGTAACT CTGGCAATAG TTCTCTGCCA 720  
30 GACA 724

(2) INFORMATION FOR SEQ ID NO:980:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 721 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1603UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

55 GATCTATTTG TGCCGTCCGC CATTAGCAA GCGGCAAGCA TGATCCAAA TCATGAGAGT 60

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ACCCTGGGC TTTCACITTC CAAGCCTTTA TCAACAAATC TGGTACACGA TACATCCATC 120  
 5 GCGACAGCAC ATATACCAGA ACGGAAAGC OGACAAGATG GCACTAGACT CTGGTAGGTA 180  
 ATCTGAGTTC GACCATATOC ACTTCGTTAA TGGTGATAGT TGATAAAAAG AAACGATACT 240  
 10 GAAAATTTTA ATGGTTACCA ATCTCATCTC ATCGCCATAC TGAAAGAATA TTGTAGGTCT 300  
 CGCAGTGGAA CAAGGATCAA GCCCAGCCTA AGACAATAAT GGTTCAGCG GAGGCAGTAC 360  
 15 AGGAACTACC CCCAGATGAA GAAGAACTGG CCTTGGCTAA GCTAGTGTIT GGCGACACAG 420  
 CAGACTTCCA TGAAGCGCTG OGAAATGCAG ACCTTAATTA TGTTCCTTCA GATGAAGAG 480  
 20 TATATGGCCA GGAGTGTTC AGTGATGAG AAGAGGGGAC TGAAATTGGT CACCTGAATG 540  
 ATGACCAATT GTTTTTTGTG GACGAGGGTG CAGATACCGA GCGAGGAGCA GATGGAGAAC 600  
 25 GGAGGCCATG GAGGTGGAOC AGGTATGCGA GGAAAGCGAC TCCGAGAGG AAACGGGTAG 660  
 CAGCGCTGCA TGGTCAGATT CGGATGACGA ACACTTAAAC GTTACAATAG GGCAAACCAA 720  
 30 T 721

## (2) INFORMATION FOR SEQ ID NO:981:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 638 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1604RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GATCCCTATT AGAAGAGGTT ACTGGGGCTC CAACCTTGGT CAGCCACACT CTCTAGCCAC 60

55

GAAGACCTCT GTTAAGTCTG GTTCGGTCAC TGTGCGTTTG ATCCCTGCCC CACGTGGTTC 120  
 5 CGGTATCGTC GCGTCTOCAG CTGTCAAGAA GCTTCTACAG CTTGCTGGTG TCGAGGATGT 180  
 GTACACTTCC TCCACCGGTT CTACCCGTAC CCTAGAGAAC ACCTTGAAGG CTGCGTTCGT 240  
 10 TGCCATTGGT AACACCTACG GTTTCCTGAC CCCAGACTTG TGGCCAGAGA ACCAGTTGCC 300  
 AGCTTCTCCT CTAGACGTCT ACGCCGACGA GCGCGTTGCC CAGAAGAAGA GATTCTAAGT 360  
 15 AGTGTGTGTA CATACCAACA GTTGTCTTCT TTGCAAGTGA ACCGCCCGCC TAAGCCTTTA 420  
 GCGCGATGCC ACACAGACTG CCGTTGGGCA GGAGATCGGT TGCTTCCGA CGCTGGTACA 480  
 20 GGGCTGGAT GCGGCTCTGC GGCTGGGGT GCATATCGGA GATATGGGC CGTGCCCGTA 540  
 CGGCAAAGAA TCAGCAAGAC ACTAGCGTCT GGCATCTTTT TTCAATGCAT TATTTAGCTT 600  
 25 TTTTTTTTTT TTTTTTTTGA GTATAGACAC ATATAAGT 638

(2) INFORMATION FOR SEQ ID NO:982:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1604UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GATCAGAGCA TCCGATGAGG TGGCACCGGC CCGTCCGCT GTGTCTTTCT TCGCGGTATC 60  
 GGCITCCGAA ATACTTAGCT TCTCAATACT TGGGACTGCC TTATCTTCAG AGGAAGCGGT 120  
 55 AGCATCTCA CTCTTAGGAG CGCCCTCTGC GCTGCTCTTA GGCTCTCCT TTGTTGGCTC 180



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CTCCGCCCTTA GCCTCTTCTT TCTTCGGGAC AGGTTTCTTA GCACCAACTA GCTTGATAACC 240  
 5 GGAGCTGGAA GCCAACTTGA GGGTCTTCTT TGGTTTGGGA GCAGTGGCAT TGGGCACAGT 300  
 TCCCTTCTCA AAGTTGTTC AAGTCACCG AGGGTGGCT GACTGGCCCT GTCCGTAACC 360  
 10 ATAGCTCTGG TTCCCCCTAC GGTCCCCCTG TGGCTGTGAG TTGTACTGCT TGTAGCTCTG 420  
 ATACCCACCT TGCGCATTGT ATTGCTGGTA ACCTTGGTAG CCAGCTTGTG CTGGGTTGTA 480  
 15 CTGCTGGTAT CCCTGATAAC CCTGGTAACC GCGGCTTGC TGGTTGTATT GCGCATAGCC 540  
 TTGGTACCCA CCTGCCTGTT GGCATACGC CTGGTAACCT CCCTGAGGCA CATACCCCTG 600  
 20 GTAATTCTGG AAGTTACTTG GGTGTGAGTA TTGGCCGAAA TTGCTGCCC CTGACCTTGA 660  
 TTTTGACCTT GATCCTTGGC TTGGGACTGG CCTTGGTCGT TGCCTTGCGA 710

25 (2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 688 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1605RP  
 40

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GATCTTCTCA AAAGTAGCAT TTACAATCTG CGTTAGCGTT GCTTGTGCAA TTCCCTGGTT 60  
 50 GGACGAGCTT AGTGACAGGA TGAAAATATT ATAGATTGT CTGACGGCCT TTAATAGTGA 120  
 TGACCGTGA CAATTGCAAT AAGGCTCATC TGTCAATATA CAGCTTGCGA GGGCGGGAC 180  
 55 TACCTGCAAC TCGACCTTCC CATCAGTGGC TTCTCCATCA AACAGTCGG TTATGGTATC 240

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AAAGGCAGCA TCTATCAGCC GCATTCTTGG AGGTGGTGTA ACACCAGAGT CTGGCAACGT 300  
5 CGTGCCCTGG TCGTTTGATG CTGCGGAATT TGGAGGGTTC ACTAAAACAT TCTCGTCTAA 360  
CGCCTTAAAG GCAAACAAC TTAGATAGACA ATCAAGAGCG CTAACTGTA TTTCTGGAAC 420  
10 ATTAGTCTTA CAGCAAGCAC GTAGTGCTC AAAGACCAAC AGAGAATCCA AAAACTTTGG 480  
ATCGTTTTC GATTGCAGGA GTTGTCTGGT CAAGTTTTC ACAGTTTCT CAACCACTTT 540  
15 TTCATTATTA GGATGTTTGT GCATGGATTT TGCTGTAGT ATACCTCTTA ACCTTAGTTT 600  
CACAAGATGC ACTGCGGATT TCATCGTCCA TGGACTACCA GAGACATTGG AATATGCCCT 660  
20 TGTGTGAGCG TTGAGATTAT CCTGCGAC 688

(2) INFORMATION FOR SEQ ID NO:984:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 725 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1605UP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

GATCAGAGCA TCCGATGAGG TGGCACCGGC CGGTCGGCT GTGTCTTTCT TCGCGGTATC 60  
45 GGCTTCCGAA ATACTTAGCT TCTCAATACT TGGACTGCC TTATCTTCAG AGGAAGCGGT 120  
AGCATCTCA CTCTTAGGAG CGCCCTCTGC GCTGCTCTTA GGCTCTCTCT TTGTTGGCTC 180  
50 CTCCGCCCTA GCTCTCTCTT TCTTCGGAC AGGTTTCTTA GCACCAACTA GCTTGATACC 240  
GGAGCTGGAA GCCAACTGA GGGTCTCTT TGGTTTGGG GCACTGGCAT TCGGCACAGT 300  
55

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TCCCTTCTCA AAGTTGTTCA GGTTCACCGG AGCGGTGGCT GACTGGCCCT GTCCGTAACC 360  
 5 ATAGCTCTGG TTCCOCTTAC GGTTCOCCCTG TGGCTGTGAG TTGFACTGCT TGTAGCTCTG 420  
 ATACCCACCT TGCGCATTGT ATTGCTGGTA ACCTTGGTAG CCAGCTTGTG CTGGGTTGTA 480  
 10 CTGCTGGTAT COCTGATAAC OCTGGTACCC GCGGCTTGC TGGTTGTATT GCGCATAGCC 540  
 TTGGTACCCA CCTGCTGTGT GCCCATACGC CTGGTAACCT COCTGAGGCA CATACCCCTG 600  
 15 GTAATCTGAG AAGTACTTGG GGTGTAGTA TTGGCCGAAA TTTTGCTGOC OCTGACCTTG 660  
 ATTTGACCT TGATCCTTGG CTGGGACTG GCTTGGTGC TTGCTTGGG ATTGAATTG 720  
 20 ATCTT 725

(2) INFORMATION FOR SEQ ID NO:985:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 678 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1606RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

GATCAAGCAT ATCAAATTTC CGGCAATCTG CGGGTCATT TTTTGGACA ACAGGGTCT 60  
 45 CCACAGGGTC CATCTCCATC AGCGGAGCTA TACGTTGGA CAGTGGCTC AGCTTGGTAC 120  
 TCTGGGAGAG AATTGAGACG CCTTGGAGC TGGCTGTATG GTAACGTGC TCCGTGCGT 180  
 50 AGGTGGTCAA AGACAGGAC TCTGAATACT CGCATTTCG ATCCCGGTTG CGCCGTACGT 240  
 ATCCGTGCGC CGTGGACTTG ATGGCAGTGG TGTCCGAGCA CGAAGACAGC GAAGGTAGTC 300  
 55

TCAGTGGCCG CGTCGGCGAT ACGTGTACT CGAGCACAGA CTCGTTGTGT CCCCTCCCG 360  
 5 TCATGTTCIT CGGCTCAGTT CGCGACAACG CTCGCGACCA TGCGTGCCCC CTCGCTTCT 420  
 TTCTGTGGAA GCGCCCAAAC ATTAAATCTA GCTGCTTCTT CCTGGTACTC TGTTCGCTCT 480  
 10 GTTCTGCCC GCGAGCCCC TCGATTCAA TCTCTGTACA GCGTTATGC CGCACTTGCT 540  
 CGTCTAATT GGCTGCCACA CTCCTGCTGC TCGAACCTAA GCGTCTGTA CGAACGCTT 600  
 15 TCGTTGACTT GACCGTTGG GCGTAATCTA TTATTGGAAC CTGTAAAAG CGGCTTCTG 660  
 TACGCTATTA GTTAGCCC 678

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1606UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GATCCGCTTG AGTACTGAGA TATTAACTCA ATACCAGGAT AAGCTTTCAA AGCACCGTAA 60  
 45 TCCTACTGTG CAATGGTGGG GACCTACTGA TTCTCGCAC TACGTCTAG CGCTGAAAT 120  
 TTTATCATAC GTGTCCCGAG ACGAACTGGG CCTTGCAGAT ATCGATGAGG CTGGACTTA 180  
 50 CATGGAAAGT ACCACGGAAT ACGGGTTAAA TGTGGCGGAC GAAGAGCCTC TAGATATTTG 240  
 GGAATTAGAA TACGAAGAGA AAAAGCTGCA ACGGTTAGCA TTAGGACCCA AGTACAGCAG 300  
 55 CATGACTTAC AGAAAGCATC CTGCCAGGGC GTGGCTGTA TTAGATACAT CCAAAAATGG 360

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TTCTAAAGAG CATAAGCGTA AAGGAAAGCA ACACAAATTA AAAAAAGGAC AGCAGTCTAC 420  
 5 AAAGATAAGG GTATCAAAAA AAAGGOGACG CGTACAACCA CACAGCATAT GOGATTAATA 480  
 ATCTTACAAT CGTACTAAGT AATACATACC GOGCTTATAG AATCTGCTGC TGCACGGAAA 540  
 10 GTTGCATATG CGAAAACATG CTATGCAGTG GATGATCGCG TACCCTTTT TAATCOGATA 600  
 AAAGTGGACT AGCGATAAAT AGTAATTTC AATAGGAATG TGAATTTGAA TTGAGAATTG 660  
 15 GGATAATGCT GTGGATTTC GTGATTATAA TACCATAAAT ATA 703

## (2) INFORMATION FOR SEQ ID NO:987:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 622 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1607RP

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

40 GATCACACGA CAGTGCCAGT CGGGGCAGCC GGTACCCGTT GGCOCATCG TGAAGCTGAC 60  
 TCCGAAGAAC CCTTCTACA AAGTCCCCGA GACCGAAGAC CTGTGACGG TCATGGGCAT 120  
 45 CCTTGGCTCC GCGTGCACC GTGTGCCCAT TGTGGACTCC ACCTCTTCAT CTATCOGTGG 180  
 CATTCTGTG CAGCGACGTC TGATGAAGTA CCTGTGGGAC AACGCCCCC AGTTCAGCAA 240  
 50 CCTGGAGGTG CTGCTCAACT CGTGCCTGCA AAAGTTGGGC ATCGGTGTGC TGGATCCACA 300  
 TACCCCTCCT ACTTGGGGC AGTGGGTGT TATTTCATT CTGACACAG AGCGCTGCT 360  
 55 CGTTGCCCTG CACAAGATGC ATACAGAACG GATATCCTCC ATGCGAGTGA TCGACCACCA 420

GGGCATGCTG CTGGGAACA TCTCTGTGAC AGACGTCAAG CAGGTTACGC GCACCTCGCA 480  
 5 GTATCCGTTG CTGCACAACA CCTGCCGCCA TTTCATCAGC GTGATCCTCA ACAACCGGG 540  
 CCTGAGATG GGCAAGGACT CCTTCCCCAT CTTCACGTT TACCCACCT CGTCCCTGGC 600  
 10 CCGCACGGTC GCGAAGCTGG TC 622

## (2) INFORMATION FOR SEQ ID NO:988:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1607UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GATCGGTGCC CGCACCTCG CCCGATTCTT CGCAGCTCG TTOGCAATGT TGGTATOGA 60  
 35 CTCTGCTTC TTATCCCAT CCACCTCCGT CCCGCCCTG TCAAAGCTC GCTTGGCTGC 120  
 GCGGCCACTC GTACCTGCCT GCGTTCTTC ATCTCAATA ACTATCACTT GCATCCCGTT 180  
 40 AGTAGCTGCA CGGTGCAGAG GCGTGTAAC CTCCCTCAG CCCTTCAAAA CGCCCCACCA 240  
 CATACTTCT CGTCTGGAA TCATGATTGC CCTGGTAAT CTTACGCTA GACTAATTT 300  
 45 GGTCATAAC TCGCTCTTG CGACTGGAA TTGGTGGTG AGATGGTGAA GTCTCATGTC 360  
 GTCCATTTCT GCGATGTTA AAATATGGT TTOGAAAAA GCGTCTTG CCCTTGACTG 420  
 50 ATGCTGACT CACAGAGGAC TCACCAGAGC TTGAACGCA GCCAGGAAGC ATTCTGTCA 480  
 TACCAGAAAG GCGCCACGGC GAGAATCAGA ATGATGTTG CATAGTCGGG CAGCAAGAGT 540  
 55

EP 0 866 129 A2

GCTCCAGCGC TCGGGGTCCG CAAGCGCAGA TGCAACAACCT CCGTGACAG CATCACAAGC 600  
 5 GGTATAGCAT GCCTTCCCA ACGATTTCG AGGTGCGGA CTCAGCAAG TATTCCCGAC 660  
 CTGGCCGGTT ACAG 674

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1608RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GATCAAAACC ATCAACCAAGT TTATTTCATGA AGTGTCCGAC GATTTCAGG TCATCATAAT 60  
 35 CGACGCAATT CGTACTTTGT CCTAAAGTT CCCAGATGAG TGGAAGAATA TTCTATCCTT 120  
 TTAAATTGAC ACTTTGAAAA GTGCAGAGGG TGGGTATACA TTCAAAAATA ATATCGTAGA 180  
 40 TGCGCTGTTT GACCTGATCC AACATGTACC TCAGTCAAGG GAACAGGCTC TGGAACTTT 240  
 GTGTGACTTT ATTGAGGACT GCGAGTTCAA TGAAATCTCA GTCAGGATCA TTTACTTATT 300  
 45 GGGTAAGGAG GGCCCTCGA CAGAAAAGCC TTCGCTTTAC GTTAGACACC ATTACAACAG 360  
 AGTTGTCTTG GAAAATTCAA TCATCAGATC TGCTGCTGTT AGCGCATTTG CCAAGTTTTC 420  
 50 CTCTCCGAAG AAAGATCCGT CGTTAGCTTA TTCCATCGAA AAATTGCTAA AGGSTATCCA 480  
 AACCGATGAG GATGACGAAG TGAGAGACAG GGCAACCAAT CTAGTAAAGC TCCTTGAGGA 540  
 55 GAACAAGGAA AAGCCTGGTG TTGCCGATGA ATTTATCCAG CCAAAGCATA GTTACGATCT 600

ACTTGGCCCTG GAAAAGTAAA TTAACGAACT ATCTCCACCA TAATGAAGAT GGCTTTGCCA 660

5 CACCATTTGA CGCGTGGAGC ATTCCAAAGT TACACAGAAG AGGAGCTCAA GGCTATTAAAT 720

TTGAAGCAGA AAC 733

10 (2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1608UP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GATCTGGCCA AGGATAAAGG TGTTCATCAA GTCATTGTGA ATGAAGCCCG CAGCCTGTGG 60

35 CGCCTTAGTG CCATTTCCTGA TGGTCCATTC TCTGACTTCG TCGGGCCCGC AGGTGAAGAA 120

CGAGATCAGA TCCAGCTTCT GTCTCATGGT GGTGATGATC TTTGGGAAGG CGGACTGGAC 180

40 GCGGATCTTC TCGCACTCCT CGACAGCCTC CTCGGGCGTC ATGTGGGACA GTCTCTCCTC 240

CAGGCACACC GAGAAGGGTA TAATTAGATC GCCAGGGGAG TACTTGTGGA TCCACTCCTT 300

45 GATCTTCAAG AGGTGCTTGT TCTTCTTTCT AATGTAGTCC CGCTCCGATA GGTGATCAG 360

GTAGATGGAT GGCTTGGCGG TTAGCAGGAA CATGAGTTG ATGACCTCCA CCTCCTTGGT 420

50 GCTCCAGGAC TGGTTTGGGA CTCTCTGACC CGACTTCAAA AGCTCGATAA TCGGCTTCAC 480

CAGCTGGGCC TCCTCCTTCT TCTGTTTCAC CTCAGGGAC TGGCCGCGTC TCTTGGTGAT 540

55 CTTCTCCACG GGCTCCAGGT GCTTCTCCGC GAACTCAATG TCCTTCAAAC GCAATTCCGT 600



GTTAATGATG TCCAGGTC TCACCGGGTC GACGTCACCC TCAATGTGGA TGATCTGGC 660  
 5 GTGTCGAAG CAACGCACGA CCTGGTAGAT CGAGTCCACA GATCTGATGT GCGATAAGAA 720  
 GGC 723

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1609RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GATCAGACGG TAATGGGGG CATGCTGGG CAGGTGGAGC ACGTATCTAG CGTCCATCGT 60  
 CTCTTGCTGT GGTGGGGGG GCGGGGCAAG GGCTGCTG CGGAGAAAT ACASTAGGGA 120  
 TCTGTGCGC CCGGCAACCA GGGCAAGGG GGGCGGAAC AGGGCGTTT GCGCCTTAAT 180  
 CCGGACAAAC GCATATAAGT AGAGGCTTAG GCGCTGCTG AGGGACGGCA GAACACACAC 240  
 AAGGACCAAT GAACACGATT ATCAACTTCC AGGAAGGCAG CGGCAGGCT CTCAGCGAGC 300  
 ACAGCATCTT CCAGATGTG CTGGTGCCA CTGCTGAAA CGGTCCATCA GGACACCTTG 360  
 TAGTGGAGTA CCGGGGCGAG TCTACAGCG TGACGCTGG GAACGTTATG CCTGTGGAGG 420  
 CTACGCAGAC GGTGCCCAAC CTGATGTTAA TCACGACCGA GCGGGGATC GTCAGGGAGG 480  
 GGGACCTATT CACGCTGGG ATGACAGACC CAGATGCTCC CTGGGGTGG GACCACAAGT 540  
 GGTGGGAATA CTGCCACTTT CTGGAACGA ACATAACGCT GGGCTGGGAT GACGGGGTGT 600

OCCACGTGGT GCTAAAGGGC ACCCCGCAGG TGGAGCACAT GGGCCCTGGG CCGCCCGGGC 660

5 GGCACAGGGG CTCACCGTA CGTGTGGTTG TT 692

(2) INFORMATION FOR SEQ ID NO:992:

10 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 720 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: PAG1609UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

30 GATCGAGAAG ATTTGGAGAA GGAAAGCGTC TTGGTGCTAG CCTCGTGACC CCGTCCCGGG 60  
CTGGAAGTGC GCGATATACT ACATAAAATA CGTTATCCCT GGAATTTGTA GCATTAAAGG 120  
35 ACTTATGGAC TATTCTGTAT ACGTGGCTT CCGCTGCCA CCGTAGCAA TGCCAAACTC 180  
ACTCGAGGC CTGCTGCTG GCGCAACAAT CGGACTCAG CGGACCGAG CCGCGCAGTC 240  
40 ACGTCCCCC CGCATTCGG CCCACATCAC TCGCTTGCC TCGCTTCGC ACCCGCCAC 300  
GGGACTCCG GCGCGCAGC CCGACGTGAT TCTAGTTGCA TAGGAAACTA GGCTAAAATC 360  
45 ACGTGAAGTA ATGCGCGGC CACATCATA CATGGGACG GACCGGACT ACCCCCCCCC 420  
CCCCGCGCG CCGCTGCAC AGCAGCGTA TACGGCGCAG GCGCAGTCG GTGCGCGCC 480  
50 TCTGAGAGG CGCATGGCG CCGATGCTG ATGGCTGCT CCGTGTGCG GAAGATGTGG 540  
AGGCACGTAC GCGGCAGCT CAGTTACCG AAGTTACCG TTCTTCTGAT TAAATTTGGA 600  
55 CTGAAACTTA AAAGCGTCA GCAGTGCAA ATCCACGTG AGAATAATTA CAGGAAACAG 660

CGGTGGACCA GCTGCGGAAC TAGACGACGG GTTGGTGTGG CACGCATAGA AGGTATGTTT 720

5

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 731 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: PAG1610RP

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GATCAATTTC CTTTGGTATA GTTGGCGTCC CAGGCTCCGA GATAGCCCCA CATGATAAAT 60

30

TGCTATCGCA CATGATGTCC TGGTTGTTCAT TGTGTGTCAG ATTGCTCAAA TCAAAAATGA 120

AACTACCATC ATCTGGTTTC ACTTTCAGTA AACTATCGTT TTTCTCTGTT GCAGGGTCGA 180

35

AATCCATATC ATCCCGTAGA TATTCTATGT ACAGCAGAAA CGGAACCTTC TCTGCTGAGT 240

TCAACACCTG AGCTTCGTGA GCAGCAATAT TTACAATTGG ATGCAGCTTG CCTTCTTAT 300

40

TAGGCGGCAA CAGTGTAGGG ATATCTAAGT CAGCTGGCAA GTCCCTATTC ATGATAGAAA 360

GCTCAGCTCT CAATGAAGTT AGGCGAGCTT CAGTGGGAAC TTGGGCAAC TTCCTGGATA 420

45

TGTTTTCTAG AGCAATCACA AACTGCATCT CGCAGCGGAA GTAATTGGC TTCAAGATTT 480

TGATTTTATG TGTGGCTGAT AACTTGGAGG GCTCCAGGTT ATAGATGTTT GCTCCATGCC 540

50

GAGATGTCTT CGTTTGTGG CTCTTCTTTA AATCATTTGA CGGAGACTGC GTGATGCTAC 600

CATTCCATG CTGCTCCAAT GATTGCTGAT CCTTATACGA GTGGAGTGAC GTGCTGGATC 660

55

GAGAATTCAG ATGCAAAATTA GGCATAGAGT TTGTGTATTC CTCTAGCTTA GCACCATCGT 720

TATCTTTGGG C

731

## (2) INFORMATION FOR SEQ ID NO:994:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1610UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GATGATCTG TACAGAGCGG TTACAACAGG CACTTGTAAA AAGCAATATC GTTACTTTTT	60
TGCATGTCAG TTTTTCCTC GAGCCTCGTC AGCGCGAGGA ATGAGTAATG GATACTTTGA	120
CGACAGAAAA AGTGAAACT TTAGCGGAC ATCGCAACT GCTCGTTAGT AGCACTAAG	180
CGCAGGTTAG CACAATGGG CCAAAGGATA CGCGGTGTC GGAGACTCT ACGGGTCTC	240
GCTATATCAA AAAGGGCAAG ACTTTAGAGA ATGACATTGA GCTACAGTC GTGACGCCAG	300
CCACCGGGA GTTCCCGAG GACCACAGG AAGAGGGGA CTACCAGGAG ACGGAGGTCA	360
AGAGGGGCT GAAGCGGG CACATCTCGA TGATCGGCT GGGGGGAG ATAGGCACAG	420
GCCTGTTTAT TTGATTGCA TCCCGCTGC GGACAGCGG GCGAGTGGG TCGCTGTTGG	480
CGTACATCTT CATCGGTACG GTGGTGTACT CGATCACCA GTGCTGGG GAGATGGGA	540
CGTTCAATTC TTGACTCTT CGGTGACGT ATTTTCAAAG CGGTTTCTGT CGCCTGGTT	600
TGGGTGGCA AACGGTATA TGTACTGGT CAACTGGCG ATCAAGTTG CTGTGAGCT	660
TTCTGTGGT GCCAGATCA TACAGTACTG GACGGACGC GTGCCAATG CGCGGTGGAT	720

TGTGATTTC

729

## (2) INFORMATION FOR SEQ ID NO:995:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1611RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

GATCATCGT GGTGTCGTTT ATTACCTGTA ATTCCATTGA TATCCTGGCT ATGCAGTGCT	60
GGAAACGCTC CTCCAGCGCC TCTATTTTGT TATTCAGCTC CAAGTACTOC GCGAGCTTAA	120
AGGTCAACGA GAGCGACCCCT GGATTGCACC TGAOCCGCGAT CTCAAGGACC TTCTCGTGCT	180
CGTTCTCGTC CACAAACATG GCGTAGTTGT ACCATATCTC CGGCGCAAAG CACATGTGCT	240
GCACAGCCTG GCGGTGCACG TATTCCAGC GCTGGCGCAG CACGACTTGG GGCAGGTGGA	300
GCTTGTTGTC CAGCTCCAC TGGATCCACT TCGTCCAGAT CTGCAGCTGG TACTCATCGT	360
ACTGACCGGG CGCAGGCAGG TTCTGCTGTG TCGCTGGTT TAGCTTCGTG GGCAGCGAGC	420
GCGCAGGCC CTTCGTCAGG TTGACCACT CCTGGTACAG CGAGCGCGCA TTCATGTAGC	480
TGCGCGAGAG CTCTCCGATG AACTTCCCGG CCGTCAACTG GTTGAOCTCC TGCTCCCACT	540
GCGTGTATTT CTCCAGTAC CGCTCCAGCG ACTCCACTGG CAGGCACAGC AGGCGCTTGT	600
ACAGCTTGCG CAGAATCTCG ACCCGGCTCT GCTCCTCCCA CTTGCTCACC GCCTTCCACT	660
GCTCCA	666

## (2) INFORMATION FOR SEQ ID NO:996:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1611UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

GATCTAAGGG ATGGGTGACT GCTGCCGGTG CTCACAGCAG TGGCAAGTAG CTAGTAATGG	60
TGCGAAATCG ATCAAAGAGG GTGGGTCTGG CGGTACAGGC AGAAAGCAAG CCGGCCGATA	120
CAAGTTCAG TTCTACAAGC ACCTGCAGTT CCAGGGTACG AGGTACCAGG TGGTGACTTC	180
GCGGCCGTAT CTGATAGAGC GGTACGGGGA GCGCAAGGCG GCGACGATCA GGTGTTTGT	240
CAAGTGCATC CATCGGAAAA TCAACGACGA TTGTACACCG ATCAGCGACG AGCGGGTGAC	300
GCACGGGGTG TCGAAGTGGG AGAAGTCGAA GCTGTTCTTG CTGCTGGTGA CGCTGTGCA	360
GCGGGGCGGG CCGGAGTACT GGCTGGACAA GACGAACGGG TGCCAGAGCC GCGCGGGCGG	420
AGACGGGCGG CGGAAGAGCG ACCAGGTGGA GGAGGGGCGG AGCGGGGCGG GCCAGAGGCT	480
CGTCTGCACA CTGGTGGAGC AGATCATGCG CGAGAACATC ACGGAGGACT ACGACGAGAG	540
CGTGCAAGAC GAGAACTACG TGTTCCTGTC GATATGGGCG AACTTCATGG AGGGGTTGAT	600
AAACCACTAC CTAGAGAAGG TCT	623

## (2) INFORMATION FOR SEQ ID NO:997:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 708 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1612RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GATCCATGCG ATAAATCTCC TAGTGGTGTG GTTTCACACG AAGCAGCTTC CGTGGTTCTC	60
GTGGTTTTTC CTGCAGCTCT GTTCAGCTT GATTMTGGTG TTTTGGGGA CGTGGACCAC	120
GAGGTGGCGC GAGCTTCGGG ACACGTTTTT TGAGGGTCTC ATAGATCAGG AACCTATTAC	180
GGGTGGGGCT GAGTCTCCCT ATCATGGCAG TTCTCAGAAC AGACAGCAGT TTGAGATGAA	240
GGACTTGGAG GCACAGAAAT AGCTTACATT ATAAATACGC TTGAGATCAT TCTAGGGCCA	300
CGGTGAGACT GATCATTCGT AAATAGCATT TTAATAACGT AATATATCAT ACGCTGGTTA	360
TTTGGGATGC AGGACTCCGA AATAGTCTGA CAATTATGTA CTGTTAAGTT ATTTATTTTC	420
AGACGGGGTA TCTGGCTTGA AACCTGTTCC AGTGACAGC AGATCCAGCA GCTCGAATAC	480
TGATTTTTTC GTATTGTTAC CTGGTCGACA GATCTCCAAG CCACCTCCA ATCGCTGCGG	540
CAGCTGCAGC ATTGCTACCG TAGACTCCAG CCTAGTGACA AGATGATCCA ACAAGGATAT	600
CCAATCGTAT TCGTGTTCCT GGCTCAGCGC TTTATCAACC TTTTATCAC GATCATATG	660
TGTGGGTAGT TGTAGGACAC TATTGTGAT TTCGATCAGA CCGCGGTT	708

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 732 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1613UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

GATCAAATAG ATGTGCGCTG CCACATAGGA CGGAGTCCGG GCTAAGCTGT GTGTTTACC	60
TGGAGGCAAC TGTGGACTC CTGTGTCAGC AATCGCGCCC CGAAGTCCGG AACAAAGGAC	120
TATATAACAA GCGAGGAAAC CACCTTGTGA TAAGCAAGGG GACCAACGAC ACAGCAACGA	180
CACAGCAACG ATGGCGGACC TGGGGCTCT TATTGACTTG ACGCGGATAT CGGAGACGGG	240
GTATGAATCG ACGAACCATC ATAGGATGAT ACACGGCGGC AAGGCGCTCT ACGGGGTCT	300
GCTAGTGGCA CAGGCGATAC TGGCGTGTG CTACTTTGTC CCCAGGGACT TTATTCCGCT	360
CTCGGTGCAC TGCCGTGTCA TGGTCGGCGG AGACAATGCT ATCAAGACGC AGTAAGAGGT	420
TGAACGGCTG CGGAAGGGGA GCAACTTCGC GCACTGTTG GTGCGCGGT ACCAGAAGGA	480
CAAGGAGCTG TTCACAATGC AGATCATCTA CCGGCGGAC CTCGGCAAGC AGCGGACAC	540
GCTGCACCGC AAGGACAACC TGGGCCCTGT GGACCGGTCC CACCTGGAGG ACGCTGGCAC	600
GCTATGCAGG CCGGATCTAC TGTCCAACCG TGAGAACTG CAGGCGGTGA GCGGTCTTC	660
GAGACGGATA AGGGCCTTAA TAACATTCTG GAGGGGTTCG ACAACAGTC GTCCGAGTAC	720
AGGCTGCTG GC	732

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid



(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: PAG1614RP

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

20

GATCGGGG ATGGACCGT GCTTGAACG CCTTCTGGG CACGGGGG CGTCTTCC 60

CGCGTGACAG GAGCAGGTG AGCGGGACTA CGGGGCGATG GAACAGTTC ACAAGTTCC 120

CGACACGATC CGTGTGACA AGTTGGTCAC GTATATATGG CGGTGTTCG AGCGGTCTG 180

25

CGTGTACCCG CCGAACCAGC AGCGCTGCCA TCTGAAGAC ATCATGCTCT TGGTGTGTA 240

CTGGGGGAG GCGGGGGGC ACCCGCTCTT GTCATGGG ATGTTTACG CGTGGGGC 300

30

ACGCTACGGG GTGCAGAAGC TCTCTGGA GCAGGTATTG ATCATCATG ACGCAAGTT 360

GCGGGGGGA CAGTCATACT TGATGATCC GCTGGAGGG AAGCAAAGC CGGCATCTT 420

35

CACGGGGG CGTTGCTCG ACACTATCG GCACACAATA CCCAACATTG CGGACCGCG 480

GAGCCTGGG CTCGCGCGT TCTCACTCC GTCACGAAG CGGGGGTG CTGAGAAAT 540

40

CTTCAAAGAC TGGTCCATCT ACTGCGACAA ATCCATATGG CGGACGATC CTGATCACTC 600

GCCCAATGGC ATTCTGGCT AACTCCGCA CTCTGCAAG CGATGGAGC AATCCATCTT 660

45

TGAGTATTTT ATGCTCTATT GGAAAACGC AACAGCAAC CACTCCAGC ACAACATTTT 720

CCACACC 727

50

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

55

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1614UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

GATCCTTTTC ACCAACAGCT GTCTGGGCCA GCTGGGGCCT GGGATGAGCT ACAACGAGGC	60
AGTGAAAGCG CTGACGAACC TGGGCTGGA CAGCTTTACA CTGCGGGGA CGGTGGGGTT	120
TCCGCTGAAC AACGTGTACT CTGTCCGGT AGAGGAAGGT GCTCAGATGG AGCTGCTGAA	180
GGGTACCTG CAGCAGTTGC GGCAGGAGCT GGCCAGCGG CTGCTGGACC GTGTGTATGG	240
GGGGAGAAG GCACAGCCCT CGAAGTTCTG GCTGGCCTTC ACAAGGCGCA AGTTTATGAA	300
CAAGGCGCTG TAAGGCGAAA TAGGTACGTA GCTGGGCGCG CCAGGAAGTA TTTACAAAGT	360
TGGCTGTATC GCTACGAGT TTTGGTGGCG TGTGCTTGT TGGAGCGAC GAGGAGTTCA	420
ACGGCGGAAG CTGGAGCTG TTCGGGTCT TTCAAGATCG CGTTCAGTC AATGCTGAGG	480
TGGTGTTTT TGGGCGGAA GCGTTGATC CGGCGCTCA GGTCTGTCAG CGCTGGAGG	540
ACACGCTCAT AGTCTGCATC TTCTTTCAG CGCTCTTGT ATGTTTGGAA GCACTGAGCG	600
ATGTCTTGA TACCGGGCTC GACTCTGCTG ATCATCTCGA TGGCTGGCG CAACAGCTGA	660
TGGCGGTGCG TGTGGGGTT CGGCTGCTA ATCATCTGCT GGATTTGTC ATCGGTCAAG	720
CCCGAT	726

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1615RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

GATCATTGAG	CTGGAGGTCA	GCCGACTACT	GTGGGACCCC	ATATTGACGG	TCCCGAGGT	60
GCAGAAGGAC	ATGGTGGAGA	TTCTGGGCGA	GTATATGCTG	GAGTCGGGGC	GGCGGTACAA	120
GCAGGGTTTC	CATGAGCTAT	GCGGCATGTT	CTACATGCAG	CTTTACCGCA	ACGGCTACCG	180
GGACGGCATC	CAGCACACCA	CGCTACATAT	GTTCAGGAG	TTCATGCGAG	AGGTAGCTGT	240
GACCTTCTAC	GACGAGGGAA	ACCTCATCGA	GTGGACGAAG	AACAGGTTTG	AACCGATACT	300
TGACACCGG	TTGCCAGGCT	TGTACGAGCA	GCTTCTAATG	CACCATGAGC	TGGACAACTC	360
GATATGGCTC	ATCCGCTGGA	GCAGGCTGCT	CTTCTCGGA	GAGTTGAGC	TGGAGTACAC	420
GCTTTGCTTG	TGGGATCACC	TGCTGACATT	TAGATACCCA	GTATCCAGC	TGTTAGCAGC	480
CATTATCGTT	GTCTGTCTGA	CACTCATTTG	ACAAGAACTG	CATTCTCTTG	AAGACCACGG	540
CGACCTGATG	TCTATTTCTAC	TGCACTACCC	TCTCGAAGC	TGCTGAGGC	CCCCAGATGA	600
TCCGCTCCGC	CCGGAGGCTT	CCTGATCTGT	GGCTGGCGGA	ACAATATGAA	GACATGCAAC	660
TCATCTCGGA	TTCACTAATT	AAGTCGACA	ACGGCGCCTG	GTTC		704

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 706 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1615UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GATCTCGTTA TTCTGGACAA CATTCGGTAT AGGGACTGCT CCTGCTTTGT GTGAGGAGAC	60
GTTGCTGAC TTAAATAAG TAAGATGAAA CGGTCAGCCT ACGGTGGGGC CCCGTTTTTC	120
AGTTTCGCAC GGAGAGGTA TCAAAGGAGG TCGAACACAG CTACGTTATT GGTTCGTATA	180
GCATGCTTTT GAAGCCCTTA GCTTCACGAG CGCTCCGACC ATCCAGCCA CCGGCCCCCT	240
ACGCCCAAGG CCAGCTCCCG CAATACGCCA GCGCGTGGG CCCCCTTTTCG TAAGTATATA	300
TGGCGTGGCC GCGCCCGCGG GCGAGGTGG CCGGTGAC AATGGCTTCT GACTTGACA	360
AGCTCCCGGA GCGGTTCAGT CGCTGCAGA GCTCAGCCA TAGACAGCTG CTCGTCCTGG	420
CGCAGGGGCT GTGCATCCCT GCGCTGTCCC CGTCCCTGCA CAAGGGCCAG AGTGGACGGG	480
TGTGCGTCTG TGGGGGGTGG CTGGAGTACA CCGCGCGGCC GTACTTCAGC GCGCATGCGG	540
CGCGGCTCAT GGGCTCGGAC CTGGTGCAAG TGCTGTGCGA GTGGAACGCT GCAAGCGCGA	600
TCAAGGCTTA CTGCGCGGAC CTGATGGTGC ACCCGCACCT GCGCGACAGT AGCTCCCTGG	660
CGCGCGGGCT GGAGCCCGCC ACAGAAGCCG TCGCGCGGCT CGTGGG	706

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 687 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1616RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GATCTGCTTC AAGAGCTOCT TCTGGTAGGA CGAGCCCAGG ATGAAAATCT TGGAGACGGT	60
GACAGGGTCC AGGAACGGCT TGAACAGGCG GAATCGGGCG GAGAAGCCGA ATGGGGGGTT	120
GATCATGTAG AACTTGCCCA TGGCTCGGG GTAGTAGTTC TGGCCGATGT TCGAGGCTC	180
GCGCACGTAG CTGAGCACT GCGCGCTGC GGAGATGGAG ATGCCCTTGA GGTCTAGGAT	240
GGTGCAGGAC GTCTGACGA GGCAGTGGC CTGTCTGGAG CTGGCCGGCA AGGGTACCG	300
CGAGAAGGAC TGGTACTCCC ATATCAAGTT CTTCAGCATG CGCTCTGGG TCGTATCTT	360
GTACATCTCC GTCAGGTCA CCGCGCCAG CTCTCGATG TACACGGCC TCCGTCCTT	420
GTCGTCTTG TGGTAGTACT GCGGGTAGAA CTGGCCACC AACGGCTTTT CCTCGTAGTG	480
GAAGTCTCG AAGATCGTGT CCACCGCGTT TTCTTACGC CACTTCTGC AGTTCTCAA	540
CATTGCCCGC GCAGCGCCC ACGTTCGAAC TTGGCGGCC GCAGAAACCG CAAAAGCGTC	600
GAGTGTCCA GACGCTTGGT GAATCCGGCC TGCTTCAGCA CCTTGGCAG CTCTCCAGC	660
GCGGCTCG TGCTCGCTC CGTCAGG	687

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1616UP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

10 GATCACCTTT TGGCAGGAAC GCCACAGAAA ATCCATTACG CGATTCTGCC CGTTCATTTC 60  
 TGTACGAATG GGGAAATGAC TCGTGGCCAT GGCACAGGTG ACTATCGCAT TTGGTTTGGG 120  
 15 GGGCGTGATG CCCAGATTTT CTTCAGAAA GCGGCCACCC TGCGGGATAG GGCCTTACCT 180  
 CACATGAGGC GCAAAGCGAC AATAATCGCA GAGCTGCTTC TTACTTCATT CTCTACCOCA 240  
 20 CTACGTAAT CGATGGGACA GGCACAGTCC TACGGTAATC CTCTGAGATA CCAGATTGGG 300  
 TTGCATAATG ATCTGGCCTA CAGGGCGGTG TTTGTTGGAG CCCATATCTC ATGCAAGATC 360  
 25 GCGATGCCCC TGACGATCCA CCTTCACCAT TTACTCGTTT CTTTTTCATG TTTTCAAAAA 420  
 GAAACGAAAA GGTGAGATAA AAAGCAAACA TTACTACCGA CATTTAAAT AGGTGATGTC 480  
 30 CAGGACTGTA CCTCATTTGTG GCGCTAACA GCACCAGCAA TGCTGTGTG ACCCCTTGTG 540  
 CTGTTTGACT TTTCAACAGA CAATCGAAC AACTGCCCC GGAATACGA CCTTGCAGTG 600  
 35 GCGCAATCT GTGTGCTGGG CCACGGGGC AGTGGCAAGT CATCACTGCT TGCTCGATG 660  
 GCTACACGGA CTGGAGAGTG GCGTG 685  
 40

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: PAG1617RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

5	GATCTTGACA CCAATGACT TCCGAAAGC CTGAGTCAAG GCCTGGTCT TGGATAGCTC	60
	CAACGAGAAT ATCTCTGACC CTGCCATGC TGTGAAGGC ACATCTGCGC CCAGTGACTG	120
10	CGACAAGCCC ATGCCAGCG CGTTTTCGC GGTGACGGC GGACCAGCA CCAACACGGC	180
	CGCCCCGCA ATGTACCGT TCTGCACCAT TTTGAGAATC ACGCTGCGG CCTCCGCGC	240
15	CTGTAAGTGG CCCACCAATC CCTGGAGCT CGCTTAGGC TGTAGGTTCT CGTCCAGTCC	300
	CAGGCCAACA ATGTGGAAT GTGTGCAAT TAGCGACAAG GACTTCAGAG ACATGTCATG	360
20	CGCTCTCTGT GTTGAATCG ACATATTATA GATCTTTGAA ACTTTGAAAC CGTCAAGAGA	420
	GTCCAATGGC CTTGTGCGAT GACCGTCTAA CTGTTCAAAC GGTGTGCAA CATAACCAAT	480
25	TTTGCCGGAG CCGAGGACT AAAACGCATG TTATACGAAG TCAAGAAGAA GCATCGTTTG	540
	AGCTGCTAGC AGTTCCTTGA CTCTCAACTT GGTCCGAGCG TGGGTGTGA TGCTTCGCAT	600
30	GGGAGAGTAC ATATGTGGTT GCAAGCCACT TTGGAACCTG TGGGCTAAG ATGTACGCAT	660
	CACCGTGAAT GGAAGCGGT ACTTGGTGAC TGGGCTCTC AGT	703
35		

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1617UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

5	GATCACTTGG TCGAAGAATT CATGTCATGC AGAGAAATGG GAAGCAATTT ATGCTCAGCT	60
	CCCTCCCCCT GTTCTCTTTC TACCGCCAGG CCATGCAGGC ATGTCAGGCG CTCAACACAC	120
10	CTAGTGACAA ACTCGCCGTT GTCTTGACAG CCTATGCGTT CGTAAATGTT AAGGCCATCC	180
	GATGTTGGAA GAGGTGACAG AAATTCCCCG TGTAAATTCT CAAAGAACT GTCCAAGGGC	240
15	GTATCCTTCA CAAAGTCGGG GCGCCGCTGC AGCACATCTT CCAGCTTCCT CTGTTCCCCC	300
	GAGGCGTTGC TCATGCTCGT GGCGATTGCA CTGCTCAGC TCGGCTCTG CAAGTACGTA	360
20	ATTTTAGCTA TCGAAAATTT TCCCTCTGG CGATGAGTTC ACGAAGTCTA CATACCGATT	420
	GACTAAGACA CTTGCCACCC GTTTGGCGCT CATGCCACTA CACCAAGGAC CTCGTGACAT	480
25	CGAGGATCAA CTTGCCATCA TTGCGGAGCG CGGCATAGGC GATCTTGACA GCTCAAGCA	540
	AATCTTTTCC GAGCTCATCG ATCCAAAGCT CCTGCCATCG TGCAGCGACC CAGACAGCT	600
30	CTGCACGCG CTGCACATGG CTGCCGCCAA CGGACAAGCC GACGTGGCCC GCTAACTGCT	660
	CTGCTGCTC GAGCCCCGCG CGGGACGCGA CTGGGG	696

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 360 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: single   |
|    | (D) TOPOLOGY: linear       |

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- |    |                         |
|----|-------------------------|
| 50 | (A) ORGANISM: PAG1618RP |
|----|-------------------------|

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:



EP 0 866 129 A2

GATCOGGCGT CCGGAAGAGC AGCTTATGCT GAAGGGCTAC CTAAGGGACA CAATCCCCC 60  
 CCCCCCAAA AAAAAAGCA TGAGACTCTG TATCAGTAGG AAGTCTATCG CATCTTCTTA 120  
 TTTAGCCTGT ATATGTCTT TCCGCGTGT GACAKTGCGT TGGACGAGTA TGCTCGATGC 180  
 GGAATATAAC GTACTTTTTT GAAGAGTAAT ATGGACTTTC GACCTGCAAA GTACCGTCTG 240  
 CCGTTCGGT GTCAGACACT CATCGGAACG CAATTGTGTC GCGATCAGG TATGCTTCTG 300  
 TTGTATGCTA TGGTAGCTAT AGGGTCTGGA CCGCTATCCA GAGAGATATT ATCCCATTA 360

(2) INFORMATION FOR SEQ ID NO:1008:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 637 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1619RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GATCAACAAT GTGCGCGGC TGCTCTGTT CCGCCCGGC GGTGATCTGG ATAGCTACGA 60  
 GCTCTCGG ATTCGTCGC ATACAGGCG CGCAGGGTG CCGGCGATCA TCGACACCT 120  
 CAAGATTAC ACCGGCATCG AAGACTTGA GTACCACGAA CCAGTGAAC TGGGCCAGTA 180  
 TGCCCTATC CTCATGATG CCGTCCCGT AGTAATCATG CTGCGCACT ACTGGTCGT 240  
 TGTGGTGTC ATCGCCCTT TCCGCTCT GTGGGGTTC TCCTGGTGT CGATGTCAT 300  
 CGCACTTGT AGCGGCGCA TGTTCAMCA GATTAAAGAC ACTCCCTACG TGGGCTGTC 360  
 CCGTATGTC AATTACGTC AGTACTTGC AATCAGGCAG CAACAGGTC AGTTGGGGT 420

GGAAACTCAA ATCATCTCCG TCATATATGG CACCOCTCAGC GCAGGAGTGG TACTACTTGC 480  
 5 CATTGGCACC AAAAGCATCA GAGCTTACTA CATCAAGTAC AACTATAGCA TGCACGGGGT 540  
 GGTCACCTTG TTGTTGTCCC TCGCCGCAAT ACTGCTTATC TATATCTCCT TCGCCGCOCT 600  
 10 GCTCGCAGTC TTCAAAGTGA AGAACTTTGA GTATTCA 637

## (2) INFORMATION FOR SEQ ID NO:1009:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1619UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

GATCGCTTGC TGGAGACCAC AGATTTTCTA GCGTTGTGG TAAGGGGAG ATGGGGTGA 60  
 CAACCAAGGA GGAAAAGCTC ATGAAGCTGA ATCCAACAGC TACAGATGG AACAATTACA 120  
 40 TTAATACTGA TACCACTGG AGCAAGCCG CTCACCTTC GTCAACAGAG GCTGGACAGG 180  
 CAATTGAACG AGAAAAAAA CTAGACCGGA GGCAGACTGA GAAGGACAGT GTAGAGAGCA 240  
 45 GCAAGGTTGA GCGCCCGGTA GTAGATGCAT CGTAAGTAGG GTGAAGCAA ATCGCCGGGT 300  
 GGAAGAGCG CGACCGACTC ACCGAAGATG ACCTGCACTG GGAGCTTGAC AGAGAAACCT 360  
 50 TTTAAGCA TGTGCTGCT GCTGCTGGT ATGGGACTG GTATCACTCC GTGGGATAT 420  
 TCTTCTCGG CGGATTTTGA TCGTTTGGT TGGGCTACTT CAAGTTCAGT TTATCACTG 480  
 55 TATCTTCTGT AATGGTTTGA ACGGCTTTC TATACCGTAC ATCGATTTGG AAGTACAGAG 540

GGTCGATAAG GGAAGCTGGT CAGAAGGAGC TCACAGTGCA GAAAGTAGAG GATGACTAOC 600  
 5 AGAGCATGGA CTGGCTCAAT AACTTCTTGG ATAAATTCTG GACCAGAATA GAGCCCAACA 660  
 TTTCGGTGAT GGTGTGGAT CAGGTGAACC ATGAATTGGC TAAGAACCGT CTGTGCCGGG 720

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1620RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

GATCAAACTA TTTCTTGTTT TGTTGGTGA AGCATACTTT CGTCAGTACT AACTTCTTGG 60  
 35 CTCCTCTCCA TAAATTGGTA TTCCCTATTG GGATTAAATT CCGGACCCAA GGTAACGACC 120  
 AAAACATTA GAGCAATAGA TCCCCACACA AAATAGGCCA TAACTCTACC ATAATCATAAC 180  
 40 AATTCTTTAT TGCCATTATC GAGTGGAAAA TTCTTTGCAA GGCTGCTTTC AAGCAACGAT 240  
 GAGGGGCTAG ATGCCAAGTT TCCCAATTGA TATGCCAAGC CCACGAAAAA GGTTTTCTGTG 300  
 45 TCTGAGTTTG GAGCTAAGCA GTGTAAATGA TGTTGGACAA GGCCCCATGC TCCTTGAACA 360  
 AAAAAGTGA GGAAGAACAC GGACACTATA ATACTTCTAT CATGTACAAA TCCCCACGGA 420  
 50 TAAACAAGAC AGGCAGCCAA CAAAATACAC ACGAGGATAA CAACTCTTCT AGAGCTTATG 480  
 CTGGAAAAAC GTGAAATGAA AAGTCCACCT ATTATAGCAC CAACGTTGGC TGCACAATTT 540

GTGACGGCTG ACTGATTGGG AGAATAACCA AGTTGTTTAA TGAGCATGGT TGGAAAGAGA 600  
 5 TCTTGAGACG CATGAGAAAA GTAATTATAA CCCGTCATAA GCAATATCAT GTAGATGACA 660  
 ATGT 664

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1620UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

GATCAAATAA AAATAGAAAT TAGCTTAATG GTAGAGCAAT CGTTTTACAC ACGAATAATT 60  
 35 TGAGTTCGAT TCTCAAATTT CTAAATAATA ATTAAACAATA ATTTAAATTT GGGTAAAAAT 120  
 TAATAAATAT TAACGTATAT AATAATTATA TACTTTATAA AATTACTCAA TGTTATTAT 180  
 40 AAATTTATTT CTTATCATTATAAATAATGATGT ACCTACTCCA TATAATATAT ATTTTCAAGA 240  
 TTCACTACTA CCTCATCAAG AAGGTATTTT AGAATTACAT GATAATATTA TATCTATAT 300  
 45 GTTACTTGTT TTAGGTTTAG TTTCTTGAAT AATAATTATT ATTATTAAAG ATTATAAAAA 360  
 TAATCCTATT CTTTATAAAT ATATTAAACA TGGTCAAATA ATTGAAATTA TTGAACTAT 420  
 50 TTTACCAGCT ATTATTTTAT TAATAATTGC ATTTCCATCA TTTATTTTAT TATATTTATG 480  
 TGATGAAGTT ATTTCAACCAG CTATAACTAT TAAAGTTATT GGTTTACAAT GATATTGAAA 540  
 55 ATATGAATAC TCAGATTTTA TTAATGATAA TGGTGAACT ATTGAATATG AATCTTATAT 600

AATTCCTGAA GAATTATTAG AAGAAGGGTC AATTAAGAAT GTTAGATACT GATACTAGTA 660  
 5 TTGTTATTCC TGTGATACT CATGTAAGAT TTATTGTTAC AGCTOCTAGA TGTATTTCAT 720  
 GAATTTT 727

## (2) INFORMATION FOR SEQ ID NO:1012:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1621RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

GATCCACCCA COGGTACCTC CTACTTGGCC GTATCTGGGT CTCGGTGGCG CTTCGCGCTG 60  
 AGATGCTGTG GGGCCGAAAT GTACTCTCAA ATGGGCTTGT TCAGTGGGCC ATACAGCTCA 120  
 TTAAGCTCAG TGGCCCCGAT GCTTAGTAGT AGCTGGGCGC CTCTTCATAC TGCTGTCTTG 180  
 TATTATTTCAT CTTCCTGTAT TTCTCTCTG TGTCCGCTCA CGCTGCAGG GGGGACTGCC 240  
 TGGCGCGGCG CGCTGTCTCT GCTTTCTCGT CTGCTGTGAA AATGACAAA CTCACAAAAA 300  
 TCGAATTGTG CGCGCCCGAC AGTTGATTAA GCTGGGGCAT CTCTATTCTC TATAAATTGT 360  
 TAAATTAACC ACACTGTGAA GCCCTGCAAT CGCACGCG CGCACGTCA ACTCTTGGTC 420  
 ACAACCTAGC CCGGGGAGTG CAGTCTCACA AATACAAGC CTGGGATATC ATGTACTGAG 480  
 GCCTCCTGAA CGTTTTGCGT TTTTCTTAAA ATGCTGTTC ACAGTCTTAG CGCAAAAAA 540  
 ATAATTTAAA AAAAAAATGT AAAGTCTTAG TGAAATGAAA AAATAAATA AAATAGACCG 600

CCAGCTGCAG AACACCTCTT CAAAGCATAT AACTAGCATA CGCATAAACA TATGCTTGTA 660

TACTC 665

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1621UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

GATCTCTTGG TTCTGCGATC GATGAAGAAC GCAGCGAATT GCGATAAGTA TTGIGAATTG 60

CAGATTTTGG TGAATCATCG AATCTTTGAA CGCACATTGC GTCTCTGGT ATTCCAGGGG 120

GCATGCGTGT TTGAGCGTCA TTCTCTCTC AAACCTCGG GTTTGGTAAT GAGTGATACT 180

CGGTGTAAG ACAAGGTTAA CTTGAAAATG CTGGCCATGG GCGGAAGTGG CGGGAGCTGC 240

GGTCTGAGCT AGTTTCTACA CTGGTATTA GGTTTGACC AGATGTTGA GTGGAGCTGG 300

CGCTTGAAGA ACGTACGACA AACAGGCCT TCCAGGCGAA TAGTATTCCC AAAGTTTGAC 360

CTCAAATCAG GTAGGATTAC CGCTGAACT TAAGCATATC AATAAGCGGA GGAAAAGAAA 420

CCAACGGGA TTGCTTAGT AACGGCGAGT GAAGCGGCAA AAGCTCAAAT TTGAAATCTG 480

GCGCTTCGG CGTCCGAGTT GTAATTTGAA GAAAGTACCT TGGTTGCTAG TCCCTGTCTA 540

TGTTCTTGG AACAGGACGT CATAGAGGGT GAGAATCCCG TCTGGCGGGG GTGCTAGTGC 600

CATCTAAGGT TCTTTGACG AGTCGAGTGG TTTGGGAATG CAGCTCTAAG TGGGTGTTAA 660

ATTCCA

666

5 (2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: PAG1622RP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

GATCGTGTA TTTTATTTT ACATTATTTA ATTAAAAATA ATGATTTTAA TAAATATTTT	60
TTATAAAAAA TAATTAGTGC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAAACC	120
ATCAACTAAT TGTATATAT TTATTAAATA TTAATTTTAC TTAATTGAAG ATTAGGAAC	180
TTATCTATTA GTCTGGGCTG TTTCCTTTT GATTATTAAC CTTATCGCTA ATAATCTGAA	240
ATATTTAATT TTAGATTAAT AATATATCTT GAGATTTAAT ATTTTAAATA AAATAAATAA	300
TTATTCCTTA AATAATATTA ATAACTATAC CATATATATC TAATATTTAA ATAATCATAC	360
TAACATATGT TTCTAGAAA ACCAGCTATT TGCAAATCAG ATTGACTTTT CTCTACTTAC	420
CATTATTCAT CAGATAATAT TGCTACATTA ACCTGTTCAA TCGTTTTTAT ATTTTATTAT	480
ATTTTAAATA TAATAAATAT ATATTTTAAT CATTTGATAA TAGTAAGATC ATCTGCTTTC	540
GGGTTAATTA ATATTAACTA AATTTAATTT ATTTTAATTA ATTTTAACAT TGTAAATAT	600
TTATATTATT TTTAATATCA TTTTATTTT TAATATTATG CTAATATTAA TTAATTGCTG	660
ACCATTTATA CAAAAG	676

## (2) INFORMATION FOR SEQ ID NO:1015:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1622UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

GATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTGGGTAA	60
CAATAAAATT CAATAATTTA TTAAATAAT GATTAAATA TCICAATATA AAATTATTAA	120
TATAATGAGA TATATATTTT TAAAAGAAT ATATAATTAA ATAATCCCAA CCAAATTG	180
TGCCAGCAGC TGGCGTAAGA CAAAGGGGGT TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240
GTAGAATGAT TATTTAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300
GTAAAGATGA AATAATAATT ATATGAATA GACTTATAAA GTGAAAATTT AAATTATATA	360
TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTCGATAC CCGAGTAGTT	420
TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA	480
AATTAAAGTA TTCCGCCTGA TGACTACGTT AGCAATAATA AAAATCAAAA CAATAGACGG	540
TTACAGACTT AAGCAGTGGC ACATGTTATT TAATTGATA ATCTCGATA AATCTTACCA	600
TTTTTTGAAT ATTTAATTAT AATAATTAT AATTAATTAC AGCGTTACA TAGTTGTCTT	660
CAGTTCGTGC TGCAAAGTTT TAGAATTAT CATAAACGAA CATAACTCTA AATATTTT	718

## (2) INFORMATION FOR SEQ ID NO:1016:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1623RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

GATCACAATC GCATGGTATG ATCGTTTTAG AATCAAGAA ATATGACAAA ATGAAGGAAC 60  
ATATTGCCAT AAGGACTTCA GGTATTACAG TOGCAGATAT TCTATCGAAG TCCACTGAGT 120  
ATGGTTTAGT ACCTATACCA AAAGAACAAT TTGAACAGAT TAAATGGAA TTAGAGCATC 180  
CAAAGTTTAC TAGAGAGATG ATGTGTGACC ACGCTGGTGA CTTCGACTTA ATTGCAGTGG 240  
AATTAAAGGA ATACAATGCG CTCAAAAGC AATGCGAGTT CTCCTTTGGT GACATTTTCG 300  
ATAGCATTAA CACTGACGAG GAAAGTGAAG CATCTGATTT TGAATATCAT GATGAAGAGA 360  
TAAAGCAGCT TAACAAGACA GCCAAACGCT TTGGGTTAAT ATGTATTCCA GAAGCTGGGT 420  
TTATCGCTAC TTCCGTGCT AGCAAGGCTG ATGTGATAA TGTCGTGTG CTACCAATAA 480  
GCTACTATAA TAAGTTGATT GCGAATGAAG CAAAGAGCCT CGAAAAGCTG ACTGACTGGG 540  
ATCTTCAGTC AGAAGCTAAA AAACGTGGCT ATCATATAAA TTTCAGCTTC CAGAAGGAGG 600  
ACGCCCCACC GCGCCTTCA ACCCTATGTC CTCACGGAT GCGAAGTTT TCCCCAAAC 660  
CGTTGCACTT TGTCAGTAGA CTCAAAACCT ACTAGAAGGG CGTTTAATGA GGCTGCTACT 720  
GTGCGCGCAC AGAGCGAATT TGAACAG 747

## (2) INFORMATION FOR SEQ ID NO:1017:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 758 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1623UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

GATCAGCGCA AAACACATCT GTATTCCAG CAGCATGTC TCCTCCACT GCGCATGGC 60  
CTGGCTTGCA AAGCCGTCCA CCTCGCGTC AAATGAAATG CTGTCCGAA TATTCTOCAG 120  
TTTCGCAACC ACAGGGTTC CGTCTGTC GTACTCTGT TCCTCATCT CCTCACTGC 180  
CTCGTCTCG CCGCGCAGT CCACGGGCT AATGCTCAG TCGGAGGCT CCTGGGATA 240  
CCGCTCCGC AGCGTAATGT CCACCACAA GTGCTGCTC TTGCTGATG CAGCCGCGT 300  
GAATGAAGAG CTTGCCAGCG GGATCAGATC CAGTTTAGG TCCACTTCAA ACTGGATTTT 360  
CGGGTACTCC CCGCACCA CCGTCAAGT ATCGGCATAG ATGGACTCAA GCACTTCCAG 420  
CTCTGCTTT TGCTCTCT GATAGTCCAT ACCTATCCG TCGACCACT ATGAGGCCAC 480  
GCGCAGCTTA GGGCTAGACC GTTACAGCT CAGGTGACG TCCGGGGAC GATGCGCTAT 540  
CGCTGGCGAA ATTTTTCGCC TATACCACCA CTATGTTAC CCGTCTATA GTGCTGCTCT 600  
CCGACTCAC TGATGGTCT GTCCCGCGG GACTGCTCC TGTGCGGC AAATCCCCAC 660  
CGTCTGAAC GCTCGTTCCA TCTGCTCAC GGGTTGACG AACGGGAATT GCGCGCGCG 720  
AGAAATCTTG GCGAACCATG CTGCACTTAG CCTTACTG 758

## (2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1624RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

GATGCGACGT CATTTTACCT ACAGGCTGGG CTTTGAAGA AGACGCTGC ATGGTACAAT	60
GTCGTAGCCA GGATCCCAAC TGTGACCAAG TTOGCCAGAG AACCGAAGCT GCATGACCCA	120
GTTAGCGGCA AGTACAAGGG CGAGCTGGAT ATAATGACGG ATAGATTAAA CAGAAACACA	180
GAGACGTACA AGACACGGGC TGGGAGTTTC GACCGGCAGA CGGCGCGGT GCACAAGCCT	240
TCTAAGCTGC GGTTTATCGA GGACAAGCTG CGGTGCTGT TTTTCAGCA GCATCCTGG	300
GAGCTGTGCG GGCGAAGGT GCTGGTGGAG AACATGGGAA ATGAGCAGTA CCACTGGTGG	360
CGGATGTTGC AGCTAGGCAA GCGCTTGAC GGTGAGTCTG TGGTGCAGCG GACGCTGTAT	420
CTGCTGAAGT CCGGCGGCGA CCGGAGATG CTGGCGGCAT ACGACCAGGC GCGTTTGAG	480
TTCTATCGTC TGAGGATGCA GCAGGAGCTG GAGGAGCAAA TAGCGTACGA GGAGGOCAG	540
ATGGTTGGCG CTGTGTTCAA GACAACCGCT GTGGAGCAGG GTCTGCAGCA AGAGCAGAAG	600
GTCTCGACA AGTGAAGGA GGACGTGGTT GCGGGGTGCG AGCTGATGTC TCGAAGAAG	660
AACTCTACAA AGCAGTCGTG GCGCGAAGCC	690

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1624UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

GATCATATAT CTTCCTGTGG TAAGGTCTGT GGAAGCAGC TCTCTGCGG GAATCACACT	60
TGTCCCATGA CCTGCCAAGA TGGTAACTGC ATGGATCCAT GCTCTGTAT AACTGAGCAG	120
AAGTGTGCAT GGAACAGAG GGGTTCTCTT GTTCTTGGC AGTTCCCCA TTCCCCAAGT	180
TGCACTGCAA AATGTGAATC ATTGATGTCT TGTCTGCGC ATCGGTGGC TGAAAGATGC	240
TGTTCCGGTA GACCCGATTC TGTCAAGCG AACTCTAGC GCGCGGTGA GAGTCCAGAT	300
GATGAATCTG AAGTTGAGGC CCAGCAAGTG TGCTTAAAG ATTGTAATCG GGTCTCTCTT	360
TGTGGTATCC ACATGTGCAA TTACAAATGC CATGCAGCA AATGTCTCTC CTGCTTAGAA	420
TCAGATTCCA ATGACCTTAT CTGTCCCTGT GGTAAACAA TGTACCAGC CCTGTCTCTT	480
TGTGGAACAA AGCTCCCTCG CTGCACTCAT CCATGTGAA ACTGCTCTT GGATACTTGG	540
CCTGCGGAC ACAGTCCACC TTGCATAAT TGTATCCCT TAGATGAAC TTGCCCCCA	600
TGTACCATCA CAGTCAAGAA AACTTGTGCG TGGGTAAAA ACGAGATCAG GACATTCTGC	660
TACAATGATG ATGTGTCTGT TTGAGACCG TGTAGAAGC CATTGTCTTA TTGCAATCAC	720
TTCTGCCAAG TTCCCTGTCA TT	742

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 725 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1625RP

(>i) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

GATCAACTAC GAGGACTTGA CGACCGCAAG ACGGGAGCTC GCGGCGGCGC TGGCCACTTT	60
GGAGAATATG TAGCGCACAA CATCAGCAAT GTTACAGTAC AGAGTCTAT CCGTGGGGTA	120
CGGCTATGAT GAATAGAAAT ATATACACAG CTGCTGCAG GCAGCTTAGA AGCGCAGAGG	180
CTTGGGCTTC TCCACGAGT ACTCTGGTT AGTGAAGTGC CCGTAGAGG CCGTAGGTAG	240
GTAGATGGGC TTGGCGAGGT CGAGCTCTTT GACAAGAACA CCTGGTCTGA GGTGCAAGTT	300
GTTCGGGATG ATCTCGATCA GCTGTCGTC GGACTTGGTG CTGGTACCGT AAGTCTGAC	360
GTGGATGGAC AGCGGCTCGG CAATACCAAT GCGGTAGGCA AACTCAACCT GCACACGCTT	420
GCACAGGCGG GCGGCCAACA GCGACTTGGC GACCCAGCGC GCAGCGTAGG CAGCGGAACG	480
GTCGACCTTC GAATAGTCTT TTCCGGAGAA CGCAACGCCA CCGACCGCGG CCGCACCGCC	540
GTACGGGTCA ACAATGATCT TTCTACCGGT CAGACCTGCG TCACCTTGTG GGCACCGATC	600
ACGAAGCGGC CGAAGGCTGC AAGTAATACT TGGTGTTTTC GTCTAGCATG TCGGCAGGGA	660
TGACCTTGCC TACGATGCGA TCGCGCAACG CGGAACGCAG GTCTGGGTC GAGATGTGCT	720
CCGCG	725

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1025UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

GATCTGGCTC TGGGCATCC CAAACAACCT GGGTGTGAC AAGAAGTACT ATGATGAGCA	60
CAAGAAGGAA TGGGCATGT ACCAGGAGAT GATGAAGCAC TATGCCAAG AGGACCTTGT	120
CGACACCAAC ATGCAGGGCG GGTTTATCGT CGGCGCGCCA CTCCACGAAA TAGAGCTGGA	180
CAACTTCAG CTGGCGTCT ACAAGGAGCT CGTAACTAGC ATGTTCCCT GACTTCATGG	240
AGTCAGCAT CGCCATGTT TTATGCCAA TACTTTTGAG ACTATACTTA TATTATATAC	300
TGATAACAA TTTCGCGCGC TCTCTACGC CCACTACTTG TTCTCGCGT AGAAGAAGTT	360
CACGGCATC AACTCGAGGT TCTTCTGCC CGCAAACTG CCACACCCA CAGGGGGCG	420
CTTCTCGTG TAGCCCACT TCAAGGACT CTGCAGGGG GTGAAGTCT CCTGCTCAG	480
TTCTAGCGC CCGGGCTGC GAAACAACAA CCACACGTAC CGTGAGGCC CTGTGCGGC	540
CGGCGCGCA GGGCCATGT GCTCACCTG CCGGGTGCC TTAGCACCA CGTGGACAC	600
CCCGTCATC GAGCCAGCG TTATGTCGT TTCCAGAAAG TGGCAGTATT CCGACCACTT	660
GTGGTCGAC CGGAGGGAG CATCTGGTC TGTCATCCC AGCGTGAATA GGTCCCTCC	720
CTGACG	726

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1626RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GATCGTGGG GACCATGGGC AGATGGGGCC CTTAATATAA GCCCCTCCTC GCAGGCATGA	60
CGTCTGCCAA CTCGACCAT TCTAAATGGC CAGCTGCTGC TTGATGGTA GGTCCGGCG	120
CTGGCGCAGA AGTAAATATA GCATTAAATT CCCCTTCTAA ATATACATTA CATACCAGCG	180
CTCAGAGGC GCTCCCGAGG CGCTCCGAG GGGCCCCAGG TCTCGCGCA GCGAGCGCG	240
TGCGAGCTGG CCTCTGGCC ACGCAGACAT GGGCGCGAC GGGCCCGT TATATACAGC	300
CTGGCCTGTC TCATATGCAG ATGGGTCTGA GCGAAAGAAG TTCCTGCTC TCGAGAAGC	360
AGTGTGTG ACCCTGGGC TCGCGGCCA ACGCGCAGC AGAGAATCTT CCAGCGCTTC	420
CCGCGACCC GCACTGGGG TACCCGTGCA GGTAAGGATA CTTGCGGCG GCGCGGCAC	480
CACCGCCCTC AGCCTGACTT GCGCAACGC CATACGCAGA GGACCCGCT GCTTCGGCG	540
TTTGTGCCT GTGCACTGA TCTACCGCC TGCTCAGCC GGCCTGTCA ACGATGGCA	600
CCAGACCCCT CAGAGGTGC CTTGTGCC AAGTCGAGC CCA	643

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1626UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

GATCCATGCA TATTTCGGAA CTTACGAAAA AAGGCGTGAA GAGGCGGAAC GTAATCTAGG	60
TTTGAAGAA TTAATGAATG ACAACATAGA CCTTGTACA GGAGAAAATA ATGAAGAAG	120
CCAGCTGAAA CAAAAGAAGT TGTTAGAGGA GCAGTTGGCA AAGTTGGAGA AATCAAAGGA	180
AAGACGACAA GCACGCAAGG CCGCGAAGGA GAAGAGCAA GATGGCAAAG TCGTGAAAGT	240
AAAAAACACC ACCGACGCT GCGCAACATG CCGTGGATC GGGCATATCA GAACTAATAA	300
ATCCTGCCCC ATGTACAATG GTGGCGTTGC AGCAAACGCA AACGCAAACG CGAATGGGTC	360
GAGTGCAGCA GCTGCAGGTT CTTCAGGGAT GGCTCAAAT AATAGCGCTA CCAGCAAGTC	420
TATACTCCT AATGCCAGTA TTCCGCCGAC TTCATTGAC TAGCTGGCAG TATAATATAT	480
ATCTAATATG TACCAATTGT ACTTCTTTG ACTGCTATAG AACTTTCTCC TCTTCTTGCA	540
TCACATGTGC AGCACTGCAG CACCGTGGC CTGCAATAC TTATGGACCG CGGCAAGGTC	600
GGCTCGTAT CCAGCGTACG CTATGTATCC TGCGGGACCC TTATTGGTGC GCGACAGGG	660
ATAGTGACA GACTCCACAG AAGTGTCTC TACAATGCAG AAGA	704

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1627RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

5			
10	GATCTTCCTT GAATTTACTT AGCAGCTCGT TAATTTCTCTG CTCTTCTGC TCTCTAAGCT	60	
	GGAATCTGTA AAAGTCTGTC TTGGCCTTCT TGTCACCAT GCTGGGAGGC TTCTCTTCC	120	
15	GTGTATGCTT AAGAAGTGA TTGGCGTTCA GAATCTACG CCTTATGGAG TTTAACGATT	180	
	TTGTGTCTT COCTACTACA AGTGTGAACC CGTCTCGTC CACAATACTC GATTGAACCT	240	
20	CATCTGCGC AAGTTGTTC CGTGTCTCA ATAACAACAT ATGCTGTGA ATGTGCTGC	300	
	GCAAGTACTC AAGGTGAGT GGCTTATAGA AGCTCTGGA GGTCGTATC GAAGGAGCT	360	
25	GGAACGCCA CTCCACCAAT TCCTTTTGT TTGTGGGTA TTGGGCAGA GCAGCCAGC	420	
	AGTTCTCCAG AGATGCTGG TCACAACT TCAACAGAGC ACTGTTCTC GTGTATACC	480	
30	TTCTGTCTC GCATCCCG GTGTCTGA AATCGAGCT CAGGCAACC AAATCACTT	540	
	CGTGCAATCC GAACTGTG TGATGTAGCA GCTCTGCCAC ATGCGCCACA GTCTGTACT	600	
35	GCGCGCAAT CCTGCCAAG CTCTCTTGA TAGAGTGGC CTGTGTCAAC AGAGGTAAAT	660	
	TGACAATAAA CAGGCAATTA GCTCCGATT CCACCTTCGT CTGATGCTC CTC	713	
40			

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1627UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

5 GATCTTTGAG ACGCGGCTG GAGAGTTTAG AGCAGATTGT TGACCAACGC ATAGCAGATG 60  
 CTAGACCTGA GTCATACACC CTCGTCCTTG TTGGAGACAC GGAATTGCTA AATTCAAAAA 120  
 10 TAAAGGAGGA GGCAGATGAA GTGATTGAGG CTATAACGCC AGCTGAACTA CAATGGGAAG 180  
 TTGGGACTT GCTGTATTTC CTCATGGTTA AAATGAGGAG CAATAATGTG ACTTTAAAGG 240  
 15 AGGTGGAAGC CAACCTAAAC ATGAAGCACA TGAAGATTAC GAGACGGCCT GGAAACGCGA 300  
 AACCAAAGTA CCTACCCGCG CAGGAGTGGC AGAAGAACA GGAACTCCT GTAGATATTG 360  
 20 CACCATCTGC CATTACTTG AACGTGTAT CTCAGATGA TGAGGCGCA TTGAAACAG 420  
 CAATTACAAG GCCAATTCAG AAACTACTG ATATATTAGG TCTTGTGAG CCTATAATAA 480  
 25 AAAAGTGAT AGAGGAGGCG GACAATGGT TGACTGAAT AACAGCGAGG TTTGATGGAG 540  
 TAAAGATAGA AACACCAGTA CTAGAGGCTC CTTTGGCGA CGAGTATTTA AAAGGATTAA 600  
 CGGAAGACGT CCGTACGGCC ATAGATATTT CGATGGAGAA TGTCGGTAAA TTTCAATGCG 660  
 30 CACAGCTGAG AGACGATATT CTCAGGTG AAACGCAACC GGGGGTGGTA TGTAAGAGAT 720  
 35 CCCGAGGCCA TAGAGA 736

## (2) INFORMATION FOR SEQ ID NO:1026:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1628RP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

5	GATCTGCCCC TTTAAGCAAC CACATATTAA GCGCTGACA CACAGACTGT CAGCGCTTAG	60
	AAATACTTCG GTGAGTGTC AGAAGCCCGA GCGCTGGAG TTATTCATGA TCACGTGATG	120
10	GGTATTGACC TTGCGATCCA CAGACAGGCG GAAATATGCA TATATGTAAG CCAAGATGCC	180
	GGCAACCAAT TGGTCTAACT GTAATGCATA ACACTGTATT CCGCGAAGCG GCTCTGAGCA	240
15	TGTATGGTAT TCGGCGCTAG ATTGTCAGCC CACGTATATT TCCAGGTGAC GCGCTGATGC	300
	TATTTACAAC ATAATCACTA TTGACGAGCA AGGATAGTGG TCGCACGTTA CGAAAAAGAA	360
20	ACGTTGAAAA ATTGGATGG TGGTGATGAG GTAGAGATAT TAACGTTAAT GGGGAGCAC	420
	GAATTTGGTC GAAGTTCTAT ACTGCCAAGC ACGTTCCGAG ATTGCTGAGT TGATGGGTTC	480
25	CAAAGTATT AAAAAGGCGG TAGTCCCTAA ATTATCGGAA AAAGCCAAGG AGGAAGAGTT	540
	GAGCACTTCG GGCTCCTCTG ATTCTACTTT AGAATCAAGT TCATCTTCCT CGTCGGAGGG	600
30	CAGCTCCAGC AGCAGCTCTA GTTCTCCCGG ACAGTGAATC GAGCTCGTGG GACAGCGGCT	660
	CCAGCTCTTC TAGCAGCAGC TCGAGCTCCT CCGGCGAATC GGGCTCC	707

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1629RP

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

5	GATCTCCAC ACTAGGCTGG GTCTTACTGT CCATGAATAG CATTGAAGA ATGGAGGAAT	60
	CGGTCTTCAA GTCAGCGGG AAATTTTCAG GGCAATATAA TGGTTCCTAA GTATTAGAA	120
10	CTTCTCGACT GTCGTCAGTA CTGGGCOOCT TTAAATCGGC TGTTCOOCTT GAAGATATAC	180
	ACCATTCATT CCAGTGTATC GTACCCGAAA AATTAGCAGT AATGGCACTT GGAACATCAT	240
15	COGGAATCGT GTAAGCACTT GCAATAACTG AAAGCTTTGT AAGAGAGGTA AAAATCGGTG	300
	CGCGCGTTCC AAAATTGTCC AATTGTGAGA TTGTGTGATC TTCATTAGGC CTACTGGCCA	360
20	GTTCCTACTAG TGATCTAAG GGGCTTATTT CAGTGGTTAG AAATTTATCC TTCTCAGTTT	420
	TGACTTACA AGCAAACTCA GTGAACAAAG GGGGTATCG ACGAGCAGCT CTGTGTGAAG	480
25	CTGCTGAGGT TTTCOOCTGT GAAATAACAT GTTCTTTAGT TTCATGTAGG GCTCCAATCC	540
	ATGCCGTTAA CTCITTATAA CTGGTTGCTT GGAAAATTAA AGTACCAGAG TTATTAGAAT	600
30	ATTCTTCTTG AGGTGAAGAA GTTAATGGAG AAGAGATAGT CATTGGAAG CAGTATTTAC	660
	GTGCOCTCTC TGGATGGTGC ATGGCACTGA GTAATAATAC TCCAAATCTG TCCGTTTCTT	720
35	CGACTGCACT TTT	733

(2) INFORMATION FOR SEQ ID NO:1028:

- |    |                                   |
|----|-----------------------------------|
| 40 | (i) SEQUENCE CHARACTERISTICS:     |
|    | (A) LENGTH: 742 base pairs        |
|    | (B) TYPE: nucleic acid            |
| 45 | (C) STRANDEDNESS: single          |
|    | (D) TOPOLOGY: linear              |
| 50 | (ii) MOLECULE TYPE: DNA (genomic) |
|    | (vi) ORIGINAL SOURCE:             |
|    | (A) ORGANISM: PAG1629UP           |

# EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

5	GATCTGGGCT CGCTGCTGGC GCTCGAGCCC TACTGGGCAG AGCGCTACCC AATAAACAAC	60
	GCCCTAATCG GCGGTGCAGA TAAATTGCAC AAGCTCTACT CAACCGATT TTGGCCCATC	120
10	GTCGCCGCCA GGACTTTTGG CTTGAACCTC GTGACAAGC TTGGACCGCT GAAAGACCTC	180
	ATAATGGCAA AGGTCAGCGG CCCAAATTAA TAGTCACGTG TACATAAAGG TTTTCTTAAT	240
15	AGCTATACAG CTTGCCCGCG TCCTCAGCTT GCAGCGGCA ACCGGCGTGC AGCCATGAGC	300
	GTCTACTTGG AAACCTACCAT TGGCGACCTT GTAGTAGACC TGACTACAA GACATGCAGC	360
20	GCCGAGAGCT ACAACTTCCT CAAACTCTGC AAAACTCGCT TCTACGACTG TCAGTGCATC	420
	TACGACCTCC ATCCTGAAGG CTCAGCAGGC CTGGCGATC CACAGGTGGG CTTTGCATTG	480
25	CGCAGCGATT TGCTGTACA CAATACCTCG ATCGAAGGCC TGCGCGACAC ACCGGCGGTC	540
	ACCCCGAAGC TCATTGAAGC CTCGGTTGCC GCTCAACCG CAGAGCGCTT CGGACAGGTC	600
30	GCCTTTGTGC TCAAGCCCGG CACTCGCCTG CTGGGATCCA ACATACTGCT CGCGCTTAAT	660
	CCCGAACTCG GCGCCACATC AACACAGTGC GCTTGGGCA GGTATCGAC GAGTGGCTGG	720
35	CAGTTCTGCA GCAGCTCAGC GA	742

(2) INFORMATION FOR SEQ ID NO:1029:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 692 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)
50	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1630RP

55

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

5	GATCGACTTT CAAACATTAT TATACAGATG GAGGGCATCT CACATCTTGC ACAGCAAGAC	60
	GGCAATCCAA CAGGTTCTGT AATGCAGCCT AAGAGGCGAA GGGTTGAAGA TGGAGCGTCT	120
10	AGTGATGGAG AAGTACGAGG AGAGATAAAG CGCAAGTATG GTATTGGGCG GCAGTTGATG	180
	GCCAAGATGG GATATAAGGA GGCAGCGGT CTAGGGAAG AAGGTACGGG ACGCACGACG	240
15	COGATATTGG TATAGCAGCG GCCGCAGGGC ATGGGGCTTG GAGCCAAGT CTCCATTTCC	300
	TCTGACTCAG AGCAGAGTGA GGTGGAGCTT GTGACTCGCG AGGCAGTGAA GTTTGAATCG	360
20	AAAGGTGTGG AGACTGACAC AAGCAGAATA GCAGACAAGA TAGCAAAGCT GGAGATCGCA	420
	GGAGTGCAAG TCCCGCAGA AGTGATGAGT TTGGGTTCTG GGACAAAGAC GCTGGGTTAC	480
25	CAACGGGCTG CAGCGATGGA AAGGGTGCTC TCGGAAGTGC TGCAGGTGGG TGAGCAACTT	540
	GCGACCTTAC AACTACGCGA AGATCAGCTG CAGCAAGGGC TAGATGCGGC CATTGAGAGT	600
30	AGTGACCTGT TGAACAAGTT CTCAACGGCG TGCAACAGCC GACTGGGCTG CCGGAGCGGG	660
	TAGCGGCATA TTGGGCTTGG AGGACCCAGA AA	692

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 712 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1630UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

EP 0 866 129 A2

GATCGTCGCC TCATCGGTGA GCTGCGCCCC ACCGGCGAAC CTGGCAGCCT GCGCGGCGAC 60

5 CCGCGCGGGG TGGGCGACCC GGTCCAGTC GCGAGCCCC GTGGTCCCG GACCATGGTT 120

ACCGTATCGT CCGCGACAAA TGGCGAGGGG TAGATGATGC CCTCCTCCG CTCGCGCGTA 180

10 CCGCGCGGCT CCGCGTGTG CGCTCCTCT GTCCGGCCTG GCGCGTCC GTCCCGAGAC 240

AAACGGTGCC CCGCGGCAC CCAACGCG AGGCTTCCG CCGCGGTGG CCGCGCGGC 300

15 CGCTCCGG CTCCGCCAAG GCGTTGCC TGACCCAGTC CTGTAGGTG CTCGTGGTCA 360

TCGAAGGGG TCCAAGCAAT TGTGTACGA TGATCTATGC CAGCCGAGC CTTCGTCACC 420

20 AGCGCGGCA GCTGCGGCAG CTGGGTTTG GTCTGTCCA TATCGTGGT TOGGTCTCTG 480

TAGGCATCAT ACATCTCCG CTATCTTCT CTTCGGCCTG CACCGGTACC GTGCATTGGA 540

25 AACCTGCTC CTGCGCGAG GCGTTCTAT AACGTTGCA GTGAAATCG TGCAGTACG 600

AACAGTAGCT CATCGGCAC CAGGCGACA CATAGGCAAC AGCTTCGGT TAGCGGGCTG 660

30 CCGCGCGAC CACGATCTC ATGTTACATA GACTCACATG ATCAGGCAGC AC 712

(2) INFORMATION FOR SEQ ID NO:1031:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1631RP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

55 GATCTAATTT ATTACATTA ATTAATAATT AATAATATTT AATAATATTC AATAATTTAT 60

EP 0 866 129 A2

	ATATTTTATT ATATTTAATA ATTATATAAA TACTTTAATT ACATAAATAC TTTAATTAGA	120
5	GAGTTAGGGT TCACCCCCCT AATGCTTATC AGCATTATGA GGTACCACTC TAATTAAAGG	180
	TAAATATATA TATTTAATAA TAAAAGGATA TAGTTTAATT GGTAAACTA TTGACTTCAA	240
10	ATCAATCATT AAGAGTTCAA ATCTTTTAT CCTTGTATA TTTAATAAT ATAAATTAAT	300
	AAATAATAAA TATGATAAAT CATAATATTA AAGATATTGA TTAATATTTT TAATTAATTA	360
15	AATAATATGC AATTAGTATT AGCAGCTAAA TATATTGGTG CAGGTATTTC AACAAATGGT	420
	TTATTAGGAG CAGGTATTGG TATTGCTATT GTATTTGCAG CTTTAATTCA AGGTGTATCA	480
20	AGAAATCCAT CAATGAAAGA TACTTTATT CAAATTGCTA TTTTAGGTTT GCTATTAGTG	540
	AAGCTACAGG TTTATTCTGT TTAATGATTT CTTTCTTATT ATTATATGGT GTTTAATTTT	600
25	ATTAAATTAT ATAATAATTA ATATTCAAAA TAAGTTATAT TAGCTTAATT GGTAGAGCAT	660
	CCGTTTGTGA ATCGAAAAGG TTAGGAGTTC AAATCTCTTA TGTAACAATT TAATTAAATT	720
30	AAATAAAGA	729

(2) INFORMATION FOR SEQ ID NO:1032:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 716 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1631UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

55	GATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT	60
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ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCTTA AAGTATTAGG TGAAGAAGAT 120

5 ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA 180

TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA 240

10 TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA 300

TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT 360

15 CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA 420

GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA 480

20 GTTAAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TTTATAAGAA 540

CCATAATATA AACCTTTACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA 600

25 TTAAGATGCA TATATCTAAT TAATCAACCT AGTTGTACAT CTCTCATAAT ATGTTCTACT 660

GATGAGAAAG CTAATTCAAT ATTAGATGAA TAATGCATAG CTAAAAAAT ACCAGT 716

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1632RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

GATCTTCGGC CGGTTGGGCG CCAAAACCCG CAGCTCCCAT ATACCCGTGT TCAGGTTGAA 60

55 GCTGATGCTA GCGTGCTGCC GCGACACCAC TTTCGCAGGC CCCAGGTCGA TGTGTACTGA 120

COGGTCTGTC GGAGACGTGT TCCGCCCGAT ACTCGTCATC ATGTCCCTTCA CGTAGTACGT 180  
5 CCAGTCTCGT CCGGATATCT TGGCGTACGC CTGTACTTCC GTTGGCGTGT TCTTGTGCTT 240  
CGAATATACT TGCGACACTG TCGTGGCTC CTTCGGGCA TCCAGCACCG AAATCACCGC 300  
10 ATTGATCAG TCTGTCTCC GTTAGTACTC GGTCTCGTGC CGCCCGTCTC GCTCCTACAT 360  
ACCTGCTGGT GCTGCTGAGA CGCAAATGGG TAATTCATCT CGTGGCTCA ATTTGCTCC 420  
15 TCCACTGGCT GCGCCAGGT AACGTGGAC TTCGGTGTCT GTGGAAGGGG TGGTGGCTCA 480  
GGTAGCTCG GTACAGCTGA TCTGGTCTT AGTATCAACA AAGCAAAAAT AAAAATAATA 540  
20 ACAATAAGCT TTTCAGTGTG TGGAACGTC CCAGAACTG ATTCCAACGC TCCAACACCG 600  
CACTTCTTGA AGCAACCTCA CGCACCTTC TGAATGACAG ATCACCTCA CTAAACGG 658

25 (2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 690 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1632UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

GATCGAGACT GTGATATAGC TGTATAAGAA GGTTTGAAA CCTAGTAAA TACCCAACTT 60  
50 TTTTAATTCG AACCTTGTAC AGGTTTATA CTCAATTGTA GCCTTGAGTT GCAAATACCC 120  
GAGGCATAAA ATCAAAGCGT ACTTAAAAAC AATCACTACA TACAGTCTC CACACCTGC 180  
55 CAGAGTGGAA TAACATGAAG AATAAATATT AAGGACAGTA ATGCTATAAA TACATGTGCT 240

TCAAATAAAT ATATGCTTGC TAAGGGTTTT CAAATTGGT TTGGGGCAA GAGTACGCAA 300

5 TAAGTGGATC TTGGGAAAGT GATGGGGGCA GATAACGACC AAACAAGTGA GTTTOCAOCT 360

TACCTATATC TTCCTCTGGG ACAAACCTGC CACTGTTGAC CATGTTGTG CTAGGTGTTT 420

10 GATGTATGGA TGGAGTATCA GCACGTCCGG TAGAGGAAGT GCGAATTAGT GAAACTAACG 480

TCCCGGAGAA ACTGGATGCC ACACGATTGT TTGGTAGTGT GGGGGGCGTG TTAGGATTTT 540

15 TAATGTTGGT TACTGGGGTG CCTGATGGCA ACGATGGGC AGAAAAGTAT ACTTGCTCCT 600

GTGCTTTCAA AGATGGGTCA ACAGCCCAAT TGTGAAAGAA ACTGGCATTG CTAGTCTCAG 660

20 GGATGCTAAT AAGCTCTTGG ACAGAGTTGT 690

## (2) INFORMATION FOR SEQ ID NO:1035:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1633RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

45 GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA 60

CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT 120

50 ATTGAGTTTA TATTAAATTC ACCACCTCTT ATTCATTTCAT TTAATACTCC TCTAATTCAA 180

TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAAATTG 240

55 GTAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAA ACTGAATATC TACATATTAT 300

ATCATTAAATA TAATAACTCT TTAATTAGAG TGGTACCACA AGAATGCTGA AAGCATTAGG 360  
 5 GGIGTGTACC TTAGCTCTCT AATTAAAGTT ATAAAATTAT CTTAACTAAT AAAAATAATT 420  
 AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT 480  
 10 GTTATATTTA AATAGATCAA AATTTCACAA ATTTCCATTT CATTTAGTAC TACCATCACC 540  
 ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTACTAT 600  
 15 ACATGGTATT ATTGGTAATA TTTATCCTTT ATTATTATCT TTATTAGTAG TTTTATTACT 660  
 AATAACTTTA TGATTTAGAG ATATGGTAGC TGAACCTACT TATTTAGGTG ATCATACTTT 720  
 20 AGCTGTAAGA AAAGGTATAA CTTAAGGTT 749

## (2) INFORMATION FOR SEQ ID NO:1036:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1633UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

GATCTTAATT TAAATTTTAA ATTAACATTT TATAATTTAG AAATATATAA TCTAGAGATA 60  
 TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA 120  
 50 AATAGAAAAC CATAAGTTAA TTGATTCATA AAGAAAAATG GAATTATTIG TGGCATCTTA 180  
 ATTTTATTTA TTAAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA 240  
 55 ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TTTAATTTAA TTTTAAATAT 300

AAATATACCA TTTTATTAA TAAATAGATT ATTAAGTTA TTAATATTAA GTGATATATA 360  
 5 ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC 420  
 TTTCATAATA TTTATTTTFA TTAGTCTAGT AATATTTCTA TTTAATAGTC TACCTTTTAA 480  
 10 TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC 540  
 TAATAATTTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTATTAT TATTTAAATT 600  
 15 ATTATTAATT AGTAAATTAT ATTTATTTAT TTTATTAACA TAATTTTTTG ATAATAATAT 660  
 ATCATTATTA AATGGTTAAT TTATTAATAA TTATCTTTAA TGATTTTAAT GATAAACCAT 720  
 20 TATTATTATA GA 732

## (2) INFORMATION FOR SEQ ID NO:1037:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 702 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1634RP

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

45 GATCCATCTG CGGTTTGTC GACGTCCTGT GAAACTCTAC CAGGCGAATA GAACTCTGAT 60  
 AGACGACTGG CAGGTGCTG TTGAGTGGCA ATAAOGGAT TTGCATCATC TATATGGGCA 120  
 50 TTCTGTGTAG TATCTATCCT TAGACTCGAT AGGGACCCAT GCTTTACAAG TTCAGGTTTC 180  
 GCTTGCGGAG CCACGACATC CTTTCTCGA TTTAGGAATG ACAAATTGA GGAGTTCTTC 240  
 55 CTATGCTTGT GTTCAAATC ACCAGCAATG CTGGCTCGTT TATTGGTACT CGCAGATACA 300

TTCCTTGAAT GTCCATAGAT ACTCGAAGAC GGCTTCCAG TGGGAGCTGG AACGGCCAGA 360  
 5 CIGTCTTGIG CACCTAGCCC TTCGTAATCG TTTGGAGAGG AAAGCATGGA AATTCGATTG 420  
 AACAACTCCA CAAACGAGCC ACCCGATTTT GTCTTCTTAT GTCTGCTCT TATACTCTCT 480  
 10 TCCGGAATGG CCTTTTCAAA AGTACGCTGC ATCGGAGATA TGCCAGGATT ACTGTAAGGA 540  
 TTTCGAAGGT CTGGGCCATC AGGCTGTTTCG TCCACAGCAG GCTGCATAAA TACTGTGGGA 600  
 15 TAGATTGCTT TCTCGAGGAA GTGTAAGAAG CTGGTGAGTT TAGGGTTTGT GGGCCGTGTT 660  
 CGTAAATGGT AATGTGCTGA TTCCTGGCTT GATTCTGCAA AA 702

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1634UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GATCAGAGCG TGGCCAAGCC CAGCATTGTG TCTAAGTTAC ATGTAGAGGT CGAACAGCAC 60  
 45 GAGGGAATGC TTTCGCTAC GGCGAATTC GAGACCTTCA GACTGACACC GCAGATTTTC 120  
 TGTGGGCTC ACCGACCTT AAATAGCTAC AGCAACACAG CTGGCCGGT GTACACTGAT 180  
 50 AGCAAAGATG AACCGGTCTA TCATTGCTC GGTGACTGCG ATGGCTCGG ACGACGCCAG 240  
 CAGTCTTCGG CATGAGCGT CGAGTACTC GCGGAGTCA GAGGAAACGC TGTCAACTC 300  
 55 GTATGGGCC TACAGCACCA CGGGAATCGT GATGACATCT GTGATGATGA ACAAGGCCCA 360

GCGCAAGGGC GAAGTGTCCG AGCAGTGGAT GCGGCTCTTC CTGGACAGCA CGCCTGTGGA 420  
 5 GGACGTGGCG GTGCTGCAGC GCGGATGTC GGTGACGGG CGCTGCTGG ACACGTTGCA 480  
 GCGCATCTTG CAAAGCATGC ACGGATACCG CCAGATGTC CCGGGCTGG CGATGTTCAA 540  
 10 AGAGGCATGG AACCTGCAGT GCTACCACGG CAACGAGGCG GACTTTCCGC TGCTGAGGT 600  
 GCGATCAAG GTCAACAGCC TGACCACACT GGCAGCCTG CTGGTGGAGC ACGCGTGTG 660  
 15 CGGTTACAGC ACGCGATCG AGCAACTCAC CACGGTGCTT CAGTACCTCA ACAAGCTGCT 720  
 GCAGGGGTGG CGGTC 736

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: 1635RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GATCCTAGGG TGGTTCATGG CACTGAGCGG GACCGTGTTC TTGGACGGGT CGAACCGCAG 60  
 45 CAAGAGTCTG AAGTGGCTGA ACGGTGGCTG GGAGCGGCTG AAGCGCAATC GCGAGGGGCG 120  
 GTGGATTTTC CCAGAGGGCA CGCGGTGTA CACAACGGAG ATGCAGCTGC TGCCATTCAA 180  
 50 GAAGGGGGCG TTCCACCTGG CGCAACAGGC GCAGATTCCG GTGATTCCGG TTGTGATGTG 240  
 CAACACGAGC ACGGTGTTCA ACCCGCGGCT GGGCATCTTT AACCGGGCA CGATCACGGC 300  
 55 GAAAGTGCTG GAGCCGATCG ACACGGCTAA CATGACCAAG GATGAGTGG ACAAGCTTGT 360

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GAGCGACGTG CAGGCCAAAA TGCAGGCGGA GTTCGAGGCG CTTGGCTACG CGCCTGGGAT 420  
 5 CGTGGACACG AGCCTACCCG AGGAGGCGCT GCGGCGGAG TTTGTGGACT GCAAGGAAGA 480  
 CATCAGGAG GTAACGGGCC TCTTGAAGTA ACCTTGGTTG GTATCATATA AACGTTGCGA 540  
 10 CGAGTTATGT ACATATAGCG CTGCTAAGTA GGCATTCACT CCCACGAAGT CATACTGGC 600  
 TGAGCTCTAC GCCCCGCGA TGTGGGCCAG ATACTTGTCTG ACCTGCGCAG CGGACCGAG 660  
 15 CCAGATCGAG GACTTGTCTG GGATGTGCTC GGGAGTAAG TCCAGAAATG CGCTCGCCGC 720  
 GGTCGTTTAC GGCCTTG 737

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1635UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GATCGGACTG ACGGTGAATA GCCCACGTG GCATGCGCG CTGAGCGCG TGGCGAGCGA 60  
 45 TAGCAGCGGT CGTCCGAGG CTCTGGTGGC CAGGACAACG ATCCACTGGC CCACCAAGGC 120  
 CAGTAGGAGG ACTGCCCCACT GGAATGACAT CGTCGACACA CCGTTGTGGA TGCAGAGGTC 180  
 50 AATTATCAAG CCCGACAGGA AGCGCGAGCA CGTCGAGGCA ATCGCAAAAT CTGGCAGCAC 240  
 CGACGCTCG CCCAACAGGC TCGACAGCGA GCGCATGTG GTGAGGAACA TCTCCATCGG 300  
 55 GCGCAGCGAC AATAGCAACA CAAGGGCCAT GAAGTACGCC GCTGGGTCTG GGAAGAAGTT 360



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420 GCGCAGCCGG CGGCGGATGT CCTGCGGCAG CAGCGGCTCG GTGGGGCTCT GCATGCCGGC  
 5 GAAGGTCAGT GTTGGGGCCT TGACCTTGAG CATAGTGACG ATGCTGTGCG CAAACCACAT 480  
 GCAGAAGCTG ATCAGCGTAT ATGCGACAGC AAGAGTCCTG AATACACGAG AAAGGTCAAG 540  
 10 GTACGGCAGG CCATTTCGAA ACCATGGTAT CTTGAGCAGC TGCGACCTTA GCACAGAAGC 600  
 CATCCCGTAA AACGTGGCGG GCAGACTTAT CGAGCACAAC TTGCTCGCGG GGTACAGTTT 660  
 15 TGATGCGGTG AACAGCGCAC TGAAGT 686

(2) INFORMATION FOR SEQ ID NO:1041:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 720 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1636RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

40 GATCTTCTTC TGCTCGATGG ACGAGCCAGT TGTATCTTGG ACTCTACGGA TAACCCACAC 60  
 CTTTTCCTTC AGCGACAGGA ACTTGGCATC GGTGGGTTA TTCGGGTATA GATATAGGCG 120  
 45 TAOGANCGCT ACCACAAACG TTAGGCTGCC GATTATAATT GACAGAATTT TOCAATGTGA 180  
 GATAGCTGGG TTCCTTATCA GCAGGATCAA GTAGGAAAGG ACGCCCATTTG GTATGGATAC 240  
 50 ACTGACCGTC GCGATAACAA AAATCGGGGC GGTGCTGCC TTTTCATTCT CTGTTAAGAA 300  
 CATCAGCATT GTGTGTTCA ATGCAGGAAT GATAATAGCC TCCGTGAAAC CTAAGCAGAG 360  
 55 ACGAAGAACA TATACACCTT TGTAATCGT CATTGCACAT TGTACCATCA TAATGATGCA 420

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CCATATCGTC AGGAGGACGA TAACAACGTT CTTCAAAGGA AACTTCTGGA TAAACAGCAA 480  
 5 GTTGATCTGT CCGGTAATAT AGCCAACGTA GAATAAGGTA TTCACATTGT TGTAACGATT 540  
 CAAGGACATG TTTACATCTT CAAAAAATCC TAACAGAGTG CTGTAGGACA ATTGCGCCTT 600  
 10 GTCTATGTAG GTGATGAAAT TAATGCTCGC CGTCAGTCCC ACGATGTACC ACATAACCTT 660  
 TCGTGCAAGC TTCTTTTCCT CGGCTTCTGT GATAGGAGGG ACATCCTTGT CTTGCTTCAA 720

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1636UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

GATCCGCAAG ATGACCGAGG GTAAGGGCCA CCTGCTTTCG CACCACCGCT TAGTTTCCTT 60  
 40 TGGAGGTGCA GGTGGTCAAC ATGCAGTTGC AGTGGCACAC TCATTGGGCA TAGAAACGT 120  
 CCTCATGCAC AGGTACTCAG CAATTTTATC TCGGTATGGA ATGCTTTTGG CCGATGCGGT 180  
 45 AAAAGAGGAG CAAGTGCCAT GCTCCATTTT CTTGCAAGAT ACATCTTCTA AAGACCAGCT 240  
 AAATGAAATA TTCCACCAAT TGATTACCAG TACCTCAATT AGCCTTCTTA AGCAGGGATT 300  
 50 GGCCGACGAT CGGCTTGAAT TCGAGAGATA CCTGAACTTA CGTTATGAGG GTA CTGAAAC 360  
 AAGTCTTATG GTTCTACAAG AAGGAGACTC GTGGGATTTT GTAGAAAGGT TCACAAAAC 420  
 55

CCACAAGCGT GAGTTTGGCT TTGTTTTCGC CGAGAAGAGG ATTTTAGTGG ATGATGTCCG 480  
 5 TGTCGGTGCT CTAAGTAAGT CTATGGTGCG GAACAGGAGC CTGTTGATCA GCAGTTATCC 540  
 CAGGTCACCTC GTTCTACAGC TGACCCCTTCT AAGGATGCAA AGTTCCTTAA GGACGTGTAT 600  
 10 TTCGTGCGATG GGTTTATTAA GACCACCTAT TTACAGGTTA GATAGTTTAC CGGTAGGTAC 660  
 CTGTATTGAA GGACCTG 677

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1637RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

GATCTGCTCA TACTGAGCGG CCAACTGGTC GTACTCCGTA TGCAAAACAT CTGTGGTTTC 60  
 40 CTGGAAGTGC GCCACCTTGA GCGATATCTC ATTAAACTTG GTAACCAGCT CTOCCAACCTG 120  
 ATGATTGACT GCACTGGTTT CCGTCAGCAG GTCCCTCCAGT TGGCCAGTTC TGGTGTCCAC 180  
 45 TTCCGCCAAG TATCCGCTGT ACAATGTATA CTCGTGGTTC GCAGACCCCA GAGCAGAAGC 240  
 TCGCCGCCAC TCTGGCGCCA GCAGCTCAAT TACCTGAGGT TCAATCTCTG TTTCAACCGT 300  
 50 TGCCAACAGA GTGTCTACTT TTTGGGGTAA CGAACTATCC CCAAAAAGCG GAGGCAGCTC 360  
 ATCGTGAGAG GAGGCACCGG GATTTGCCGC TACATCCTGT ATGACTGAGT TCTTCGGCT 420  
 55 CCTAGGCATG GTGCAGTTGC TGCTCAACG GCTTTCCTCC TGGTGCAGGT CTGCAGTGGT 480

TCGTGCTTAT GCGCAAGCAG AATACCATGT TGAGCCGGCG AAATCTCATC ACGTGATCAT 540  
 5 CATCTTGCAA CGGCTCGGAG GACGCTGATG CACTGTTCCTA TAGGCTTAGG GCGCAATTAT 600  
 ACGCTAGCTA GTTATATTGA TAATATGTAC ATGATGCCCTT CGGCACGACA GCGCACTCAG 660  
 10 TGCTGGGCGG CCGCGCCGGG CTCCGGCAAG CTCTGTCTC AACTTGGGCG TTCTCGGCTT 720  
 CCACGT 726  
 15 (2) INFORMATION FOR SEQ ID NO:1044:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 683 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: DNA (genomic)  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1637UP  
 30  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:  
 GATCTTGCGG TCCTTCTTGT CCAGCTGTAG GTCCGGATGA GGGTACGCTT CGCTCAGGTA 60  
 40 CTCAGCCCGC AGCTCGCCGC TCTCCATGGA CGCTCCAGG ATCGAAGGCG CCGGCACAGC 120  
 CTGGAGGGG AGGGGCGGCT GCAGGAGGGG CATCTCCTGT CGCTCCTGGT GCATCTGCAG 180  
 45 CGCCGCAGCG CTGGGCTCCA GCGCCGGGTC GAAGTACTTC ACATTCGTCA GGCCCGACTT 240  
 GTACAGATTC AGGATGCAGC CCTTGAGCTG CGCACGGTGC AACCGGTACG CAGTCGGGAC 300  
 50 ATACTGGTAC CCGCTCGTCC CCCCTCCCGT GAAGTGCGGC CGCTCCGATC CGATCGAAGA 360  
 CAGTGACGCT GTTGGCTGGT GGCTGTATCG CCCCTCGCGC GCGGGCGCTG CGCCCTGGCG 420  
 55 CTGTTCACCC CACCCGAGCC GAAACACAGT CCGTCTGTAC GTCTCCCGGT TCAGCCCGCC 480

TCCACGTGCG ACCGGCGAGC CCGCCGGCTG CGAGCAGGGC GACACCTGCT CCTCGCAGCG 540  
 5 CGCACCCGCG TTCATGTCTT CACATGTTCAG CGTCGGCTTG TGCGCTTGCC CCGTCGGCAC 600  
 CTGTAACTGC ATCGGGGTCT GTGGCTGCTG CTGCTGCTGC TGCGTGTGCT GTTCGGGTTT 660  
 10 GCCTGTTGGC CTTGTTGTGT GTA 683

## (2) INFORMATION FOR SEQ ID NO:1045:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1638RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

GATCCTGTGCG CTGGAATGT CCGGACGAG AACAGACAAC CGTGGGGGC GGGCGGATCT 60  
 35 GCCGAAGCT GTCCGAAGGA GACCAAGAAG GAAATTGTAA AGCTGCAGCC AGGCGCGATT 120  
 CCACAGAACT CTCGTGGAA ACCGGTGCAG ATGGGGACGG GGGCCGACG GGCCACCGAG 180  
 40 GACGGCGCT GGCTTCTGC GCAAGAGGTT GCGACAAAGC TTGCTGACGA CGGCAGGGG 240  
 CGGGGGGCT CGCAACCGAT GGTGACGACC GGAAGGAGA AGTGGGTGCC AATGAAGCCG 300  
 45 GCCATGCTTG TGCCCGGCA GGGCTTGCGC AAGATGCAAC GCAAGAAGAA AAACGGGCAG 360  
 GCGGTCAACG GCGGTGCGC GAAGCGCAAG ACCGGAACA AGGCACCCCT CAGCCAGCAA 420  
 AAGAGAGCTC CAGACTCCCA CAGGAAGGCG CATGACGAGG CGAGCGCGC GAGCGCCACG 480  
 55 CCATCTGCAC CGAGGAGCA CGTGAACAG CCGAGCTCG GCGACAGCA GCAGGTCCCT 540

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GAGGCGGCAG AACAGGGTGC GGAACACCCG ACACAGCATA TGGGCGAGAT GCAGCCCCAG 600  
 5 CCCAGAAGAC GCTTCTACGG CGGCAGGCAG CAGCACTCCG CTGACGGACA CAAGCCAGTT 660  
 TGIGT 665

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1638UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GATCTGAGAA CTA CTGTGTG TGGCTAGCG CAACTTATC AGAATTCCAT CAACTCACCG 60  
 35 AACCATAGCA CATCTACGTC ACCTCCCCCT ACCGCTACAG ATACCGGGAA TGATCAATTT 120  
 TTGGGIGTTC ATGCTGTAA CATTATCGCAT GATGACAAGT ACCTAATATG CATGAGCAAT 180  
 40 GACACGTACA TTGATGTCTA CGACATGTCA GAATTATCGC CTGATTGTGA ACGCTGCGAC 240  
 GAAATTAGGA CTCCTAGACT ATCTAGACTT AATATTGGGA AGCAGATGAT GTCCATGAGC 300  
 45 GGGCCAGTTG GACCCGATGA TTCGCTTTTA CTAATCAGTG TACAGCCACA CGAGCTTCAG 360  
 CTATGGGATT TCAAAAGGCA GATTATGGTC CAAAGATATG TAGGACAGCG GCAGGTGGCA 420  
 50 TACATCATCC GTTCGTGCTT TGGGTATGGG GACAACCTAG TTGCTGGAGG TTGGAAGAC 480  
 GGAAGATAT ACATTGGGA TAGATATTAT GGTAATATTA TTGGCGTTCT ATCTGGGCAT 540  
 55 AACATGGAGA GACCGACGA CTCCAGAAAT AAAAATTCC CAATGACCAA AGTTTGCAAT 600

ACTGTAGCAT GGAATCCCGT CAATTCAAGA CTATTTGCOCT CTGGAGGAGA TGAOOGTCTG 660  
 5 GTGAAGATAT GGAAGGTIGA CCTAATTGA TGAATCCTAT AGCATGAOCT TATTGTCTA 720  
 TAGAACTTCG AGAAATCCTG CCGATCTGTT GTTTCCTAAA TTGTA 765

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1639RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

GATCCATCTG ACTATTGTTT CACGOGATTC GGGGACCAAC TGTGCAGTCA GGCCOAGGAA 60  
 CCGGGAGAAA TAAGCCTTGA ACGAGCGCTG GTGATATTA CAGTTGTGCG CACCTTGACA 120  
 TCTGCOCTCG TACAGGGTGT CGTTGCTGAG GAAGATTCTG GCGCTGTCCA AGAAACGCAG 180  
 TGTTCGCTGG TGCCACAGCT CGTCCTGGGT ATGGTTGTAG ATGAAGGCAC AGOCTGCCAT 240  
 GATCAGOCCA TGGTTGTAAG TCCACTGCAG CTTATTTAAG TTGGTACAGT TGTCGTTGAT 300  
 GTCTGTACCG TGTAGACGA CGTGCCAGTT TGGCTGCACA ATCGAGATCA GOCOAACGCC 360  
 ATACATCCAG TCGTAAACCC GTTCGCCCCA CTCTAAGTAT GTGGCATTCC CGGTGTAAAG 420  
 CGTTAATCGT GCGCCATGT GGAACAGCGC ACCGTTGGAA ACGGAGTTTT TGTAGTGGTA 480  
 CCGTGTGTTT CAGCGGAAAA TCTGCCATCT GAGCCCGCCG TTGCACGTCT CCATATCCCA 540  
 GCGCAGGGCC ATGGTATTAA ACACCGCCTG CGCCAGGCC AGCCATTGCG GCTGGTCCGC 600

GGGCGGGTTC GGAAGTTGC GCTCCGGGCG AGCATCACC GCCATCCCC AGAAAAA

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(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 730 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1639UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GATCGAGCGG GTGAGGGACA CGGTGCACAT AACGACTGG GACGGTGCT GCTATGTTTC 60  
CAAGTGGCGG ATTGTGACCG TGGCGCAAAG CGTGCTGGAG CTGTCTCTGA AACCAGAGCG 120  
GGTGCCCGGG CGCATTGAGT TTGCCCCCCC CCTCAACGAC AACATCAAGT CTGGGTTTGA 180  
GCGAGCTCAC TACGCCTGCG TGGGCAAGAT CTTCCTTGAG TTTGACAAGT GCACCTGGGA 240  
CACGCAGCGC CCGCGGGTTG CTATCGCAGC CAAAGTTCCC GACGACTTTA GTGGCAGGT 300  
CCGTAAGGCC CAAGATTTGC AGGAGCTGCT GCGATCCGCC AGTGCTCAGA CTGAGGTGAA 360  
GCTGGGACAA GACTGCTTTG ACTTTCCACA AGAGTTTCAG AACATGGTTG CGCTGGCAGG 420  
GATACCGACA CTTATTGGGT TCACGCAGAC AACTCTTACT GAGCAAGTGG AGCGCTTATC 480  
AAAGCAAGAG ATTGTGGACT ACTTCAAACC CGCAATTGTT GTTGCACTAC GTGCACTGGG 540  
GTCCAAGGAG GAGTGCTCTT TGGACCTGG AAACACGCAA CGCAAGACG ATAGTCATCC 600  
AGGCCCAATC CTAAGAAGCG TGATCTTCAA TCCGTGGTCA CAGGATACGT ATTCTCGTGG 660  
CTCATACACC GGTAGTCAAG TGGACGACGA CCAGCTGCCC TTGAACGTGG CCTCAACAA 720



CGGCCAAGAT

730

## (2) INFORMATION FOR SEQ ID NO:1049:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1640RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

GATCAAGCCG AGCACGCTGA CCTTGGCTCC CCGACGCAAC ATGGGGTTGA CGGGCTCCCC	60
CGCGGTGGGC TCCTCGAGGC CATCGCCAG CTGGGCACTG GCGGGTGGC GCGCGCGGC	120
GAGGCGCGCC ATGTCCATGA AGACGGGAT GTACGAGCCC TCGTGATGG TGTATATAGT	180
GTTACAGCAG AGCATCAAGC AGTACAGCAC CGACATCAA ATGAGCGGCG CGTAGGTCTT	240
GCTACCTTGG CTGACAAACG GCGTGGCAAG TCGCGCGTAC ATTACAATGG ACAGCGTCAT	300
GAGCCACTTG CGGTAGTTTG AAAAGTCCG CAAACCCATG AGCACAATGG CAATGAGGCC	360
CTCGATGGAC GTGTACAACG CCCGCATATA AAGCACATAT GCGTGAACT GCACGTCCCT	420
TCCGCCACG TAGATGTAGC AGTCATGGC GCGGGGGGG CAGTGGGGG CGGGGTGGC	480
CTTGGGGTGC CCGAGCTCGT GTGGGATGGT CTGTAAAGAC GCAGGCACAA AAGAACGCAT	540
CATCAGTAG GTGGGCGCG TCGAAAAGCA CACAAGGAGC CATGCAGGAA ATACCCACCG	600
GCCCCGCCAC CGGCGCAGCA CTCCTGTTGG GCGCGCTGGC CGCCACTAG CGGCTGCTGC	660
TGTTCCAGCG TCACTGACAC CTGCATGTCA GCGCCCTTGC TT	702

## (2) INFORMATION FOR SEQ ID NO:1050:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1640UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

GATCAACGAG CTGGGCGAGC TGCAGCTGGA CGATGCGGAG GAAGGCGCTG AAGAGGCGGG 60  
 TGGTGGCGAG GAGGGGCGCG CGCTGTGGGC GCAATTGGAC GGTGACGAG ACCTGAAGGA 120  
 GTACGACTTG GAGCACTAGC ACGAGGAGGA TGGGGGCGCG GGTGCAGAGG TGAAGATGTT 180  
 CCGGGGGCTC TGGGGCGAGG CGCGCTTCCA CGAGGGTGAG GAGGGGCGAG ACGGTACCT 240  
 GAGCTTGCCA ACGTAGAGG AGGAGCAGGA GGAGCGGGCG GAGCTGCAGG TGTACCGAC 300  
 AGACAACTTG GTGCTGGCAA CCGGACCGA AGACGACATT TGTACCTGG ACGTGTACGT 360  
 GTACGACGAC GCGGCGGGGT TCCACGACGA GCGGCTGCG CAGGAGGCGG GGCACGCGCA 420  
 GGACCCCGAC GTGGGCGCGG GGCTGATAAG GGACGCGTCG TTGTACGTGC ACCACGACCT 480  
 GATGTTGCGG GCAATTCCCGC TGTGCGTGGA GTGGGTGAAC TACCGGCGCG GGTGGAATC 540  
 TGACGCGCGG GCAAACTTTG CGGCGGTGG CACCTTGGAC CCCACGATG AGCTGTGGAA 600  
 CCTGGACTGT GTGGACCGCG CGTCCCGAC ATGATCCTCG GCGAGCGCGC GGACTCTGCG 660  
 ACCGCGTCCA AGAAGTCGAA GAAGAAGAAG AAGGCG 696

## (2) INFORMATION FOR SEQ ID NO:1051:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1641RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

```

GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGOCATT GAGCTCTTAC GAACTGCACA      60
AACCTACTCG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTCAACTGC TTTCGCATGA      120
AGTACCCCCC AGGCTATTTT TCTTACCCGC CTGGTGTGTTG TCTATATACC CGGTGTATT      180
TTTGATAAAA AACTCAGCTC TTCTCTACG GCAGAAATAT ATATCCAGTC CTTAGCGCCA      240
TGCGAAAATC TGCTTTTFTA CGCTGTGTTT TCCAGTCTT AGCACTGGCA GAAAAAAGAT      300
GTATGGCGTA TAGGCGCTGG CCGCGGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA      360
AAAAGACGTG GGCCGCCCCG CGGCGAGACG AAGAAAAAAT AGGCGCCAC CCTTCCAAGC      420
AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGA AGAAAGTCTT GTGCACGCTC      480
CCGGCTCAT AGCTGCCAT TCTGTTCAT CCGGCTGCA AACCCAGTAG TGGCATGTCA      540
AAGCATGTCT CCGAGCTCC GCTGCTTGC AGTGACATC CTCTTCTAA CCCCAGCCAG      600
ACTTCCATA CTTTGCACTT CACATAGCAT ATCACTTTTC AGATCACTAC GTGACATTOG      660
GTACGGAATG GCACTCCAAT GCCGACAACC TCTTCTACC CGTGACTTAC CCGATGTGCC      720
AACTA                                          725

```

## (2) INFORMATION FOR SEQ ID NO:1052:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1641UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GATCGGGTAG TGAGGGCCTT GGTGAGAGCG GCGAAGTGIG CTGTGGTCT GTCTCGGGG 60  
GCTTGCTCTT GGGGACGGAC TGCTTGCGTG CTCTGTCTA GACGGCCTTG GTAGACCATC 120  
TCTGGTGTG GCTTGCTACA ATTAACGATC AACTTAGAAC TGGTACGGAC AAGGGGAATC 180  
TGACTGTCTA ATTAAACAT AGCATTGCGA TGGTCAGAAA GTGATGTGA CGCAATGTGA 240  
TTTCTGCCCA GTGCTCTGAA TGTCAAAGTG AAGAAATCA ACCAAGCGCG GGTAAACGGC 300  
GGGAGTAACT ATGACTCTCT TAAGGTAGCC AAATGCTCG TCATCTAATT AGTGAAGCGC 360  
ATGAATGGAT TAACGAGATT CCCACTGTCC CTATCTACTA TCTAGCGAAA CCACAGCCAA 420  
GGGAACGGGC TTGGCAGAAT CAGCGGGGAA AGAAGACCT GTTGAGCTTG ACTCTAGTTT 480  
GACATGTGA AGAGACATAG AGGTGTAGA ATAAGTGGG GCTTCGGGC CAGTGAATA 540  
CCACTACCTT TATAGTTTCT TTAATTATC AATTAAGCG AGCTGGAATT CATTTTCCAC 600  
CTCTAACAT TTAAAGTCT ATACGGGCTG ATCGGGTTG AAGACATTGT CAGGTGGGGA 660  
GTTTGGCTGG GCGGCACAT CTGTTAAACG ATAACGAGA TGTC 704

## (2) INFORMATION FOR SEQ ID NO:1053:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1642RP

(vii) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

GATCGGGTT TOGGAACGGC TTGCTTOGCA CAAAACACAG GGTTGGAAGT TACATACTCT	60
TCAAGAAATT GACGAGGCGT TGAAAGCGCT GGAGCTACGC GGGTCAGGA NIGATGGTAA	120
TGCTCATAT AAGTCAACT GCCAGGCAC TATGCATCT CTTTTGAGC TAGCCCCAAA	180
TTGCTGAAC TGTGGCAAAA TTATATGTTG CCGAGAAGGT CTTTATATGG ATTCTGCAG	240
TTATTGTGGG ACGCTGCTGA TACCGAAGCA GCAGCAGCGG GATATAGAGA AGGTGTTGCA	300
GGCGAAGCG GAATTGGTAA AAGCCAAGAG ACAAGAGACC GGCTGACTG GCAAGAAGAA	360
GGAAAAGGTC TTTAAGATTT CGAACGCAAA GGGGAGAAAT ATGTTGAGTG AGCAAGAGAG	420
GCTATTGAC AAAGTTGACA GGCAGCGGGA CGTGAAATGA AAGCAACCA GGTACTTGGG	480
GCAGAGGACT GTCTCAGGAG GAGGACTCGA TTCTGAAGGC TGAGGAAGTC GATCGGAAC	540
TAAGGGCGGC CAGGCGCGCT TGGAGAATCT ATTGCACTTT CAAGACACTA GCGAAGAGAG	600
GACTAAAATA ATAGATACTG CCAGTGACTA CAGTATGTCA AAGACGCAG GAATTTGGGG	660
GTCGGCATAT GAGAAGGC	678

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1642UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

GATCTCGTAC CCGGTACGGT GCGGAGCTT GCGGCGGCA GCGGCGGCT GCGCTGCTTC	60
TCCGCGGACA GCGGCGCAA TACCGTGTTC TACAAGCTGC ATGGATCGCT GCCACAGGCC	120
GTGCGTGTTC CGACGCTGG GCACCTCTCC TCAGACGCTG CGGCAACCG GGGGAAGCAC	180
CTGGTCTGT TTTGTACGA CGTCGCTCG CGTGGCTTGG ACCTGCGCG TGTACGACT	240
GTCATCGAGA TGGACCGCC CTTCGGGTC GAGGACCATC TGCATCGTAT CCGGCGGACC	300
GCGCGTGCG GTGTGGCTGG CGAGTGTTC CTCTCTCTGC TGCGCGGGA GGAAGAGGGC	360
TACATGGAAC ACATCGTGC CCACCACTT CGTGGCTGG AGCTGCTTC CTACGATCGA	420
GACCTACTGG CGCGGCGCTT CGCGGCGCT GTGCGCGCT CGACCGTCC GACCAACGCA	480
ACGGACGCG OCTGGACAG CAACGCGACA ACTTGGCACC TCAACGTCCA GCGCGTGTTC	540
GCTCGAAGAC CCTCGCGAA GGATCTTGC ATCAAGGCT ACACAGCCA TATCGCGCA	600
TACGCAACCC ACATCTCTCA GGAAAAAGG CTCTTCAAC GTTGGCTGTC TGCATCTTG	660
CCACCTGGCG AAAGCCTTTG GACTTCGGA GCGCCCCAA GCA	703

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 616 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

EP 0 866 129 A2

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1643RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

GATCGGAACA AGGAGCAGCA GTCCATCCAG CTGTGCGAGC AGCAGCAGGG CACACTGCAG	60
GACAGGAAGC CGACATACCA AGTCATGTCT CTCCAGAGCG ACACGACGGT GACCAAGTTC	120
AAGGTCGAGC ACTCCATCAG CAAGCGTTTC GAGTTCATGA ACAAGCCGAA GGCCAAGCGC	180
GCGACCGCGC CGCGGCAGGC GCGGACCAGC AGCCCTGCAA TGGCCTGGGG CGCCGGCAAG	240
CGCGTGACCA AGCCCAAGGT GCAGCAGGGC CGCGCGCGCG CCGGCAGGC CGATTGGGG	300
AAGCAGAGTA ATACGCCAG GGGACTTGGG TGCGCTCGGA GAAGACCAAT CGCTGCAGGA	360
ATTCTGTGCG CAGTCGAGA TTAAGAGCGA TCTGTTGAA CTGGAGGAGC AGAACGACGA	420
GAGCGCAAGC TCCAACAAGG AGAAGCTACC CCGAGCTCC TCGTCGTTGT TCCAGCAGCA	480
GCTTCTGCCC ACAGATATGG ACGACTTTT CAACCTGAC CTGACCATTA TGAAGAACAC	540
CGATGATGAG TGGTTCAGG GCTGTGTTGG CACTCTCGG GACGCGACCA CCTGCAACAC	600
CATGCCCATC GAGGAC	616

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1643UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

5	GATCGTTGCA AAGAAGCTAT TACGGTGTCT ACACGTTGCA GAACAGCGCC CGATGCCATA	60
	TCCACACCG CCGCTGTCAA ACGGTCTCTT GGCACGAGC GCTGACGGG GGAGCGCGC	120
10	AGGGCTGGCG CAGCAGGCG CCGAAAATC GTACTACCG CTGGTGCGG ACGGCGACA	180
	GCTCAGCGG CCACTGCTGC CCGTGTCCAC GCGCGCGAT GACGCGGCG TCTACCGCTA	240
15	CCACAAGCAG ATCAGCAAGT CGTTCAGGA CGACCTGATC TACTGCCCG GCGCGCTGCT	300
	GAGCAAAGTC GAGCTGAGC AGTGCTACCA GCTGGACATG CTGCTGCTGA TGGAGCAGCA	360
20	GCAGCAGGCC CAGCCGAGTG TCAAGTTCAA CCCATATACG TGCAGAGCT TCAACCCCGC	420
	GGGCCCCGCA TGCCCCGCT CTTAGGGCG GCGGCGCGC CGGGACCATT TAGTTGACN	480
25	GAATCNCTAT GTCAAGACTG ACGTTGCTC GCATCGGGT TTATGTTTIA TTCCAGTT	538

(2) INFORMATION FOR SEQ ID NO:1057:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 560 base pairs
	(B) TYPE: nucleic acid
35	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40	(vi) ORIGINAL SOURCE:
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(A) ORGANISM: PAG1644RP

45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:
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50	GATCCTTTGC AAATTCGTCC ATAGGAATGT AAACGACCT GCGCTCCAC CTCCTGGTAT	60
	TGCAACAGG CATCTTGAGT TCGTTGGCC ATTCCATCTT TATATGCTGT TCTTCATGC	120

55



AAGGCACATT TTCGTCTTCT TGGGCTTCT CAAAACAAC CTTATGCACT CTCTCAGTAA 180  
 5 TATACACAGG GTACGGGGTC GCCGTCCCTG AACATTAGGA AGAACCAGCC AAATGGGCTT 240  
 GTGCCTGGCG ACTGGCCCGA CTTCTGCACK AAATCCACC TCAAGTATAT GACCATCAAG 300  
 10 TCCCTGAACC GCGTGCTAAA CTGCTGGTAT GTTGTGTGGA TATCTAGGG ACCGGGAGCT 360  
 AGCGAATGG TATGCGGCAC TTCCAATAGG TAATGCCCCG GCGTTTGGA CCGATGGTAT 420  
 15 ACCCTAGTAA CTTTGCCCTGC AAACCAATA TGGGCTTGG GCTTTTTCCTA GTGGGCTGG 480  
 TTGTAAATIG GTATCAATGT CTGGGAGAT GAGATGGAGC TGTOGCTGGA AGATATGTCC 540  
 20 TTAGCAGGT TATCGTCTTC 560

## (2) INFORMATION FOR SEQ ID NO:1058:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 706 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1645RP

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

45 GATCTTGGA GAGGAGGACT ATTCAAGTAA AATGCCACGG CGGAAGATA AGATGAAGA 60  
 GGAGTGATA CGAAAGTACG AGCGTGAGAA GAAGAAGAGA AAGAGAGGCG CATAATCCCC 120  
 50 AGTGTAATAA ATCAATTCCG CCGGTTGGCT GCGCTGTAGC ATAATAATAT GTACGATAGT 180  
 GGTCAGATAA GGTATTTCAA AAGTTAGGCA ACCCATGAAA CATCAAACCTT TTCAATGCAA 240  
 55 TGATATGTAA GTTCATATA TTACGAGCTG TGAAATAGAG AAACCAAAAT GAATACTTTT 300

EP 0 866 129 A2

ACCACACCAT AACAAACGCA CAATGTTACG AGAATGAAGA CGATAATGCA GCTTGAATAG 360  
 5 TGCCACCATG GCGGCATATG GTACCTACTG AACAGCAGAA GCAAGCTAAA CGAGCTCAGC 420  
 ATGAGGGACA CCACTAGAGA TACCAGGATC AACGCTGTGA TATAATTACT ACCTTCAAAC 480  
 10 TCAGTCTGGT CATTTCOAAG AGCGCTGAAC AATGAAAACA TGATTCCCAC AGTGGTACCT 540  
 GTGGTTATGC AAGATACGAG CAGGGTCGTC AGGTAAAACA ATGAGACCAC CTCATCGTGC 600  
 15 TTGTATCCAT ATAGGACATC AAGTTCATCG TAACATACTA GCGCAGCCTC GTCATCCCAG 660  
 TTTGGAACIT GCAGTTGGCT ACCACTCCCG GCAACGTGCT TTGCAC 706

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1645UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

GATCAGCGGC GGCTGCGCGC GCTGTTGCCG TAGCGCTGCA GCAAGCTGCG GCGCGCGCGC 60  
 45 GCGCTCTGCG CCTGGCCCTC CCGCTGCCGC GCACCGCGCT CCGGCGTCTG CCGCCCAAGC 120  
 TCCAGCCGCG TCGGGTTGCG ACTGATCAGC TGATCCACCG TGCTGCCGTC CCGGCCGCGC 180  
 50 CTGTCCGCGC CCGCCGCGCG CTCGCCCGCC GCGCCATGCG CCGGTACAC ACGGCTCTTC 240  
 GGATCGTACC GCGTCTCTTC GCCCGCACG TCGTCGAGGT ACCGCGCGCG GTCATGCGCG 300  
 55 GCGCGGATCG CAGGCGCGCC CACGCCCGCC CCGCGCGGCC GCGGTTCCAG TCCCAACTTG 360

TACCGTTCCA CTGCTGCGGC CGCGTCTCTT GCGCTGCGG GCGGCTCCG CGCGCGGGC 420

5 GCCACTGCGG GCGCCACCG CCCCTGAAC CCGTACCATC GGTCCCGCTT GGCTCAAAG 480

CTCAGCGCAT TCTGTCCCG GACCTGAAAC GCGGCTGCG CACCATGGC CGCGGCTGT 540

10 TTGCGCGGCC GGAGCAGGCA GTCGCGCGG TCATGATTGG CGCGCAGTT TCGTGCAACG 600

CCCGGTCCG CGCCCCCGC CGCGCGCGC TGCCCGCAC AAAACGGTCA CTTATTACG 660

15 AACCTGCTGA GCCACGAGA AGTCTGAGC GCGCTGCGG GGCTC 705

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1646RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

GATCGAGAAC CGCATGGACG ACAAGCCCAA CGTGGTGATC CTGGGGTCCG GCTGGGGTGC 60

GATTTGGTTC CTGAAGCACA TCGACGCGCG GAAGTACAAC GTGACGGTGG TGTGCGCAGC 120

GAAGTACTTC CTGTTCAAGC CGCTGCTGCC CTGAAGGCC GTGGGCAACG TGGACGAGAA 180

GTCGATCATC GAGCCGGTGG TGAACCTTGC GCTCAAGAAG AAGGGTAACG TGTCTTACTA 240

CGAGGGGGAG GCGACGTGCA TCAACCCGCA GCGCAACACG GTGACGATCA AGTCGGTGTG 300

GACGGTAGCA CAGCTGTGCG ACCCGGACAA CCACCTGGGG CTGACGCAGC AGGACTCCGC 360

GGAGCTGAAG TACGACTACC TGGTGTCTGC GGTGGGCGCG GAGCCCAACA CGTTGGGCAT 420

EP 0 866 129 A2

TCOOGGOGTG GAGGAGCAOG GCAACTTTT GAAGGAGATC CCACACTOGT TOGAGATCAG 480  
 5 AAAGCGCTTC CTGTGGAACG TOGAGAAGGC GAACCTGTG CCCAAGGGOG ACCCOGAGAG 540  
 AAAGOGTCTG CTGACCATCG TGGTGTGGG CGGTGGTCTT ACCGGTGTGG AGACCGGGG 600  
 10 TGAGTCCAGG ACTACGTGA CCAGGACCTG AAGAGATTCA TGOOCTCCAT OGCTGAGGAG 660  
 GTGCAGATCC ACCTGGTGA GGCCTTGCC AACGTGCTGA ACATGT 706

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1646UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

GATCAAATGG GTTAGCCCGT CTCACAGAG CCTGCAACA TAGTGGCAGT AGGGTGTGA 60  
 40 GTCTGGATC GTCTCAAAC CGCTCAAAT AACTTCTCG TCCAGATGT AGTCTGCCAT 120  
 GCGTTGCC ATCTGTGTG TGATGTCTG AATCACTGC TGGTACTGG GCTTCAGCTT 180  
 45 GTGGAATCG GCTAGAATCG TGCTGAATC CACGACAG TCAGGTCTT TCTCGTCTT 240  
 CCGTTGCCG TCGAAACTCC AGGTATCCAG CTTCAGTTT TGGTGAAT CCGGAGTAG 300  
 50 CGCACTTT ACCTGGGAC TGATGTCTT ATCTCTTCA ACAGTATCA GCGACGCG 360  
 AATCAGGTAG AACAGCATCA CCGGTGCG CAGCTCGGA TGTAGCTCA TTATCAGGC 420  
 55 CGCAAAGAC TCGAAGTCCG CTGTAGCAG TGGTAGCAC GCTTGAAGCT TGCAGAGCC 480

TGCGTGTGTT CCGCAGGATA AAGCGGTTC CTCAGAAATT TGAGCTTCAG AGCTGCTTC 540

5 AGCTCCAGTG GGTGTGTGAA TAATTGAACA ACGTTCCCA TGGTCAGAT TCGATTAAGT 600

AATTGCCAAT TATGTCAAGC GCGTGTCACT TGGTGATGTC GCGCTTGCTT GTACAGG 657

10 (2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: PAG1647RP

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

GATCCAGCTA GATAGCGTGC CAATTGCTGA TAAATCCTGC CAGAATGCGA TAACGCTCT 60

35 CTGAAACGGC CAACGCTCC GGAGCGCCAG GAGCTGTCC GAGATCGAG GCGTCTGGAC 120

TOGATGCACA ACTAATATTG AATTCACTAT CCGCAGTAG GGGGTACAT AACTGCTTAC 180

40 GTACTCCAC TACGACACTG CGCCCCGCAC GCTGCAAGTG CGATCGGCT TACAAAGACC 240

AAGTCCTTG CAACACCTGG ATATGGTATC CATCGGGTC TCTGAGGACG GCGAGATTCT 300

45 TGATAGACC CTGTGTGTAG CGCAACTCC ACTCCAGGTC CGGTAGTC TCCTGATGT 360

CAGCGCAAAG AGCGCAGGG TCACTGAGCG ACACACCCAT GTGGCTGTAC CCGTGGGCT 420

50 CTGCGTCCC GTTGTGATAC GAGAAGTCG CGTCATCTC GTTCCCCAA TTGTGCTCA 480

GCTCCAGAAT GCTCTCGGC TTCAACCGCT CGTCCGCTG CGGATACCC AGGAAGTAGA 540

55 GGGTGAATTT CGCATTTGG TGCTCGCTCA CCTCCAGTAG CGACATACT AGCACATTCT 600

GGTAGAACTC CAGOGACTTC GTTGCCTCCT TCACACGTAG CATCGTGTGG TTAAACTTGG 660  
 5 GCOCCAGGTC CACTGGCTCC GGTCCGACA AGTTGTACTG TATCAACTCA ATCCAGTATC 720  
 CGTCGGG 727

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1647UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

GATCCGAGCA CGGTGCGGGT GCAACAGAGG AATATATGG CACTACAGAC AGTGACACAGA 60  
 TGCAGGAGCT GCGCGCGCTG GCGCGGCAGC GCTATCTGGA CCGCGGGGAG AGGGAAAAGC 120  
 TAGACTGGGC AATACGGGAC CTTCATTGT TAGAAGAAGA CGTAAAGAAG TACCGATGGG 180  
 ACAAGCTGAC GGAACGGGAG CGAAGAGAGA TTGGGACCAA GCGGCAGCTC GTGCAAATTG 240  
 TGCGGAGCG CGATGCGGCG GCGCGGCGG CGGAGCGTCC ATTCCATATG CCGCGGAGAG 300  
 CCGTTGTGGA GGCTACTGCG CGGCAGGAGA AGAGCTGGGA GGAGCAGCAG GTGCAAAAGG 360  
 CCGTGCGGCG CGAGGGGCGC TCGACATAA TTGAGGTGGA GGGCTCTGAA CAGTACGAGT 420  
 TTGTTCTGGA CTGCGGTCC GTTGTGCGCT TTACAGAGGA AGAGAGCTG GCTCCCGGCG 480  
 AGCGTGTGGA GAAGCAGCTC GAACAGAAGC TCGAGAAGGA AATTAAGCGC GTGGCGTGA 540  
 TTCAAGAAAC TAGGAGGCAG CTTCCTGTGT ATGCGTACCG CGACGAGCTT CTGAAGGCGG 600

TGCGCGACCA CCACT

615

## (2) INFORMATION FOR SEQ ID NO:1064:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1648RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

GATCCAGCTC ATGCAGTGGC CGATTCCAGC CCTGCCCTGTC GTTTAAAGTC TTGAAGTAGT	60
TGGTGCTGAA ATGCTTGTCA AATTGTGACA GGTATGTTTT CGAAGATTTC GAGAATAGTC	120
CTTCCACCAC TTTCAATGGG TTCTCTCGA ACTTGTGGAG GAATGAATTC TCAGCTTGG	180
AGAATGCATG CTGTGAAGAG TATATACGAG ACCCAGCTTT CGCCACGAAT TTGATGAGCT	240
GATTGAAGTC GTTGGCATG TCGCTCTGG GTATGAATCG TGGCAGTC AGGTCAAAG	300
CTCGCTGGT CATAGGACGG TATGGTCCG GTGGGTACTC GTGGACATCG AAGTTATCAA	360
GCAGATAGAA ATCCTTGATT TTGCCCTTGT CTGCGAGAGA CCGCAGGTAC GCCACGAAAA	420
GGTGGTACAG CGCGCTTCCC CGGTACGGT AGATCTTGTT CAGAATAAGT TCGTCGTGCT	480
TGCTTCATC GTTGGCATCC TTGTACTCTT CTACCGCCTT GCAAGAGGGG AAACACACCT	540
GGCCCGGGT GAATATTAAG TCATCTGGC TCGTCTTCTC CACCAACAGG TCCGTACGCC	600
CAACGATCGT CACCAGGATT TCCAGAAAAG CGTAAGTCGT GCACATGT	648

## (2) INFORMATION FOR SEQ ID NO:1065:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1648UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

GATCTAGCAG GTGTTGAACA GATAATGGAA TGGCTCTCTT ATATTCCAGC TAAAGTAAAT 60  
 ATGCCCGTAC CTATACTGCA GTCAGAGGAC AACTGGGATA GGGATGTTGA ATACACACCA 120  
 ACACTTCACA GCCTTATGAT GTACGCTGGA TGATTGAAGG CCGCCAAGGA CCTGATGGAT 180  
 TTGAATATGG TCTGTTTGAC AAGGTTTCTT TCCAGGAAAC ATTATCAGGC TGGGCGAGAG 240  
 GCGTCGTGTG AGGCAGAGCT CGCATGGGTG GTATCCCGCT CCGTGTTATT GCGTTTGACA 300  
 CTCGTACAAT TGAAACTGIG ATCCCTGCOG ATCCGGCAAA CCTGCAATC ACAGAAACTT 360  
 TGATTGAGGA GGCAGGCTTA GTTTGGTATC CTAATCAGC ATTTAAAACT GGCAGGCCA 420  
 TAGCTGATTT CAACCACGGA GAACAACTTC CACTCATGAT ATTAGCAAAC TGGAGAGGGT 480  
 TTTCTGGTGG TCAAAGAGAT ATGTTCAATG AGGTCCTGAA ATATGGCTCC TTCATTGTTG 540  
 ATGCTCTAGT GGATTATAAA CAGCTGTAT TCGTATACAT AACTCCAACA GGTGAGTTGA 600  
 GAGGTGGTTC CTGGGTTGTG GTGGATCCTA CAATTAACTC TGACCAGATG GAGATGTATG 660  
 CTGATTCCGA CTCGCGGGCA GGTGTGCTAG AACCTGCTGG TATGGTTGGT ATAAA 715

## (2) INFORMATION FOR SEQ ID NO:1066:

## (i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 714 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1649RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

20	GATCAAAAGC AAAACTGTGA CGCAGAAAAA AGTTTGGCTG ACAGACGACA TGCTCGCAGG	60
	GCACCAGGGG GTGGGCAACG GAGCGGTGCG GTTTCAGCG ATGGACCTCG GGGCGACCAC	120
25	GAATCTTTTG CTAAACAACA CTATCAACAA GACCAAGTTC AGTCAGCTAA AAAAAAGGCT	180
	AGATAGTATC GAACTGCATA ACCAGCAGCT GCGCGCAGAG AACCAATAGTT TGAAAATCGA	240
30	ATTCCAAAAG ATGAGTTCCA GATATAACTC CATGGTGGAG AACCTGGTGT CTCTTAAAAA	300
	CTACAATAAT TCCTCGTTG AGAACTTCAA TCTGCTGGTA TCACGCTCG CGCAACAGGG	360
35	CCTGAAGGTT CCCCATOCAT TAAACCTGG CAACTATGCA TCTTCACAGG TTGOCAAAAA	420
	TTCATCTGCT TCCGACGTTT AACCGCATGT ATCGCCGTTG GGTACTGTAG CACCTACGAA	480
40	CATACCCCTG GCGCAGGCTA CCCCCTCGAA AGAAGAGGCG AATCCTCCCTA CAAGCCTGCG	540
	CCCAGGCTTC CATGTTCTGC TGGTAGAAGA ATGATTGGGT TTGTATCCAA CTATGTTCCA	600
45	AATTCCTGAG AAAATATGGC TGTTCGGTGG AAGTCGTAAC GGACGGCCTA TCTGCTATTG	660
	AAACAGTAGA GAAATTCCAG TACGACCTCG TTCTGATGGA TATCGTGATG CCGA	714

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1649UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

GATCGCTGGC GGGGGCAGCC ACATGCGGGG GCATTTCAGC TTCTACCACA TGCAATCTAT	60
GGCGGCTGTG CGGGGGTTCG GCGCGCAGGG GAAGTACGGG CTGGGGGAGC CGCCAGCGGA	120
GGCACCACCG CGGGGGTTCG CCGACGTGGA TGTGGTCTG ATGCGCGGTC TAGGGTTCTG	180
CGCGGATACC GGCGGGGCGC TCGGACGGGG GGCAGGTTC TACGACAACT ATGTAAGCGG	240
TACGCAGCAG CTGCACGGCA GGAGACGGCT GCTGGTGGG CTGGGGCTCA GCCAGCAGCT	300
GATGTTGCAC GTCCCGCTAG AGCGGCACGA CCAGTCTCTG GACCGGGTGG CCTGGGGGGA	360
CGGACAGTTG AGGTGGGGGC ANCGGGGGC CGGGGAGATA GTTGATATAT AAGTGTATCT	420
AGCCTGTAGT GAAGCTCCCT TTGCACGCA CGAATGTCCG CGTCCCGCTC TGGTTGATGA	480
TCTGGGCTC CAGACGGAGC TTGTTGCCGT GGTCTCGAC GCGGGTGGTG CGGACCACAA	540
CGAACTGGTT CGCCAGGGTC GGGAAACAAT ACAAGATCTT GATGTGCTCG GTTACCTCCT	600
AATCGGTGCC GGTACGAAT GTGACTGCCT CCCGCATCAG GTGCTCAGC ACGTGGCCA	660
GGA	663

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 706 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1650RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

GATGCTCTG CCGGACTCG ATTTTGTGC ACCGCCACG CAAGAAGGAC CTTGGTGCA	60
TCATGTACAC CTGGGCTCG ACAGGTGACC CGAAGGGTGT GTCGTTGACC CAGCTAACA	120
TOGTGGCGGG CATTGGCGGT GTTTCGGTTG TGATCAACCG CGCGATTGTG AAGCCTGACG	180
ATCGTGTGTCAT CGCGTTCCTG CCGCTTGCGC ATAFTTTTGA GCTTGTGTC GAGTTGACCT	240
GTCTCTACTG GGGGGCTTA ATTGGCTACG GCTCCGTCAA GACGTTGAGC GAGGCTTCGG	300
TCCGCAACTG TAAGGGCGAC ATGAAGGAGT TCCGGCCGTC CGTCATGGTC GGTGTGGCAG	360
CTGTCTGGGA GGGTGTGAGG AAGGCTATTG TTGGCGAGGT CACTAAGTTG CCTCCGTTC	420
AGCAAAAGAT ATTCTGGGCG GCTTACCACA CCAAGCTACG CATGAAGAAG TGCCACATTC	480
CAGGCGGCGA TCTAATAGGA AGCATGATCT TTAAGAAGGT GCGTGAGACC ACTGGTGCCA	540
ACCTTGGCTA CATCTTGAAT GGTGGCTCTC CATTGTGCGG GGATACGCAA GTTTTATT	600
CCAACTTGAT TTGCCCCGTG TTGATTGGTT ACGGCTTAAC GGAGACTGTG GCGAATGGCT	660
GTATAGTGCC TCCACACCAC TTCAAGTACG GGGTTGTGGG AGACAT	706

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 674 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1650UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

5			
10	GATCCATTTC TCATGGAGAT TAACGCTATA TCGAGGGAAA GCAATAACAA GAAGCAAGCC	60	
15	AAGAAGICTG TTAAC TTCTC TATGCTAGGG TTGACTGATT TTACCAAAC CAAAAAGGC	120	
20	GATACTACAG ATGCTCTGGAG AGCGTTTAGG ATGTACGACG AAGTACAAAT GAAAAAGAGA	180	
25	TTTAGTTATA AATGGGATTA TGATAAAGTG TCCAGGGAAT TGGATGAAGA GACATGGAAT	240	
30	AAGATTATTA ATAGGGAAAC TTGAATTTA TTGCAATTAG TGGAAAGATA TACGGTAAAG	300	
35	ATTGAAAACG ATGCCAATAT AACCTATTGG AGTTCTGTGG TTATGCGCAA CTCTGTGGC	360	
40	AAGCATGAGG CTACAGGAGT GAGGCAATGT GCCAACTTCT TCTGTGGTAA ATGGGAAGAC	420	
45	CACCGAAGC AGTTTCCCAA GTGCGCGCGT TGCAAGGCA CAAATATTG CAGTTGTGAG	480	
50	TGTCAACTAC AATCTTGGGC ATATCATCGG TACTGGTGCC ATGATGTTGG CTCGTCTTC	540	
55	ACGGGCACCT CCTCAACGGC AAACACCACT GGGACACATA CGCAAATGC TGTGGTCAG	600	
60	TGGCTGGAA CCACGACCAC TACTACCAG GGGCTAAG AGGTAGATCA ATCCATTTTG	660	
65	ATGACAGCAA GGGG	674	

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1651RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

10 GATGGCGACG TTTACCGAAG AGCAAAAAGA AAAGTACGCG ATGGCGTTGA AGGACAAGGG 60  
GAACGAGTGC TTTAAGGACC AGCGGTACGA GGAGGCGATC AAGTTCTACG ACTGCGCGTT 120  
15 GAAGCTAAAA GAAGACCCGG TGTTCTACTC GAATCGGTGG GGTGCTACG TGOOCTTGAA 180  
CAAGCTGGAG AAGGTTGTGG AGGACAACCAC TGCTGCACTA AAGCTGAAAC CCGACTATTTC 240  
20 TAAGTGTTTG CTTCGTCGTG CAACAGCTAA TGAATCGTTG GGTAATTATG CTGATGCTAT 300  
GTTGGATTTA TCTGCCGTAT CTCTATACGG CCGGTACAGC TCGCAGACAA TTGAGCCCGT 360  
25 GCTGGAGCGG AATATGAACA AGCAGGCTAT GCAAGTATTG AAACAGAAAC TCTCTGGTGG 420  
AGAGAAACAC GAACTTCCTT CCAATACTTC CTTAGCGTCT TTCTTCGGCA TCTTCCTTC 480  
30 GGAGACATCG TTGGAGAACT ACGATGAAAC TTCCGAGCA GACCGCATTTC TTCTCAAGGG 540  
ATTGTGCGCC CTACACGGCC GCGAGGCAGG CTCCTATGAA ATTGCTGATG AAGCCTTTAC 600  
35 CGATGCTGTA GAAAAGTTCA CC 622

(2) INFORMATION FOR SEQ ID NO:1071:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 679 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1651UP

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

5	GATCGTGATT TTCGCGGGCT GCATCCTGCA GGCTCCACAT CATGCCGTGC GCCAGGCTAT	60
	GCTGAACATC CCCAGCGGGG TCTACTGCAC GTTCCGTGGG CAGTCATCGC CTGOGATCCA	120
10	GTACGGTATC TCGTCTACAA ACTTCATCAC ACACGTGAAT GAGATCGAAA CCCAGACCT	180
	GGACCGCTTT CTCGAGGTGG TACGCACGAT ACCAGACAAC ACCTACTGTA AAATCCGTCT	240
15	TGTGACCTTC GACAACGTGC CTTTGTCTAT CTCCTGAAG ACAAACTACC ACTACTTCC	300
	CACCAGCGAG CTCTCCCGCA ACTCCGACAC CGGCGCTGG ATTGAGCACC TCTGCAACGC	360
20	TACCCCGCT AAAAAGTAGC AATAGACTGA TATCTTTAT AGAAGTATA AACTATTAC	420
	ATGTAACCCG ATCAGGTGAC GAGCGCTGCA CGCAGCTCGT GCAGCATGCT CAGTGGTATG	480
25	GCAGTAGGCG CCGCAGAGCG TTCAGATGGG CACTCGCCGC CATGGTCCGC CCAGAGAGCT	540
	GCTTCAGCGC GCGCTGTCC AGCCTGTGTT ACGTGGCTG CGGCCAGCCT TCGAAGCTT	600
30	GTACCTCTG CAGTCTTCG CCATCTCTTA GCTGCGCCTT TGTGGTCTT CATTAGTGT	660
	CGCACCATGA TCAGCGACG	679

35 (2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 692 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: single   |
|    | (D) TOPOLOGY: linear       |

45 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- |    |                         |
|----|-------------------------|
| 50 | (A) ORGANISM: PAG1652RP |
|----|-------------------------|

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

EP 0 866 129 A2

	GATCTTCGTT CGTGAAAACC TTGCAAGTCT TCATGAGCTC AAGAATTGOC TCTGCATCTA	60
5	TTCTGTCCGG TTGGATTCTG CCTTCCTTAT TGTCCTGAAT CATGCGGCGA AAAGCGCGCG	120
	GCGTCCAGTC ATGACGGGAT CGGCCCTTAT AGGACTTCCC TGCAAGCGGC ATGAGGCTCC	180
10	GCCAGCCATT TTCTTCAATA ATATTGACAA GTCTTTCGTT TTCCAACACG ACCTTGTTTCG	240
	CGAGACTGTG GAACGTGTTT ACGTCTATCT GCTCAAGTAT TTCTACCCCTT TCCTCAGCAG	300
15	ACCATGCGAA GTTGCAATCT GCTCTTGA ATGCTCCAT AAGCTTTTCA TTGATGTTAT	360
	CCACTGCTTT ATTTGTCAAG GAGAGGATTA GTATTTCAAT AGGAGCTACA ATCCCTTCGT	420
20	AAACCAGGTT GTAGACTTTA TGCAGTAGTG TCACGGTCTT GCCAGACCA GGTCCCGCTA	480
	CCACATTGAC AGTTGTACAA GGCTCATATG GATGTGTTAC TACTCGTGAT TGGGACGTGC	540
25	TCAGTGCTTT CATTTCATGA TGATACATGC TCGAGCGTCG GCGAAGGAAA TAAATTCTGTG	600
	AATTTCCGTT TTAAGATACT CAAAAGAAAT GAGATAACCG CCCGCAAGGG CCGAGTAGAA	660
30	TTACAGCAGC TATTGAATAT ATTTAGTTTA TT	692

(2) INFORMATION FOR SEQ ID NO:1073:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 697 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1652UP

50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:
----	--

55	GATCTCCCCA CCAATCTCTCT CCAGCGCCCTT CTGTAAGCGT TCCCGCGGTT GCTCTCTCCG	60
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CTTTTGCTTC TTCTCCTTAC GGATTTTCGC ATACAGCGGC TTATTCAGTT CGAACTGTTT 120  
 5 CTCTTCCAC TGTTCCTTCC ATTGCGACTT CGACATGCOCT TCGGGAACGG GCGGCAAGGC 180  
 AGCCCGTGGT TTTGGCCGAC TCAATGTTTC ATCATTATTA GTTTCAGGAG TCATTGCOCA 240  
 10 GTTTCAGGAC TCTTAGCGCA AGGTCTTGTC ACTGAAGTAC AGTAAAATGG ATGCCCTTTC 300  
 GCGGTGATGA GGCAATGACC TGGTGAAATT TTTCGCCCAT GGTGAGGCTG TATAGTGGTC 360  
 15 ACGTGACAAC AGTTCAGCCC ATATATGGAG CCCCTAGGTC ATATAAAGGG TCAGGAGCCC 420  
 GCTAAAGTCT TTGTATTCTG ACCTTTTATT GGGGAGCTTT AGGGGCTGTG TCTCTATCCA 480  
 20 GAGCCGTGTG GTGAAAAGCG TCTCAGCTCA GCGGTTCTA CTACACTGAG ATTTAAAAAC 540  
 CAACAGCGAA GCAGCAGAGT ATGACGTCTT TAGCAACTAA ACTCGAAGTT CCATGGGTTG 600  
 25 AGAAGTACCG GCGGAGCTG CTGAAAGATG TGTGGGAAAC GAWGAAACGG TGGAGCGCCT 660  
 GCAACAGATG CCAGGGATGG AAATATGCCA CACTTGA 697

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1653RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

GATCTTTGAT GCTATTTTGT ACCTTAAGGG CTGTTCCGTG CTGGAGATGA TCTCCGGCTA 60  
 55 TATAGGGGAG ACCGTCTTCC TGAAGGGTGT TGCTTATAT ATAAAGCGGA ATAAGTTTGG 120



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	CAATGCTACC ATGGAGGACC TGTTTGGGGC CATTAGTGAG GTAGCAGGCC TTGATCTCAT	180
5	GGCGAAGGCA AAAGATTGGA TTCTAAAGAT CGGTACCCG GTTCTGGACA TCACTGTTGT	240
	TGATGGGAAG ATTCACTGT CACAGAGAGC GTACCTTTCG AGGGACAAG CTGACGCCAA	300
10	TGACGACCTA ACCACCTGGT GGATTCOCCT GGAAGTACA CAGGACTCAA CTGCACTAC	360
	AACAGAAATG GTTCTTAAAT CCCAAGAAAC AGAGATCTCA GCTACGATT TTGIGTTCTT	420
15	TAACAACGAT GCCACGGCT TCTTCGGGT GCATTATGAG GATGAGACTA TTCTGGCTAA	480
	CATCTGCAAG AACATAGGC AGCTGTCTC ACGCAGTAA ATTGCGTAA TTTCGGATGT	540
20	TGATGCCACT GGTACCTTCA CGCAACTCAT GGTGTCTTG TCTGCATTCT CTGCAACGCA	600
	TTGCAAGAC TACTATGTA TGGAACTCTG CATTGTCCAT TTCCACTCG GCCTGCTCAA	660
25	TCATATATCG CGATGCGTCG CAGAGATCCG CAAGAAGCTT GCGGCGT	707

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1653UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

50	GATCTAATAC TGGGAGCGAC TGGGCGTTGT GCGGTGTCT ATCTGTATGC GAACGAGCA	60
	GGCTGTGATG GAGACANATT GTACTACGAT GGTTGGCGC TCATTGCTGT GAACGGCGA	120
55	GTTGTGGGCC AAGGCTCGCA GTTTTCGCTG AGGGATGTCG AAGTGGTTAC TGCAACTGTA	180

GACTTACAAG AAGTGAGAGA TTACCGGATG TCTGTGATGT CGCGAGGGTT GCAGGCAGTA 240  
 5 TCGAATAACG TGACTTTTGA ACGTATTCAA GTACCTGTAG AACTGGCCGC GATGCAAGAT 300  
 AGGTTCAATC CTACGATTAA CCTGACGAAG GCGAAAGCCC CATACTATCA CAGCCCAGAG 360  
 10 GAAGAGATTG CGCTGGGCCC AGCTTGTGGG TTATGGGACT ACCTAAGTGG TTGCAGAGGA 420  
 ACAGGCTATT TTCTTCCACT ATCTGGGGGC ATTGACTCAT GTGCCACTGC TGTAAATTGTG 480  
 15 CACTCTATGT GTCCGATGGT TGTCACGAA ACATCTGAGG GTAATCTGCA AGTAATTGCA 540  
 GATGCGAGAA GATTGGCTGG TGCTAGGAT GACTGGATTC CAACCGATGC ACGTGAATTT 600  
 20 GCAAATATGA TATTTACAC TTGTTTTATG GGAACAGCAA ACTCCACAAA TGAGACTCGC 660  
 AGTCGGGCAA AGAACTTGC GGAACACCT 689

25 (2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 598 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: PAG1654RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

GATCTTATTA ATTTTGATGG TGCTATATTC TAAATTCAAG TAATGATAGC GCGTGATGCG 60  
 50 GTACGTACCT ATACATATAA CGCACAGTTC TCCATGGTCT ATGCGTGTAT GAAAATCACT 120  
 CCAGCCGTGC GACACGCCAC GTGTAATCTA GTGAGTTTCA AGTTCTTCCT CCTCATCGGC 180  
 55 AGAAAGTTGG CCGCGGGCGG TGAGGTTCTT GAGCGGCTCC TTGAGCTGCG CGATAAGGCT 240

ATTCTCOOCTT TGAGCATGCA TGGGATAACC CTCTAGAGAC ATATGAGCOG AATCTGCACC 300

5 ATCTAAACCA TGTTCGCTGT TGCTGCCAGT GGCAGCTGCC AGTTTGGGAC TGGACAGACC 360

TGCTGTCCA TCTTTGTAAG AATCCTCGGT CGTTGCCGAG TTGGAATTCA TGGTTCCCAT 420

10 AGTGTGCAAG ATTTTCTCCT CTCTGTAG TTCCAGATGG GTACCTGTCA GATTGATCAA 480

GGACCTGCCG CTTTTACGGC GCGAGAGCTT GGCAGAAGA GAGTCCCCGG GTTGGCGTCG 540

15 CTTACCAAG GTTTGTAATG GAGGTGTGAG ATCTGGAGT CCTTGGTAGT CTCAGACA 598

## (2) INFORMATION FOR SEQ ID NO:1077:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1654UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

40 GATCGGGGC GGGTCGCSG CAACCAACGA TGTCAAGTGT GGATACCAGC GACCTGGTAG 60

GCGTTACGGT GGGAGGAGCA GCGTTGGCG GAAAACCGGC AGCAGAGCAA GTACTGGCTG 120

45 AAGTGGGGC CGTATCTGTC GGAGCGGAGC TGGGCGACGG TCGGGAGGA CTACTGTTT 180

GACGCGACG CGTGGCGGCA CTTCOOGTTC GAGCAGGCGA ATGCGGGGT CTTCOOGTGG 240

50 GCGAGGACG GGATCTTCGG CGTGAGCGAC AACCGGCAGC TGGTGTGCTT GAACGTGGGG 300

ATGTGGAACG GCGTGACGA GCTGCTCAAG GAAGCGGATG TTGGGCTGA CCGGGCGCA 360

55 GGCAACCAC GGGAGGACT GCAAGGAGCT GTACTACTAC CTGGACAACC TTCCAGGCA 420

TGCGTACATG AAGGCGCTGT AYAAGTACCC GNTCAAGCGG GGGTTCCTCGT ACCAGGAGCT 480  
 5 TATTGCGGGC AACGACGGGC GCGGGTACGC GGAGCGCGAG CTGAGGTGT ACGAACTTGA 540  
 CCGGCTGTAC CGGAGGCGG CGACGGGGA C 571

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1655RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

GATCCACTTT CCACTCTGAC ATCGGTCAAT CAAOGCTGGG CACTCAGGTT CAGTTCIGAA 60  
 35 GCAATTGCAG TCCCGCAGT TACCTTCAT TTATTTAGAG ACTTAGTGGT GTTATAAGTC 120  
 AGTCTATCG AACAGCTCTC GACAGTCATC GGAAACGAGA AGTTACCGC CCTTGAGACA 180  
 40 CAATCTGTTA CCGACTTTG ATTTACATGC GTTACCGCT CTGGGTCAGG TGCCGGGAAG 240  
 CACATGACAA AGGCGAGAG CTAGTTACGT GAGGCTCATT GGGGTATGCC GGAAACTCTA 300  
 45 ATGACTAGAT CATCGAGAA GCACCGGTAT ATAAGACGCA TCACGGTGGT GCTCGAGAGA 360  
 GTGTGTAAAA TGCCAATTGC TTAGCCACTG ATGCCAAATA CACTGGATAA GAGTTACGTA 420  
 50 CAAAACGGCC CTTGGAGGGA CCGGGTGTTC CAAGGGAAAG TGGTCTTGGT CACTGGGGG 480  
 GCCGGGACGA TCTGCAGGT GCAGGCGGAG GCAATGGTGC TACTTGGTGC CAAGGCTGG 540  
 55 ATCATTTGGC GCAATGTGGA GAAGACTAAG AAGGCGGAG CGGAGATGC GGAGTTGGGC 600

GACTGGCTG ACTGGGTGCT CGGAATTGGC GGCGTGGACT TCCGGGAGGT CCGGACATG 660

5 AAAGCGCGCG GTGGAACAGA CGTTTGGCGC GTTT 694

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1655UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

GATCTCTCTG ACCGCCCCCA AAGCTGCTC CGGCGACATT GACACTGGTG TTACCAOCCA 60

30 TTATGTGGGC GCGCGTTTCA TCCAGATGC CCTGGCCCGT CGTCATGGTT TTGATCGGTT 120

CCCGTACTCT GGCACCGATC AAATACTGGG TATTTGAGTG CATATTGCTT TATTCATAG 180

35 TCTGGGTACA TAAGCCGGGG TTTCAGAGGG CGGGTAAOGA TGACGGGTAA CGTTTCTTTT 240

TGTTGATATG TAAAAAGAAA TGTGCAAACA TTTTTCATGA GATGAACGTT ATACTGGCTT 300

40 GTTCTCTCTT TGAAGTCAGC AATCTCTAAC CTTTGAAGGT GATTAAATAGG CTGTTGGGTC 360

45 GTGTTGGAAC ATTGACGGAG CTTTGGTTGT TGTAAGCGAT TAATCTGTGT TGGAGTTTC 420

ACTTTCTOGA ACTGGTAGCA GGTCTGACGG GTCTGCGAAG GGCGTGGGAG ACTTGCAAAT 480

50 ATAGGCGCAA GACAACTGC GAGATACAGG GGAGCTGCTG CAGCGAACAG GTGGAGTGCA 540

GGCGGATCTT GAGGACTAGC TGCTCTGGGA CGAGATGGCG AAGGAAAGCC TGGGATAGG 600

55 CGTAGCAAGC ACGGAGCCCA AGCGGGTGAA GGTGTTTCATC CTGGAAGACA GCGAGTGGAG 660

AGACACTGGG ACGGG

675

## (2) INFORMATION FOR SEQ ID NO:1080:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic).

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1656RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

GATCTAGCGA TCAATCGCAG CTAACAGATG CTCTGACATT ATGCATGAGC GCAATCATGA 60  
 TGGACACATC GAAGCTCAAG CATAAAGTAG AGGACTGGGA CATGCAAGCG TAGGCCATCT 120  
 GCAAAAGCGT GTTGACCAAT ATGAACGAGG ATGCGTACTA CAAGCGCATG AAGGCAGCAA 180  
 AGAATGACGT AGATGGCTTC TCACTCGATG AGATTCTTGG TAAGGACTAT AAAGAGTTGG 240  
 TGTTCOCGAG CCGCAGTGCA GATCTACGTG TTGGCGTACC TACTGTGTGG CCTCTTTTGG 300  
 AATGGATGCG CGAGAAGTTC GCGGACAATG GGAAGTACGAA GCTCTGGCAC AGTTTCCTTC 360  
 TGGAGCATAA GTTAGATTTC CTCGTGGTGC TCACAATTAA GAAGGCCAAC GAGGGTTTGA 420  
 AACGGGAGTT GGCTATCATG GCCAACTCCT GCGAOCGTGC GCAGCAGGTC GAGTTCCTGA 480  
 TCCAAAGCCT CACCCAGAG TTGCAGTTGA GCAAGACCTC TGTCTTCTCC CCGGCTCAC 540  
 TCGTCATTGA GACGTGCGAC CAGAGAATGC TATCTGCCAG TCGCAAGCAA ATAGTACCTC 600  
 TCCTCAAGAG AACCGTGGCC GAGTTATAGC ATGCTTATGT AACTAACGTT CCAGTTACCA 660  
 TCTTCCACA TCTCAGCGGC AATGTGCGGT TTGTGGTCTC CAACC 705

## (2) INFORMATION FOR SEQ ID NO:1081:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1656UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

```

GATCTCTTCC TACCCGTGTAT TTCTACTTAG CAGGAACCTA AATATGTGGA AATCATGGCT   60
AGTAGGATGT TTTTCTTACA ACACAGACAT TTACGCCAAC CAGAAGCTA AGGCATGCAG   120
TATCTCGGGG AGTATCTGCC TAGGATGGC GTAATGCTAA TAGTGGTTGC GGGAGAGGCT   180
GGTGAGGTTG AACTGGGAAA ATTGGGTGGG CATAGGTTGA CTGTACAGT AAATGGAGCG   240
GCGAGGTTGA TCGAATTGCC CTGTGAGGTT GATCCGCTAG CGCGGCGCGG TATTAGACAC   300
TCGAAGGTTG CATTGAGGT CCGGCTGAAG GCGGTGAATG GGACTGAGGG CGGGGCGCGG   360
GACTTCACTA TGCTGGCTGC AGAGGACGGG TGGGGCGGAA AAGACCTGGC GGTGCTGAA   420
CTGGCTGGG CGGGTGGGA CGGGCTGCTG GTTACGGGG AACATGCAGG CGGTGAGCG   480
CGATGCCCTC CGAGTTTGG ACGGAGCTGA TGGACTACTG GCACTGCCAC AAGCCTGGGG   540
ACGAGTCTGC GGGCGCACAG CAGTACCTGA CGAATATATA CGCGCTGCTG CCTGCGGACG   600
GGGAGCTGCT GGTGGGGGAC ACATTGCTCA CGGTGGGGA GGTCTGCTG TCAGAGAAGC   660
TGGCGATGAG                                         670

```

## (2) INFORMATION FOR SEQ ID NO:1082:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1657RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GATCGATTTA GATTTCACCT TCAGGCACAC TAAGAGATGG ACTCCTTACA CTAAGGGTGG 60  
 GCTGACGGGC GCGGTGAAC GTGTTTGTCT CGACGGACAG ACTGTGTGTG TAAGCGGTGA 120  
 CCTAGTACCA TCTGCAGCTC TAGGTGAGGC CGTTGTACCT ACTTCAAACA ATTACACTTC 180  
 GACTCCTCTA TTGAACGGGG AGCCATTGCA CAGCTTTGTT CCACCTTCTA GCTGGGTAA 240  
 GAAGCGGTTT TCCTTCTCCC GCGAGCGGGG AACTCGTTT GCTTCAGCTG GTGACCACGA 300  
 GGAAGCTGTT ATCGACCAAC CGCTGGAACA AAGGTGATG TCTTCAAGGC CACCAAAGGA 360  
 GCTGTGCCCC CCAAGTGGC TGAGAGAGCT AGTCGTGGG CACAATCAT TCAGAGGAAG 420  
 GAATATCTTA TCTGTTAACC AATTCAAAG TTCGGACTTC CAGCCTTGT TCGTGTGGC 480  
 CCAAGAGCTG CGTGCGGCTG TCGAGAGAGA GGGCGTCTC GAATTGATGA AGGGCCGCT 540  
 CTTGACGACC ATATTCTATG AGCATCAAC GGCACATCC TCCTCTTTTA TCGGGCAAT 600  
 GGAGCGCTC GTGGGTAGAA 620

## (2) INFORMATION FOR SEQ ID NO:1083:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1657UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

```
GATCAAGTCC TTCCAGCCGA GCCAGTCTCG CACCGCATAC CAGAAATGCA TTGGCGCACC      60
TAGCGGGATA TTCTGCGGCG TGTACTCGGT CCACGAAAAG GCCCAGCGGT GTGCCAACGC      120
AAAGGCTACC ATCTCCAAAC AGAGCGCCAC ATTGTGGTAC ACGTAGCCCA TGTTCGTGCG      180
CSGCGAGTCC TGAATCACGT TCAGGTAGTG GAGAAGCGTG ATKACCATAC CCTGCCAGTA      240
GGATGCAAAA ATGATCAACT TAACACATAA GAATTTAGGC CATGGGTGTG ACTTGGGCAA      300
CTCGTTGTAC AAGCACTTCC AGAAGAGCGC CAAGTTATAG AGCGACCATG ACGGCTCGC      360
GTTGTATACA AGGTCAACC ACTTACATCC CAGATCCAC TCCAACACT GGAAGCAGA      420
CATCCCCAAG CAGTACACCG GCTTGAACCA CCGTACTGT AGAATGCCCC GCTTCACAGC      480
CAATAACGCC TTGGGGTCCG CCATATCGAC CATGGGCAAC ACCCAACGTC CCACAACGGG      540
AATCGGGTGC TGGATCCTTT TCTGCTCCGG CGCAAGGT      578
```

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1659RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

```

5   GATCAAAAGT TGATTAAACT AATAAAAGAA TTATTTTATG TATATTGATT GTATAGTCAT      60
    TTTCAGACAA AAATCGTGGG AATTTTAGCG GCCAAACATA AAAGTCAGAC ATTAGAAACT      120
10  GACAGATACT TTATTTACTG CATAATTACA CTAAAAACAA CTGTTCTCAA AAACACGGA      180
    TTATTGACCG CCCCCTCACT AATAATGTAC TCCTTCTATC GGTTTCTTGC GGGTAGAAGC      240
15  ACGTAAAGAG ATCAGTTTCA CTTTGCAATT TGGGCACTTT TAGCTTTCCA CTTAACGATC      300
    ATTCTAGTGT ATTTTATGAC CAGGAAAGAA AAGGAGCCTA AAAACCTGAA GGCAGCCAGA      360
20  CCAGCGACTG ATCCCAAGAC AAAAACCAAA TATTTGTTAT TAGAGGTTTC TTCAGGTGAG      420
    TATATTTGGG TTATCATCAT GATCAAAATC AAATTGGAAA GCATCCATAA CATGACAATT      480
25  CTAGTCCGCA CATCACGGTA GIGATCTGCT TGCTTTTGGG TAGGATCAAC TTTTATTTCT      540
    ACCACTTCAT CGATTTTAG ACGACCTTGA TTTCCTGGTA TTTATTATCG ATGTCTGTG      600
30  GCCATTCAGT ACCCTCAACT ATTTGTTTGC CACGGGGGCC TGGGTAAOCA TAGCTTCAGA      660
    CTTTGGCTTG GACCCCTGGG AAGCGCCTTT TGT                                  693

```

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1659UP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

5	GATCGAGTGG TCCACCAGGT AGTCCCTGGCC CGGCTTCACG TTGGGCGGGG TOGAGAAGTA	60
	GACCCGGTAC TGCTTCACG CCTTCTTCAC CTCTCTGTAG CTGCCCCGTC GCCCCACGAT	120
10	GTGGGGGTGG AACTGGGCA GGTACTCCTT CAGCACCGCC GGCGGGTCCC GCGCAGGGTC	180
	GCACTCACG AAGATCGGCT GCACTCGAT GCCCCGTGTG TTCAGTCGC GTAGCCACGC	240
15	CGCCAGCTTG TCCAGCTCG CAGGGCAGAT GTCCGGGCAG TGCGTGAAAC CGAAGTACAC	300
	CAGCGAGAAC CGCCCGAGAA GGTCTTCTC CGTGAACCTG TTGCCGTGA AGTCCACCAG	360
20	CTGGAAAGGC CGCCCCACG CGGGCGGCC GTACCCCGG TTGCGCTCG CCTCCGCTG	420
	CACCTCAGC CGCCGCTTCT CGCGGAAAA CAGGTAGAAC AGCCCGCGC CGAGCACAGC	480
25	AGCACCGCG CGCCCTTCCA CGTGTGAAC TCGATCGCC CGCCCTGAC CGCTCGAGT	540
	GCGTTCTCTG CGCCCCCAGC GGGATCGGC TCAACGGCG CGCTTGCC GCGCCTCTG	600
30	GCCCCCGGC GCTCTCTGG TCGCCAGCG TGTTCGGAG AACTCCGCA CCCCCCAA	660
	CGCTGCTCTC TGCTTGCA TTCCCGCAG TTGCTGCA ACAACGAGTC CTACTGATCA	720
35	TCCTG	726

(2) INFORMATION FOR SEQ ID NO:1086:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 720 base pairs
	(B) TYPE: nucleic acid
45	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50	(vi) ORIGINAL SOURCE:
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(A) ORGANISM: PAG1660RP

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

5	GATCAATTGG ATGCCAACCA AGATGAAGAC CATCTGGGTG AGTTAGCAGT GCACTCTGGG	60
	GATACATGGT CTGAGACCGA TAGGAATCTA ATTTTGAAAT TATTGGGCAA GTTCAAGAAT	120
10	ATCAAAGCTA TTTACAAATC CGAAGATGTC CGCCAAAGGT TGATGGAATT ATTGGGTAGT	180
	CGAACGCTGG AAGTGCAGAA ACTGGCCCTA GATGCGTGTG TAGCATACAA GGATCCAGTA	240
15	GCTGTGAAAT ATAGGGACAA TCTGAAGAAC TTATTAGATG ACACGTTATT CAACGACGAA	300
	GTAACAAAGT TATTTGCTCA GAATGAGTCA AGGGTTATTG TCAACACTGA TGAAGATTA	360
20	TTAATGCOCT TCATTTTGGG TATTTTATTT GGCCGTGTTT AGACACCTAA TACCACTGGG	420
	ATCAAAAAGA CAAGAAAAC TGCGGTCATA ACTGTCTGTC CAAATTTAGG TGAGAAGAAT	480
25	ATTACTGACT TCTTGGCTCT GGGTAGTAAT GGTATCAACT ACCAGTACTT CTTTGAAGAG	540
	AATGCGGTTA TTCTGACAG TGAGCTTACA GCGATAAATT TTAGGAGAAT GCTTGGCTTC	600
30	ATAAATGTCC TAAGTGCCTC GTTGAATGTT TTAGGTTCCA ATTTCOCGGA GGCGGTCAAG	660
	ACAACTATTA AACCTCTCGT TTACGCAATT CACATGTCAG GTCGTACTGG ACAGAATAAA	720

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1660UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

5 GATCTTATAG ATTTTCATCC CCAAGCTTAC AAAGAGAAGC TTATCCACCT GTTTTAGCCA 60  
GGCTTGGATG TATTTTTCAA TGGTACCCAT GTTCTCCTGG CCCAAGTTCT TGAACAAGTT 120  
10 AGTTAGTAGC AGACTAGCCA TCTTCTGCA TTTAGGAGAG TGTTCATTTA CTGATAAGTT 180  
TGCTAGGAAC ACGAAGAATG AGGATGAAAG TTTCATTAGT AAAGCGGGCC CAGATTGTGT 240  
15 GATCAGAAGG TTAAGCAATT CCATAACAGA TTGAAGACCT TCTTGAGATG GATACTGCAA 300  
ATTGTTGACT AAAAATTCA ATTGTTTTTC CAGCCTGCCT TTACTTTGAT CATATTOCAT 360  
20 GAAGAACTGG TAATAGACAC TCCTGGCAAC ATCCCTGATT TCCTTAGCAT GATTGTTGAC 420  
CATGACTTCT GCAACGTTAT CAATAATATC GTACAGCTTC GGAAGAACA TATGTTTGA 480  
25 AACCAAGGAT TTCAAAAATC CAAAAGCCAG ACCTTGCTTA TTGGGCTCCA TCAAATCTGG 540  
TTCAATCCGA CCCAAAACAT ATTGAGGCGC AGAATCCTTT AATTCAATGT CTTTATAGC 600  
30 GATAAGCGCA GATAAAAACT TCAGACGAC TTGACAAAGT TCACCAGAAG T 651

## (2) INFORMATION FOR SEQ ID NO:1088:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1663RP

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

55 GATCGGGTT TCATCTCCCC ATACTTCATC ACCGATGCGA AGGCCAACAA GGTGGAATTC 60

GAGAAGCCAC TGTTGCTTTT GTCCGAGAAG AAGATC

96

5 (2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 583 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1664RP

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

25

GATCCTAGGG TGGTTCATGG CACTGAGCGG GACGTGTTCT TGGACCGGTC GAACCGCAGC 60

AAGAGTCTGA AGTCCTTGAA CGGCTCTCTG GAGCGGCTGA AGCGCAATCG GCAGGCGGCG 120

30

TGGATTTTCC CAGAGGSCAC GCGGTCTTAC ACAACGGAGA TGCAGCTGCT GCCATTCAAG 180

AAGGGGGCGT TCCACCTGGC GCAACAGGCG CAGATTCCGG TGATTCCGGT TGTGATGTGC 240

35

AACACGAGCA CGGTGTTCAA CCGCGGCTG GGCATCTTTA ACCGCGGCAC GATCAGGCG 300

AAAGTGCTGG AGCCGATCGA CACGGCTAAC ATGACCAAGG ATGACGTGGA CAAGCTTGTG 360

40

AGCGACGTGC AGGCCAAAAT GCATGCCGAG TTGAGGGCGC TTGGCTACGC GCCTGCGATC 420

GTGGACACGA GCCTACCGA AGAGGCGCTG CGGCCGGAGT TTGTGGACTG CAAGGAAGAC 480

45

ATCAGGAGG TAACGGCCT CTCGAAGTAA CCTTGGTTGG TATCATATAA ACGTTGCGAC 540

GAGTTATGTA CATATAGCGC TGCTAAGTAG GCATTCAGTC CCC 583

50

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 598 base pairs

55

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1664UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GATCCGACTG	ACGGTGAATA	GGCCACCGTA	GCATGCGCGG	CTGAGCGCGC	TGGCGAAGA	60
TAGCAGCGGT	CCTTCGAGG	CTCTGGTGGC	CAAGACAAAG	ATCCACTGGC	CCACCACGOC	120
CAGTAGGAGG	ACTGCCCACT	GGACTGACAT	CGTCGACACA	CGTTGTGGA	TGCAGAGGTC	180
AATTATCAAG	CCCGACAGGA	AGCGCGAGCA	CGTCGAGGCA	ATGCAAAATT	CTGGCAGCAC	240
CGACGCTTGG	CCCAACAGGC	TGCACAGCGA	GCCCATGTTG	GTGAGGAACA	TCTCATGGG	300
GCCCAGCGAC	AATAGCAACA	CAAGGGCCAT	GAAGTACGCC	GCTGGGTCTG	GGAAGAAGTT	360
GCGCAGCGCG	CGGGGATGT	CCTGCGGCAG	CAGCGGCTGG	GTGGGGCTCT	GCATGCCCGC	420
GAAGGTCAGT	GTGCGGGCT	TGACCTTGAG	CATAGTGAAG	ATGCTCGTGG	CAAACACAT	480
GCAGAAGCTG	ATCAGCGTAT	ATGCGACAGC	TAGAGTCTTG	AATACAGGAG	AAAGGTCAAG	540
GTACGGCAGG	CCATTTCCAA	AACCATGGTA	TCTTCAGCAG	CTGGGACCTA	GCACAGAC	598

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1666RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

5  
10  
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25  
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40  
GATCCTTGCG TACTAAGAGT TAGACTTTAA TTAATAATAT TATTTGTAGA AGATAGAAAC 60  
CATACTGACT CACGTGCTAT TTAACCCATC TCACGTAAAC TTTTAATTGA CGAACAGTCA 120  
AACCCTACTT AGCTGTTACA ACCAAGAGGA TAGGTTGAGT CGACATCGAG GTGGCAAACA 180  
TAACCTACAA TAGCTACTCT ATCGTTATAT TACCTGTTT AATTTTGTTA TCATAATAAC 240  
ATTTAATTAT TATTTCATA ATTCTCATTA TTGTTGAGAC TATTTCATTA TGTATTATTT 300  
ATTAATTAAT ACATATTGGG CTTTGTGGA TATAATTATT GTTAATCCTA CTCATATATC 360  
TAGTGTGTA ACGTTCTTAT AACTTTATAA AAAGGATTGT TATAAGCTTC GCTGCAGATT 420  
GTCCTTTATT ATTATAAAAT AATATTAGGA GTTCTTTGCA ATTAACCCAA TTTACTCAAT 480  
ATATTTAAAT ATTGATAATT AAATTTCACA ATTTAATGGG ACTATTAAAT AATCCCTAGC 540  
GTAACCTTTA TTGTTATCA AATACCATTA CAATATGTAT ATTTTGTGTC ATTATGCCAA 600  
ACTTAAGTGA TTGTTCTACT TGTAGGTAAT ACAATTATAG CACAGTTATA CCATTATATT 660  
TATTTAATAT ATTATCCCTA TATTATGTTT TATTACATA TAAACTGTA CAT 713

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 677 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1666UP



EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

5	GATCCTTATA AAATGGGCAA TAGACGTGTT ATAATATAAT ATACAAAATT ATAAATAAAT	60
	ATTTAATAAA ATATAAAATT AATAATTAAA GTATTATAAT AATTAAATAA ATTATTTTAT	120
10	AATAAGTATG GATTTTAAAC TGAAATTGT TAAATGAAA TAAGAATTGC TAGTAATCTA	180
	TTAATAAGAA AGTAATGGTG AATACTCTAA CTGTTTGGCA CTAATCACTC ATCAAGCGTT	240
15	GAAACATATA ATTAAATAAA GAATATTAAT TAATTTATTA ATTATTAATT ATTATTAATA	300
	TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAAATGG AAGTTGAAAT	360
20	ACAGTTACTG TAGGGGAACC TGCAGTGGGC TTATAAATAT CTTAATATT CCATTTTTAT	420
	AAAATAAATA TATTTTTTAA TATATTTTAT AATAACTATA ATTAAATAGT TAAAATTTAA	480
25	ATTATAATTT AATAATTTAA TAACTTATTA ATTAGAGAGT TAGGGTACAT CCCCCCTAAT	540
	GCTATGCATT ATGGTTGGTA CCACTCTAAT TAATAACTA TAATAAATAA ATACTAATAT	600
30	TTTATATCAA TTAAATTATA ATTATTTTTT ATTAATATTT TAATATTATT TAATGAAATA	660
	TATAAATAAA GTATTAT	677

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1667RP

EP 0 866 129 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

5	GATCCATCGT GGTGTGGTTC ATTACCTGTA ATTCCATTGA TATCCTGGCT ATGCAGTGCT	60
	GGAAACGCTC CTCCAGGGCC TCTATTTTGT TATTGAGCTC CAAGTACTCC GCGAGCTTAA	120
10	AGGTCAACGA GAGCGACCCCT GGATTGCACC TGACGGGAT CTCAAGGACC TTCTCGTGCT	180
	CGTTCTCGTC CACAAACATG GCGTAGTTGT ACCATATCTC CGGCGCAAAG CACATGTGCT	240
15	GCACAGCCTG GCGGTGCAGG TATTCCAGCC GCTGGGCGAG CACGACTTCG GGCAGGTGGA	300
	GCTGTGTGTC CAGCTCCAC TGGATCCACT TGGTCAGAT CTGCAGCTGG TACTCATGCT	360
20	ACTGACGGGG CGCAGGCAGG TTCTGCTGIG TGGCTGGTT TAGCTTCGTG GGCAGCGAGC	420
	GCGCAGGCC CTTCGTCAGG TTGCACCACT CCTGGTACAG CGAGCGGCA TTCATGTAGC	480
25	TGCGGAGAG CTCTCCGATG AACTTCCGGG CGTCAACTG GTTGACCTCC TGCTCCCACT	540
	GCGTGTATTT CTCCAGTAC CGCTCCAGG ACTCCACTGG CAGGCACAGC AAGGCGCTTG	600
30	TACAGCTTGC GCAGAATCTC GACCGGCTC TGCTCTCC ACTTGCTCAC CGGCTTCCAC	660
	TGCTCCAGAA ACTGCAGGTA GTCTGCCAG AACTGCATCG ACCGGG	707

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1667UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

EP 0 866 129 A2

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GATCTAAGGG ATGGGTGACT GCTGCCGGTG CTCACAGCAG TGGCAOGTAG CTAGTAATGG 60  
 TGGGAAATCG ATCAAAGAGG GTGCGTCTGG CGGTACAGGC AGAAAGCAGC CCGGCCGATA 120  
 CAAGTCCAG TTCTACAAGC AACTGCAGTT CCAGGGTACG AGGTACCAGG TGGTGACTION 180  
 GCGGCCGTAT CTGATAGAGC GGTACGGGGA GCGCAAGGCG GCGACGATCA GGTGTTTGT 240  
 CAAGTGCATC CATCGGAAA TCAACGAAGA TGTGACAAGG ATCAGCGAGC AGCGGGTGAC 300  
 GCACGGGGTG TCGAAGTGGG AGAAGTOGAA GCTGTTCCTG CTGCTGGTGA CGCTGTGCA 360  
 GCGGGGCGGG CCGGAGTACT GGCTGGACAA GACGAACGGG TGCCAGAGCC GCGGGGCGG 420  
 AGACGGGCGG CGGAGAGCG ACGAGGTGGA GGAGGGCGGG AGCGGGCGGG GCGAGAGGCT 480  
 CGTCTGCACA CTGGTGGAGC AGATCATGG CGAGAACATC ACGGAGGACT ACGACGAGAG 540  
 CGTGCAAGAC GAGAACTACG TGTCTCGTC GATATGGGCG AACTTCATGG AGGGGTTGAT 600  
 AAACCACTAC CTAGAGAAGG TCATCATAAC CAAGTCGAG CTGAAGGTGT GCCAGCAGCT 660  
 GTACCAAGCC GATGATGAAG ATCATCTCAC TCTATAACGA ATACAACGAG CTCATGGACA 720  
 AGA 723

35 (2) INFORMATION FOR SEQ ID NO:1095:

40  
 45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 722 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

50  
 55

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1669RP

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

# EP 0 866 129 A2

GATCAACAGC ACCTCCACCT GCGACAGGTC GAACTCATCG TAAAAAGGCA GCGACGGGAT 60

5 ACCCTGGTGG GCGGGATGCA CACCGGCATC CAGCATGACC GTCTTGCCCT TATACTGCAA 120

TATATGGCAT GAGCGTCCAA CCTCATTGCT GCCCCAAGC CCGAAGAATC GGAACGAATT 180

10 CGTATCTAAC TTCTCTCCG TCATCCGCAA TTGTTTATG TCTGCTGCT GCGAGGTGCT 240

GTGCTCTCTA CCCAATGCT GCGACACTGG CTACTGAGAC AATTCCACGT AGCTGCTGCT 300

15 GCAACTTTTT TGCAGCTATG GAAATACCGT GGTTCGGTAG ATTTGATTCT GTGGAGATGA 360

ACGATCAAAC GGGAACTCTG GTTATCGGTG ATGGGTGTG TTAGTACCCA ATCAACCGCA 420

20 GAGACAAGTG CCACTATTAA TTGTAGTACT TACAGGAACA CCGATCGCAA GAACTCTTAA 480

CGGCTCCGTT TACCAACGAT CAACACTTTT CTCTCGAAC GTTATGCTGT GCGGCGGTGG 540

25 CGATTGCGAA TGATTGTTGA ATTGAACCAG AGAGCGGAAA ATTTTGTGTC TCAAGTGACC 600

GTATCTTACA TAAGCTACTG AACTATATGA AATACCGACG TTGCTCGAGG ACGCTAGCG 660

30 CAGTGTCTCA AGCAGTGATC ATGAGATTGA GTTGTCTGA TGTTACATT GAGAGTACTG 720

GG 722

35 (2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: PAG1669UP

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

EP 0 866 129 A2

	GATCAACAAG TGCAACAGCA AGGTGCAGTT GCGCATGTG CCCTCGGGGA TCGTGATTGA	60
5	GTGCCAGGCA ACCCGCAGCC GCGAACAGAA CCGCAAGCTG GCGCGGAGA AGCTAGCCGC	120
	CGCGCTGGCG CAGCCCCCGG GTAGCGCCAG CGAACGGGAG CTGGCGTTGC GCACGTGGGC	180
10	GCGGCAGGGT AAGCAAGGCG AGGCGGGCAA GAGCGGGAG AAACAAGAGC GCGCGCGGC	240
	CGAACGGGAG GAGCTGGGCG GCGCGCGGA CGCGGAGGAC GCGAACTTC TCGTCAGCT	300
15	GCTCGGGAAG CCGCGCGCA CCTCTAGTG CCGCGGGGG CCGCGGGGG ACGCAGGGC	360
	GTCTTTTTCG GCAATTCCAA ATAGACACC TAGTGGCTC TGCTGCGGC GAGCGCAGAG	420
20	CAGGCAGCTA GCACACCACC GTCCAGGCG AGCGCTTTTG CTGGCGAGTC GTGCGCAGT	480
	CCGCTGGCTC TGGTGTGCAC ATGCGCTCC GCGTGGCAC CGCAGTGCAG AGCTACCTAC	540
25	GTACGTTTGC AGGCTTCGCA GTAAGCTGA TACTGGCTCT GGTGAACTT CCGACAAGA	600
	GTAAATCTC ACCAAGAAC AAAAGATAT GTTAGTGAGG ATATCTACA TTCTGTACT	660
30	GGAAGTACAC AAAGT	675

(2) INFORMATION FOR SEQ ID NO:1097:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 697 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1670RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

55	GATCCGGCAA GATCGTCGTT CAGTTGACCG GCAGATTGAA CAAGTGCGGT GTCATCTCTC	60
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EP 0 866 129 A2

CAAGATTCAA CGTCAAGATC AACGACGTCG AGAAGTGGAC TGCCAACTTA TTGCCAGCCA 120  
 5 GACAGTTGGG CTACGTCATC TTGACCACCT CGGCCGGCAT TATGGACCAC GAGGAGGCCC 180  
 ACAGAAAGCA CGTTGCTGGT AAGATTTTGG GTTTTGTCTA CTAAGGGGCT GCTATATAGC 240  
 10 GTATCTAGCT CTAATGTACG ATACTCAGTG TCTATTACGA CGGCGGGAG CTCCACGGGC 300  
 CACATACGAG GGCAGCGGC GACGGCAAGC GGGAAITCAG ATCGGTTAAT TAGCAGTAGA 360  
 15 TTAGTAGTAT ATATGTACAA ACAGCATACA CATGAACGGC GTGCGCGATC ATAATCTTCT 420  
 ACCTCTTCTA CCACCCCTCT TTCTGGTAGA GTGGGATGG ATAGGAGTGA CGTCCTCGAT 480  
 20 ACGGCGGATT CTCAGCGCG ATCTGGCCAA AGCTCTCAAA GCAGCCTGAC CACCTGGACC 540  
 TGGGGICTTG GTCTTGGTAC CACCGGTAGC TCTGATCTTG ACGTGCACAG CAGTGTATGC 600  
 25 GACCTCTTA CACTTGGCAG CGAGCTCTG AGCAGCCAAC ATGGCAGCGT ATGGAGAGGA 660  
 CTGCTCTCTG TGGGCTTGA ACTTCATACC ACGGTA 697

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1670UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GATCTATTTG TGCCGTCCG CATTAAGCAA GCGGCAAGCA TCGATCCAAA TCATGAGAGT 60  
 55 ACCCTCGGGC TTTCACCTTC CAAGCCTTTA TCAACAAATC TGGTACACGA TACATCCATC 120

# EP 0 866 129 A2

GCGACAGCAC ATATACCAGA ACGGGAAAGC CGACAAGATG GCACTAGACT CTGGTAGGTA 180  
 5 ATCTGAGTTC GACCATATCC ACTTCGTTAA TGGTGATAGT TGATAAAAAG AAACGATACT 240  
 GAAAATTTTA ATGGTTACCA ATCTCATCTC ATCGCCATAC TGAAAGAATA TTGTAGGTCT 300  
 10 CGCAGTGGAA CAAGGATCAA GCGCAGGCTA AGACAATAAT GGTTCGAGCG GAGGCAGTAC 360  
 AGGAACTACC CCCAGATGAA GAAGAACTGG CCTTGGCTAA GCTAGTGTTT GGCGACACAG 420  
 15 CAGACTTCCA TGAAGCGCTG CGAAATGCAG ACCTTAATTA TGTTCCTTCA GATGAAGACG 480  
 TATATGGCCA GGAGTCGTCC AGTGATGACG AAGAAGGGAC TGAAATTGGT CAOCTGAATG 540  
 20 ATGACCAATT GTTTTTTGTG GACGAAGGTG CAGATACCGA GGAAGAGCA GATGGAGAAC 600  
 CGGAGGCCAT GGAGGTGGAC CAGGTTAGCG AGGAAAGCGA CTCGGAGAG GAAAGCGTA 660  
 25 GCAGCGCTGC ATGGTCAGAT TCGGATGACG AACACTTAAA CGTTACAATA GGG 713

## (2) INFORMATION FOR SEQ ID NO:1099:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 743 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1671RP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

50 GATCGCTTTC AAACCATCCT GTAACCTACG TGAACACAC TTTACAAGAC AACGGCATAT 60  
 CGACAATCAC AAGACTTCCT CGAGACATGC CGGCCACCA TCTTCATCGT GTACTGACGG 120  
 55 ACTATAATCC AAGTGGCCAT TTGAATTGCG AGCATGATGC CACGCTTTCC AACCTGAGCT 180

CGAAACTGG AGATGTACAT CGGCTTCCA ATTCTCTTC GAGTTTAAAT GGAGCACAA 240  
 5 AAAGGGCTAG CATCCCAAAT ATCTTAGGCT CTGCTCCACT TAGTAATCAA TCAAGAACTC 300  
 CAGACAACCG TTTAACACAT GGTACATCGA TCCATGAGAA CCGGCGTTA GAATTAAACG 360  
 10 GTGATCAGTC TTTACTCTTT GCGGTAATA CAGGCGAGC ATCGGGTAAC TTGGGGGTC 420  
 TTTACCGGC CGAAACTCC CGAAGGAGCA ATTGCGATGA TCAGAGCAA TATAGATTAC 480  
 15 ATTCCAAGC TTTCATTGG ACTGCCCCC CAAACGAAC TTCTAAGAAC ACTAGTCCAG 540  
 GTACAACGT TGCACCTGG AGCGTTGTTG GTACAAACAC AAGGAACACA CAACGTGGAC 600  
 20 CCACGGGAGA TGTTCCCAA GAATCAGTCG AACAGCGCA ATCAGCTTCG CGGCGATCG 660  
 ATGAATCTAG CGCAAGAATT ATGTCGCTA GTCATCATAC GGAGCCAGTA GGTCTGTTT 720  
 25 CGACAATCTC TTCTAACACA CGC 743

## (2) INFORMATION FOR SEQ ID NO:1100:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 661 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1671UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

50 GATCAGGGAT GCGGAGGACA TTCCGCGAGC TTATCGGCGA GCACGACCTA CCGTCTGGA 60  
 ACTATGTCAA GTACGGCAAG AAAGCTATTA AGGCTTCCG CTTCTGCGA GACGCATATA 120  
 55 TTCAACAGAT CATCCAGCTA GCCATCTACA AGTATGTGG CAGACAATTG CCAACCTACG 180



AGGCTGGGTC GAACAGAAAG TTCTTCAAGG GTAGGACCGA AGCGGGCCGC GCGTTTTCTC 240  
 CGGCCTCCGC CAAGTTTGTG AAGACTTGGC AGTCGCCGA AGCATCTCCA AGTGAGAAGA 300  
 TTGCTGCTCT ACGTGAGTCT GCTAAGAACC ATTGCTGCT GCTAAAGATG GCGGCGGACG 360  
 GCCAGGGTGT TGACCGCCAC TTCTTCGGTA TGAAGAACAT GTTGCGTGAT GCGGAGGAGC 420  
 ATCCTGCACT CTTCGCGAC CCGCTGTTCC AGCACTCCTG CACGTGGTAT GTGTCTACCA 480  
 GTCAGCTATC TTCGGAGTAC TTCGAGGGAT ACGGCTGGTC GCAGGTGAAC GAAAATGGCT 540  
 TTGGTCTGGC GTACATGATC AACAACTACT GGTTACACAT CAACATTGTT ACMAAGCCTA 600  
 AGAAGTCGGG CTATAGTGTG CACGAGCTTT CACTACTACT TGACCGAAGC AGCAAAAGAG 660  
 A 661

## (2) INFORMATION FOR SEQ ID NO:1101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1672RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GATCGTGTAT TTGTCAGGCC CATCCAAGCC CTCCCCCGCA CCCAAACCCA CTATGATGGG 60  
 CAAGAAGTGC TOCAACGTCG GATGGGCAGC CTGCAACAGT TCTGCTCCCT CCGCGCTCGA 120  
 GAAGAGACGA AGTAGTCTGC CGAATTTACA GCGTTGGGC GCGTGGTTA GCAGGAAGTT 180  
 GGACAGTCCC CAGTGAAAGG CAGATGAGCG CGAGTGGCTT TTTGCGATGG CAGATCCGCA 240

EP 0 866 129 A2

GAAGAGATCT CTCAGGTTGT GCACAGCCAT GCCAGACGTT ATTATCAACC CGCAGAGGTC 300  
 5 GCGGTACCTG GACAGGAGGC GCCCAGCGC ATACTGGTCC CGCAGGTGCT TTCCCGCCGC 360  
 CAGTGATATT TGGACCAGCG GTACCGGGAC ATCCCAATCG TCATCCACGC ACTTCGAAGC 420  
 10 GGAGAAGCCA ACTTTTAGGG GGACCCAAAC GCCATGGTCT ATGCGCGGTT CTGTGAGCAC 480  
 AGGCGATAGC GGGCTGCGTA TGTGGTTGAT GGTGTCCCG ATGTGGGTAA CTAAAGCCAT 540  
 15 GCTTGATTTC CTATGGAAC CTCTCTGTA CATCCGGTC GAGAAGCCAT AAAAATGTA 600  
 TATCAATTGG TTCTCCAACG GGT 623

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1672UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GATCCCAGAT TAGATATTAC TTAAACGTC CACAGCTTTT TGATGGCTA GTTCTGCTGC 60  
 45 ACGTCTATAA TGGTCCATCG CCTGTGCAT GTGGGATGA CAGCCGACCG CGTCTCCGT 120  
 ATAGAAGCCC AAGGCATACT CGCTTTCCG TAGCCGGCCT TCGGAAGCAA TGGATGCTTT 180  
 50 ATACGCCCAT TTGTAAGATT CTGAAGCGTT GGGTCCAGC ACGCCCTTGA CACCACTTAG 240  
 GTACCAACCA CTCAAAGCGA GCATAGCCAT GGCATTTCCC TTGTTGCTG CGTTTCAGC 300

CTTCAAGTAC CACACGATGG ATTTCTCAGG GCTATACGGC AAGTGTAATT CAGCGTACTC 360  
 5 GTAGCAGTGT CCCAGCTTCC ACTGAGCAAG CGGATAATTA AATTTAATGG CACATCTGAT 420  
 GTAAAGGTCT AGAGCCTTTA GGGTATCTTG TGGAACTGTC TGCAACTTGA CAGCCTGCTG 480  
 10 CAGCTGTGGA TGCAACAAT CAAATTCATA GATCTTTGCG AGTTCTGTATA ACGCCTGGGG 540  
 AGAGACGGTC TTGTCTGTG CAGCAGCCCG CTCGAACCAT CGTATAGCAG AATGACATC 600  
 15 CTGTTCACA ATAATTCAC CTGTGTCATC ATCCACCAGG CCATTCAGTT GGGAACATAC 660  
 CCAACTTATA CATGCTACTG CTCTGTCCGG AAGA 694

## (2) INFORMATION FOR SEQ ID NO:1103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1673RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GATCCAGCT CTTACGCTCG CTCAATTGAA AACCTTTTCT AACTAGCTT TCTTATCAAG 60  
 45 GAAGGACGGC TAGTCCTAGA AGATGACGAT GAGGGCTTCC CGGCATCCG ACCCAAGGAA 120  
 CCCCTCCCGC AGGATCCCGC CGAAAAGGAA CTGGAACGGC AGGACGGAA TGAOGGOGC 180  
 50 CAGAAGCATA TCATCTTCCA AATGGACATG GCCACGTGGA GGAAGCTTAT AGACAAGTTC 240  
 CACATCACAG AGTCATTTT ACCGTGATCA TGTATAAATA GCGGCATCT ACGTATCACC 300  
 55 CGCTGGCCCG GCGCTGACC AACCAGGCAC TGCTAGCAGC TCATCTATCG GCCACTTCG 360

AATGGTCAGC GCGCAACGT CTGTGTCAG GCGGTGTCC TCGTAGAGCT CGATGCCCC 420  
 5 CCAGCCGATC ATCACCGCAT TGTCTGTACA TAGATCTGGA GCTGGATAGT GAAAGGAGTC 480  
 GAACGGTCTG AATAGTTCAG TCTCGAGTCT GGCACGCAGG CGCCGGTTGG CGCATACGCC 540  
 10 GCGGAACAC ACAAACTGTG CCACATCAGC AACCTTATCA GCATTTGAGC CGCAGCACCA 600  
 GGTTAATCTT GGTAATCAAA TGGTCGAAAT ATGGCCTCCT GAATCTGAAW TGCTGCTACC 660  
 15 CGCGGTTCGG CCTC 674

## (2) INFORMATION FOR SEQ ID NO:1104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1673UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

GATCGCTCTA CCGACGTACT GCATGCCTGT CTGGTCTTA AGTTAAAAAC CACAGCACCC 60  
 40 AATCGTTTAC ACCGCAATCT TAGACCAGGA GCTAGTGCTT GCGAGCCCTT GTCGTTCAAA 120  
 TGGCAGGACT GTTGTTTGGT TGTGAACCTC GCGACTGAG GAAAGGGGGC GGAAGATCTA 180  
 45 TTTTGCACCT ATTGCAACC GTTTAGATAT TGAAAGCAGG GCAACACTAG TAAAACTCGA 240  
 AATTAGGACA TTCTGAACA GATGTGAGCA GAGGATTCGG GATGCGCTTC GAAATGATGA 300  
 50 GGGCGCATGC TGCATACCTT GGCCGTCCGG CGTAGTGTAG ACCGTGCAGC GCATGCTGCA 360  
 AAACAACGGC GCGGTGGCGT CGGCATGCAG GTAGCACAGC ACCTGCAGCA GCGCAGGGGT 420  
 55

GCATCCAAGA GTAAAGCCAC ATGTGGGGG CGTTGCTCCG TATGTACAAG TTATGTCATT 480  
 ATTTCTACAG ATATCATGTT GAATATTAGC CCGGATCAT CTAACAATG GTATCGTTTG 540  
 GTCTATCTCG CTTACGTCAA GATGCAGGCT CCGCCGGGG ACTACGGCC AGGGTGGCA 600  
 GAGCAGTTTG GTATAGGAGA ACCATGATAC TGCTTTGGAT GCTGGTCCAG ATGAACCTGG 660  
 GGGCCACACC GCTGAAGGG CCACCCAGTC CCTGTAGCG AAGTACGACT AACAAAGCTGC 720  
 GGAAGA 726

## (2) INFORMATION FOR SEQ ID NO:1105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1674RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GATCTCATTG AGGTACACAG ACACAGCTGG CAGCGAGCC CAGGCTGGA TGGACGAGTT 60  
 GGCGAAGCAA TCAITCCGGT TGTTTGCCAG CCTGTGCTG TGTTTGCTT TCCTGTGGA 120  
 GCTCTGGAAC ATAGCAGAAC TACCAGGGGA ATAGCCAGT GTAGATCGTC GGACCTAGA 180  
 TATAGTATGA AAGTGCAAGT GTGCCACAAA GAAGAAGTCT TTGTGGTATG TTGTCCGTTT 240  
 CGTAGAGAAA GCTTCCGACC TTATTAATAG AGAGTGTAAC GTGTAAACA GAAGAGGGGT 300  
 ATGTCACCTT GTGCAGCATG TAGATGGACT TGGGTATCTA GTCAGCCGTT GTGCTTGAAG 360  
 GTGGACCAAA CTAATCCTTA GTGCATAGTA TTATGTGGG GGGGCTTTG AACCAGGCTT 420

TTGGGATGCT CGAAGGCGGA ATAATACTOC ACGTGACAAT AATATACGTC AACTATTAAC 480  
5 GGCTAAATTA TCCCTTGCGA GGAGAACATC CCGTAAATTA CAATTATCAT TCTATATTAT 540  
AAACATATTA TAAAACGTCC ATCTTGCTAA TATAAAAACA ATCTAGGTCG GCTTACCAAC 600  
10 CATATTACAT CAGTAGGCAG CGCGATCTGC ATCCGTCATG GCGTGGAGTA TCCAGTT 657

## (2) INFORMATION FOR SEQ ID NO:1106:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 695 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1674UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

35 GATCATCATC AACTATATCG AGAAGGAGTG TGACCGCGGC GTTGCTATGG GTAAATACCC 60  
GTCTACCCCTT GACCGGGAAG CGGTCCGAAA GCTGGTGGCA AAAGATTGG AGAACTTCGG 120  
40 CGTAACCAAC AGCCTCAGC TGAACAGTCT CTCCTATAC TTTCGCAACC TAACACGGGA 180  
GCAGCGGGA ATATGCATAT ACAACAACCT CACCGACTGG AGCTTGCTAA TCCTTCGGGA 240  
45 AGAGGAGAAA ACCAAGTACT GCAAAAGAAA GCAGGGTTCT TCGTCAGAAT AACAGTAATT 300  
GTAATATAT AATCTGGAGC TTCTCCAGC GGTAGAAGGT CCAATTGT AATGTACTAC 360  
50 TACCTGAGCA CTGTGTCCG CTCATCGCT CCTTAGAAAC TGTGTTCAG GAGCTCGGAT 420  
GGCATCTGAC ACAAAGGTTG CAGACGCAGG AGAGTATATC TCCAAAGCCT TGGGTAACT 480  
55 TTCTAACCTA ATATTTTGA AATAAAGCCG AGTCGCAGTG TATCACTGCT CCAGTCAGTA 540

GATTCTGACT TCGTAAAATA TGTGTTCTAT GGGTGAACA TTITAAGTCA TAGTTTGTCT 600  
 5 TTTTCCCTG ATATACTTCC AAATACATAT ATCACTGAAG TTCCATCGGA AGCACCTCCA 660  
 CAGTACGGCC TAAGAAGAGC AGAATAATTG CTCCA 695

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1675RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

GATCCGTGCA ATAAACCGCT TGAATGCACT GTGGAAGTAG TTGCGGGTCT CGATATCAAA 60  
 GTCGACAAAG AATATCTGCA GGTGTGTAGC CAAATGTCA AGCACATATC CAAGCACTGG 120  
 ACGGAGGCC TTATGCGAGT AAGTTAGCAC TTCAAATGCA CCGAGCTTGT ACTTGTGGAT 180  
 TCGCAGAAGG CTTTCCAACG TCGACAGCAT GATCAGCTTG TCTTGTGGA ACGGCTCTC 240  
 CTCTATCCCG AGCTCTGGC CAATTTTGAG AAGCGGTAGA AGGAGAGCAG GGTGCCCTG 300  
 CATGTTCCGC AAGATAAACA GATCGAAGAC CTTCGGCGGA ACGGTCCGAA AGAGCGGCTC 360  
 CAGCACTAT AGTTGCACTC GTTTCGGCA GGTGCCCTCA AGAAGATGCT GAACCACTG 420  
 CTGCTCCAC AACTGCAGC ACATCTCCAG TTTATCTCT GTATAGTGTC GCACATATAT 480  
 ATTGGCCAGC AACTGTGCA CACTCTTGCC AACGCGGTC GCAAGAGAGT CCGACCACAT 540  
 GTATCCAGA GCGTGGCAA TGAACTCCG CCGACCTCT AGAACAATTC CCAGGTCAAT 600

CCGCTCCGAT AGCACGTCCA CCATGAAGTA CACGAACCTC TTTGAAGGAC TCAG

654

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 715 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1675UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

GGATCCGCTT CCACACCGAA AACGCAGAGG ACCAGGACCG TGTCTCGAAT GTGGTTGGCG 60  
ACGCCATCAC GCAAGTCAAC ACGCTCTTTG GCGACAAAGG CATTCAAGCC TAGGTTGATA 120  
AGAACATCGT GTTCGTCCAG CAGTCCGGCC TGTCCGTGCA GGCCCTCAGG TTCTGTCTCA 180  
ACCACTACAA CTGGGTGAC GACACCCCTG GCTCCACCCC CGGGCACTCC CCGGCTGTCT 240  
CGCCCGTCAT GACCCCGGTC AATTCTCTGC TGGCCATGTC TCCAAGCACC GCGCATCTA 300  
AAACCCCTC GCGCGGACC GCAACAGCCA GCTACTTTAG CAATGGCGGT TCCACCAGTC 360  
GGTCGAGTT TGTCTGTGTC ACTGGGACTT CATCGCCGGT CCTGGAGCCG CTGTTCCAGT 420  
CTATCAATGA ACTGGCCAAA AAGGGGACC TGGCCTACGG ATCACTGTG GCCTACGGCG 480  
ACGCTATTAC CACATACGCT AAAGAGCAG TCGAAGGTT CAACGAATTA TTTGGCATTC 540  
TAGACAACT GAACTTCATT GGCTGCTGAG CGCCCTGTT ACATAGGTTA TTAATCAATT 600  
AAATCCTTTC TCTGGAACCT TATAGAGCCC TGCACCTTGC GCTCCGGACG CATATCCTTG 660  
CTGACTAGTT GTCAGCGGTA GCCTTTAATA AATTACGTAA TATGTGGTAT TATCA 715



## (2) INFORMATION FOR SEQ ID NO:1109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1676RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

GATCCCGACA CCAGCATGCG CTCGTGGAAC GGGTGAAGT CTGTGTCCAG CACCTGTGCC	60
GTGTGCCCCG GGAACAGAGG AATTGTGTCT GGGGCTTGC CCACTCTCTC CACGGGCACT	120
ACCGGGAACG CCGCTCCGCC CGACGAATTC CAGTAACCG AAATGAACTT GCGTTAGTC	180
TTGATGAGAT TGGAAATCCA AGCATTGATT GTCACCTTGA GGTCTCTGTA GAAGAGTTCC	240
TTCTTTGTG ATTGTCCGAA GACGTGTCTA TACTTGGAAG CCGGCACAAA CTTCCCACTG	300
CAGTGCCGTT AGTTTGCGT CCGCACAAAG TCAGTCTCTG GAGAGTATGA CATACTCAT	360
CCTTGCAATT CTTTGGGGTT TAGCAGCTCT ATATGCGTGT ACACCGTAAA CATCCGTAAC	420
TAAATATGTA ACGTGGAAC GAAGGGTACT GGAATCTAAA GGGGAAAGAA GTACCCGTTG	480
ATGGTGATGG TACTGTCAAG ATGGCTAAAG CGAACCTCTG GCTTGGTTGG AACTCAGAAA	540
GGTCACCAGA CTCCTCTTAT TCTTGTTT	568

## (2) INFORMATION FOR SEQ ID NO:1110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1676UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GATCGCGCG CTCGTGCTC GCGTGTATTA CTACGCCACG AAGCAATTGT ATAACCCACA	60
TATTGTAAAG TTTGTACTAT CCTCCATGGC CTGCCCCACC CGACACGCGG CCTTTCTGTC	120
ATTGCGGTGC CCGTGGCGC CCGTTTCAA CTTGGGCCA TGGCTCGGC ATTAGCTGCC	180
AGTAGCGATG CAACCGAAT GGGAAGATG GAGCGGCAT TGGTGGGTAC GAAAAAGCTT	240
TTTACGGTA CTGTTTCTG GTCTAACGA TCCAGCCAC GAGCTAACC AGTATGAATA	300
CCGACCTCTT TGGCAGCTG GTACTTGTC CGATCTCG GTCCCCATA GCGTTTGTG	360
TGCTTCTATC ACGGTATGCA ATGTTATGAT GGTGTGTCC GGAACATGT WCTAACAGGC	420
GACAGCGTGC TCGATACGCC GTGCGCGGG CTGGCAGCG CACTGACGGT GTACACAGTA	480
GTGTGAATG CGTGCTAAG CGCAACGG CGGCCAAGC TGGCAGGCG TGGACGCCAC	540
TGGAGCAGAT GCCGACGCG ACTTGCGT	568

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1677RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

5	GATCTGCAAT TAGGGCATAT AAAGTGTGGG TACTGTGTCA TCACTAGTOG GCGTATGCAC	60
	TGGTAGTGCC AACTATGCGA ACAAGGGGAT ATGAAGATGG CCTGGCAGGG CTTAATTTTA	120
10	CATAGGCAGA TTGAGCAATC TTCTCTCTCA AGGCTGCGG TTAGCTTTTG TAGGTTCGGT	180
	AGCGGGGCTA GTGCTCTTTT GTTGAACGGG TTGGCCCTTC GCTTCCAGGA TTGTTCAC	240
15	TGACTCTCA TTTTGACGCA TCTATATATC TTCTCTGTGC CGCCACGGAA ATCATTGCC	300
	AGCTGCAATA TGTCGCGTC TTTCAAGGGG TAGTCTTTTG ACATAACGGA TGCTGTGCA	360
20	AGCCGCATCT GATTAAAGGA CGTCCCGGAC GAGGACTTGA CGTCGGGCAC ATACCAATTG	420
	CCCTGCTCAT CCACCTTAAA CACCCCGTGT GTGGCGGACA CAACCTTGCT CTGAATACC	480
25	ACGGGGTGGA AATGATCCGG GAGCGAGCGG ATCGCTCGC GAACCCGTTT TGTTAAAGC	540
	CCGATAACCA ACTGCGAGCT GGGGCTGGG GTCGCGACGA TGGGATCAAA AAAGAGCCCC	600
30	GGATTATTGG TGGTCAGTGT GTCAATGAAC GCGGTAAAC GGAGCGAGAA GAA	653

(2) INFORMATION FOR SEQ ID NO:1112:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 625 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1677UP

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

55

GATGTGGCC TTAAGCCCTT CGCGGCTGC GCCTGCGCAG CCTCAATGC ACTCGTCCG 60  
5 CGTCGGCTAC ATCCAGAGC ACTTCAGGC GCGCTGCTG TTTGCGCAGA CGCTGGCTT 120  
CTTTGCGCAG CGCGCGTCA CGCCAAGCT CGTGCCCTTC CCTAGCGGCT CTGGCCACCT 180  
10 GATCCAGGGG CTGACGCGG GCGAGCTGA CCTGCGGCTC GGCTCACC GGGGTTCGT 240  
GCGCGCATC GCAGACAGC CAGCGGCGC CGCGCGGCG TACCAGATTG CCGGCACTA 300  
15 CGTGGCTCG CCACTCAACT GGGCGTCTC CGTGGCGGC GGTGCGCC TGGAGCAGT 360  
GGACAGCTG GACGGCGGC GGTGGGGT GTCAGGCTC GGCAGCGCT CGTACGTCAT 420  
20 GAGCTATGTG CTGCGCTGC AGCGCGCTT CGCGCGGCC TTTGCGGCG ATCGGTGTG 480  
CCACACTTT GCGGCTGC GCGCGCGT CACGACCG CGCGCGGAC GCTTTCTGT 540  
25 GGGAGCACTT TACCTCCAAG CGCTACAG ACGGGGGA GATCGGCTG CTGGCAACA 600  
TCCCCACCC CTGGCGCTG TGGGT 625  
30

## (2) INFORMATION FOR SEQ ID NO:1113:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 643 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: PAG1678RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

50 GATCGCTGT CGGCATCATC GGAGACATG CCTCCATGTT CCGGATGGT AGGATAAAGC 60  
55 AATTGTACG CCAGACTTGG GTCACAGAT TTATCAAGAA AACAGAAGT AACCCCACT 120

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TTAGTCAGGC AACTAAGGAT ACTGCTAGAT GGGCTAGAGA ACAACAAAAG CATCAACTAA 180  
 5 CCCTATAGCC TTACTATCCA GAATAATTTA TCTTATTACT CATTTTCTTC TGCGTTATCT 240  
 CGCTCTCTC CTGTTATCTT ATAATACTTC CCTGCAATG TCTTCATTAT TGTGTCGOC 300  
 10 TGCGACAGA CGCTTCGTT GTCTCTTCTT TTGTTGACC CTGCACTGAC CTGGCCATGC 360  
 TGCTCTTCTT AGTGGTTTGG TACAGGTGCG GGGTCTTTT ACACAACCTT TCTACTAGT 420  
 15 CTTCTATCTA ATCCATCTA CTTTCTACT TTCTCTCTT ACTTTATCGG TGGACCCGC 480  
 TGCTGCTCTT ACGTGGCAGC TTGTAGCATC TATATAATTG TATATATOGT GGTGGCAACT 540  
 20 ATCTACGGCT GCTATACATC TGCTGCCCGG TCTGATGGC CGAGCGGTC ACCAATGCAG 600  
 TAAAACCACA TAACTTTTA AGAGTTACAA GCTCAAAAAC GTT 643

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1678UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GATCCGGGTT CGAGTCCCGG GAGGGGCTGC AGGCAACCAG CGCTTCTTTT TGGGCTGGT 60  
 50 AGTCGAGGAT TGTTGACTGC TAAACCCATA CAACCACATA TTGCACTGGT GGCTTGCCCG  
 CCTAGGCGGC CTTGCGGCTC CCGGTAGCC CGCCGGGGG ACCACGCA CGAGACCGTG 180  
 55 CGGGCCCGGC ACGGCGATCA CCAGCGGCAG CCGGTGCAGC GTAGGGGGA CAGCTGAAAA 240

GTTACTACAA TTTGAGGTCT CGCATACTGA CACAGAGGGT CTTACACAGC ACCAGACGAA 300  
 5 TCAGCAATGG CTAAGCAATC TCTAGGTATG TGACAGAAAG ATGTGGGCTC CGAAACATTG 360  
 GGAATGAGCG TCTCTGGCGC TGOGATCCGT GGTAACCTGG GCATACGGCC CAGCGGCGAG 420  
 10 GCGGACCTAG CATAATCCAG TCGGTGGAAC AAGTTGGTGG CCGGCACAG TACTAACATG 480  
 TGTGCAGAGC TTCTCTCCGA CAGAAGAAAG GGCAGAAAG CGTACTTCAA CGCGCCATCT 540  
 15 TCCGAGCGCC GGTGATCAT GTCTGCTCT CTATCCAAGG AGTTGAGAGA GCAGTACAAC 600  
 ATCAAGTCTC TACCAATCAG AAAGGACAAC GAGATTATGG TTGTGGGTGG CTCCAAGAAG 660  
 20 GCCCAAGAGG GCAAGGTCT TCTGTCTACA GATTGAAGTA CGCTGTCCGC GTGACAAGG 720  
 G 721

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1180RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GATCGGCTG ACGGTGGTGG AGTTCGGAC AAACGCGGTG CTCTTTGACG AGATCGTGCA 60  
 50 GCCACTGGGC GAGATCATCG ACCTCTACAC CCAGTTCAGC GCGTCCACG AGATAGACCG 120  
 CGCTGTGGCG AAGACATTG AGGAGGCGAG GGAGGTATTT TTGTGCGCGG CGATGATTAA 180  
 55 CGAGAACAGC ATACTGATTG GCCACGGCCT GGAAAACGAC CTGAACGTAT TACCGATTAT 240

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ACATGATAAA ATTATTGATA CAGCTATATT ATACCCGAAT GGTAAGTTCA AGTCCTCCCT 300  
 5 CCGGAATCTA GCCTTTCAGG AGCTCAGTAG ACGGATCCAG ACGGGGAGC ACGACAGCTC 360  
 AGAGGACGCC ATTGCAGCAA TGGACGTGCT CAAGCATAAG CTGGGCATCC CGCTCGAOCG 420  
 10 CAAGACGTGG TAGCCCTACG GCTGCTCCTC CAGCCGGGTG AGCCTGTCTT CAAGCTGGTC 480  
 CTGCCTCTCA ATTAGCGTGT GTATAAGCTG CTTAAGGTTC TGTAAGTCAA TCGGATCAT 540  
 15 CCTATCTTCT GGAAGCTCGA ACTTGACGTT CCGCTGCGG GTCACGATCT GGCTCTTGCC 600  
 CACCTTGATC CTCGATGCGT CCGGAATTTT GCC 633

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1680UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

GATCGGGGCG CGCGGTGGCC GGCATTTCCG GAAGCGGCCA CGGAGCAGAG GTGGCGCAAT 60  
 45 CGAATCGCAT ACGTCTTCGC CACGCCGGAA AAAAAATTTT CGCTATATA AGGAGAGGCG 120  
 GCGTCTTGC TGCAGGCAGT TTCACTTTCT CTAAAACCAA AGAACATCGA TTTCTTTAGT 180  
 50 CACTCGCTTC CTTACACCGA AATGCAATTC TCACCGTGG CTTCCATCGC AGCCGCTGCC 240  
 GCGTGGCCT CCGCTCAGC CAACGTGACC ACGGCCACCG CCACCAGAAA CCAGACCACC 300  
 55 TTGGTCAACA TCACCCACTG TGAGGACAAG ACCGCATGCA CTGCCACGT CTCTCCAGCT 360

5 TTGGTCTCCA CCGCCACCGT CACCATCGAC AACGTTGTGA CCTTGAGCGA GAACCTGGTGC 420  
 CCACTATCCA CCACTGAGGC TCCTAAGCCA CCAGTTTCCA CCGCCAAGCC ACCTGCTTCC 480  
 10 TCCAACGGGA CTGTTCTCTC AACTGAGACC CAGTGTCTC CTCCTTCACT GGTGCCGCTG 540  
 CCAAGGCCCT ACCAGCTGCT GGTGCCTTGT TCGGGGGCCG TGCTGCTTTG TTGTTGTAAG 600  
 15 TTTAGTTCCG CCGGTGAGC CCTCGTTTCG TTAGAGATA TATAGGAAC TATGTGACTG 660  
 ATTCTAAGCT TTTACACCAG CATGATTGG TTCTGGGGCG CACCGA 706

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1681RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

40 GATCATTTCTA AACAGATTAA CCTTCTCTCA AATTACTTTA TTTCCTTAAT CTCGATAAA 60  
 TGGTTACATT GCGACAATAA GGTGCCCGTG GTGCTTACAG ATATACATCT ACCGAGAAAA 120  
 45 TTTCGGCCAC AACTCGTAT AGAAGAAAGA AATTGATTG AACTTCTGA GCTAGATCCG 180  
 ACGTTCAGTG GACTCTTCCC ATTTAAGGTT TTCAACAAAT TCCAACTCA TGTGTTTAAT 240  
 50 GCCTTGTACC ATACCGATGA AAATGTATTT ATTGGAGCTT GTAAGGGCTC GGGTAAAACT 300  
 GCAATGGCAG AATTAGCTTT ATTGAGTCAC TGGAGAGATG GTAAGGGACG TGCCGTCTAT 360  
 55 ATATGTCCAT CTCAGGAGAA AATTGATTTT CTGGTGAAGG ATTGGCGAAA CAGATTTTAA 420



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AATGTGGCAG GTGGAAAGGT TATTAATAAA CTCACATTGG AATTAAGTAA CAATCTTGA 480  
 5 ACGCTAGCCC AGTCGCATTT AATCTTAGCG ACCCAGAGCA GTTTGACCTG CTTTCTGTC 540  
 GCTGGAAAAG AGAAAAAAC ATCCAGACAT TAGAGCTGTT GATTCTAGAT GATCTTCATA 600  
 10 TGATCAGTAG TGACTTGCTT GCGCAAGGT ATGAAAATAT AATATCCAGA ATGCTGTICA 660  
 TTCGGGGTCA ACTTGAAAAC GGCTTGCGT ATAGTC 696

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1681UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

GATCAGGAAT GATCCTCAA TTGTCAGGAA TTATGGTTC ATATTGGTTG AATTGCCAA 60  
 GATTACTCCT GATGGTATGG TANTGTCTT CCCCTCATAT TTATATATGG AATCATTAT 120  
 40 TTCAACTTGG CAGACAATGG GGATTCTAGA CGAGGTTTGG AAATACAAGC TCATCCTCGT 180  
 GGAAACACCA GACGCACAGG AACTTCTCT AGCTTTAGAG ACTTACCGAA AGGCTGCTC 240  
 45 GAATGGGCGC GCGCAATAT TACTTTCTGT GCGCGTGGG AAGATTTCTG AGGGAATTGA 300  
 TTTTGACCAC CATTACGTA GGACTGTATT GATGATTGGA ATTCTTTTC AGTACACTGA 360  
 50 ATCGGTATT CTAAAGGCGA GGTAGAGTT CCTAAGAGAA AACTATCAGA TACGGGAAA 420  
 TGACTTTTTA TCCTTTGATG CAATGAGACA CGCGCTCAA TGTTTGGGAA GAGTCTTGAG 480  
 55

GGGTAAGGAT GATTATGGCG TGATGGTGCT CGCGATCGG CGATCTCAAG AAAGAAAAAC 540

CAACTTCCAA AATGGATCGC ACAAGGGCTC TCTGATGCTG AACTGAACCT TTCTACTGAT 600

ATGGCGATAG CTAATACAAA ACAATTCCTA AGGACGATGG CACAAGCAAC TGATCCGAA 659

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1682RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

GATCGTAAAA TTGCTATAC AATGGTTTGG GTAGGTCTT TAAAAGGTGG TCAATCTCAT 60

AGTCGCTCAC ATCAAGGGGA ATGTTTAAAA AACGCACTCT CTGATGTGTA GGCGGAGGAG 120

GCCTTGCGTC TCGCGGTCC CTGAAAGGTG AGCGGCGGGA GGGGCGGTAC TCTCGCGCCC 180

GATACGTGCT TTCCCCAGA CCCATGGGTG AAGCTAGTCC ATTACGTAAG TCTCGAGGCG 240

GATATTGCTA TAATAACAAT GTAATCGTTA ATACTCAGC TCAAGTAACC TTGCGGTGGG 300

TCATGTATCA CTTAAGGTAG TAGTGGGTG TGTCTTTTGG CCGTTAGTAT CGATGAAGT 360

TTGGTATCGA GGAGAAAAAG ATGTCATAC TTTCTACCA GTACCCCTGGT TCAAGTGTTT 420

GTCAACAGAC ATTGTCCCTT CCAAACTATC CTGTTTGAAG GGCAAAGGCT GTGTGTCAAG 480

AACGAAGTTT TCACCATTTT TCCGAAGGC TCGGGACAGC GATCGAAAGA AATAGGATAT 540

ATACGTACAC CTTTCTTTAA ATATCATTTA AAATATCCTG GAATTTGGAT ATGTGGCCAT 600

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ACTGGCTCTT CAGCTTCCTT ATCCATGAGA TAGAAGGAGC AACTGTGCG AAGGTGCCCTT 660

5 CCACAGTTAC TTAAGTTTCC GTAAGCAACA AGGAGTCTGT ATGCGGC 707

(2) INFORMATION FOR SEQ ID NO:1120:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 700 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1682UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

30 GATCCAGTGT GTACGGCCAG AGTGGGCTG GGGCACCAGC AGTACCTGCT CCGTCTCGTT 60  
 GAAGTTGCA ACATTCCCGT CCGCATCAGC ACCGGGCGCTG AAGTATCTTG TACCGGCGCT 120  
 35 GAATCTGCTC CCGCGGCTGA TCAGACCCAC ACTAACTGGC GTACTCTGCA ACACAGTGTC 180  
 TACCACTTIG ACGTAGCCGT AGATTAGGG CAGAAGAAC TCGTTGGCCA GAGCGTTTTC 240  
 40 CTCGGCCAGG TTTCGCAGCG GCTCTGTGGC ATAGTAGTTC CAGAAGAAC GCGTGTCTGC 300  
 AGTGGGCAC GAGGCTGGCC CCAACCTTC GTTCGGCTGC ACAGAGTGGC TCAAGTCATA 360  
 45 CGGTACGAA TAGTACAGCG TTGCTTTCG GAGGTGGTGG CCGAGTAGCG CAAGATACTG 420  
 GTGTCTCTCT GCAGATGGCC GGATACTGGT GTTGACCAGC ACCAAAGAGT GCGCGTTCAC 480  
 50 TTGTAAAGA GAATGGGCAC CCAGGTTTCC CACCACCTCC ACCGGGTCCG CCGTTAGCAC 540  
 CACGCGACTA TTGGGCAAAT GTAATATCCC GATCAGGCCT GCGATCTTGC GAGTTTCTCC 600  
 55 ATCTTTAGGG AAATTGCTGG GGTCTACGAG TGTCAAGCCC GAATCGTGAT GCGAGATAGA 660

CAACACCGCT TCACTCTGGG AAGTATTAGA TGGCTTGAAA

700

## (2) INFORMATION FOR SEQ ID NO:1121:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 652 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1683RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GATCTATATC ACCAATCATC ATGGTITTTGA AACATTGGT GCTTAAAAAG GGACACAGCA 60  
AACTACAAGC AGGCAGCAGC AAGCACTCTG CAGACTAAGG GCAGGCTCA TCATAAGATG 120  
CTTAGGGCTG AGCTAGTAAA TGCCATTCOG TGCCAAGGTG CTCAGTGIGT CGCTGTGGTT 180  
GATGGGGTTC GACAACTTGT GGTGGTGCGA AATAATAGGG ACTTCTTGGT GTACTCCAGT 240  
ATGGACGAGA GAGGCTCGC TCTAGTTCAG ACATATACAG AATTGCTTGG CCGAATTAT 300  
GGTGTAGAAG AGCTGCTGTA CTCGGAACGG CTGCGGACAA TATTGCTCG CACGACCAAG 360  
TGCTTACTGC TACTTCATTC GAGCAACTTA CAACATTACG ACAAGATAGT TGACAAACGA 420  
GGCATTGACC ATGCTTGGCT GTTGAACAT CCATGTGGGA AGCTGAGAC GTGGATGACG 480  
GTGCTTGTTT ACTCGGTCAC AGGGTCGAGC AAGATAAAGA TGCTGACATG GGTGGGGCGG 540  
CAGTTCCAAG CGGTGCATGA GGTCCACTA GGCACCGAT CGGAAGTCAT CCAGCTCAGT 600  
AAGTGGCGGC CCGCATGCTG TGTGGTGTCT TACCTCGAC GACTGTATAC CA 652

## (2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1683UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

GATCTGTCA AATTCTGCTC TAGCATTATC AACTTTGTGA CCACAACCTTA GAATTCCCCC	60
ATCATGCATT ATGTTTATAG ATGTACAGTT CTAAAAAATT CGGTAATATA ATGAGACCTA	120
TCTCTTTTTC TCATCCTTAT AGTCACCCAA AGTTTAAACA TGIGACATGC TGCCAGATTT	180
ACAGTCATCT GCGGCTATGA TTTCTTGCG AGAOCCTGCC CAATTATAAT GTGTTAATAT	240
ATTGCTTCCT CTGAGGTGA AGAGCGAGAA AAGTTCACGT CTCCTAATG TTAAATTCCT	300
CTGGCAAACG TAGCAGCGGT TATCTTCATC TACCACCAA AATTCAGATA TGATCTGGGA	360
TAAGCGATAG GTGCTTCGA TGAGGTGAC TTTCAAAGA TTGTTCTGTA TAOCGATTG	420
GTTTTCTTC ATGGACGCAC TTTTAATCCT TCTACTTAGG AATTCGTTAA GCGTGTATTAT	480
CGAATATTG GCGGCAGTT TCTCAAACAA TGTTATCGCA TCTAGCTTCG AACCATTCTC	540
TAGCAGAAAC AGATGAACGT TTCTCCATCC GCTAAATCT ACCTTCGCAA GCAGCTTTTC	600
AAACAAGTTC ATGAGAGCTG CTGTGCTGC ATTTTGTGTT GTGGCATAGA GCTCATTACA	660
ATATAGAGAA GCTTGTTTAT AATTCCTAG ATCATCAACT AGGATCCCTA ACGCTGTT	718

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1684RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

GATCTGTACA CTTCAATATC GAACGAAGTG TCACCGGCAT ATTCTGCAGA GATTTGAAAA	60
AGCCAACAAA GCAATATGAC ATCAGGGTAG AGCTTGGAGC GAGTAATCTC CGGTGATTGG	120
TCGATCTCCT TTAACCAAGC AGCAAACCGT GTCTCATGTT GCTTTTCCCA GCTAATAATC	180
TCATGCACCA CAGCCATAGA TTCAGCATAA TGAAGGTATG TTGCGCGCGC CTCATTACAC	240
CATTIGATAT ATATTTTCCC CAGGCCATCG ATGAAGTTCC CTTTGGTCTG CAGCTTCCCA	300
AAAATAGGTG TCAAAAGCAG TTCCTTGTC AAGTCAATCA GCGGATAAAA GATGTCAAAG	360
GCAAGAGAGG CGAAGTTTTC GTGGGTGGGC AGCAACGCGG GCGAGAATTG TGCGCGTAG	420
ATTTCTACGG CAGCATGGGC CAGGTTGAGA CTTTCTCTTT CGAGCACAAT AAGGTCAAAT	480
ATGTAGCTCT GCGCTTTTAC TTCTCTAGGA TTAATCTCTG AAAGCTCCTC GTCCGTCACT	540
TTCCAGTACT CGGTCCAAAG TCCACCGGG CGGCTGA	577

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1684UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

10

GATCCATGAC GAGCAGCTGG ACCTGCTGCG CGCTCTGGGC CTGGGCGCAG AGAACAAGGA 60

AACGCTGCAG AACCTCCCGC TGGGCGCGGT CAGGTCACG TTCAAGGACG TGGTGAAGGA 120

15

CTACTGCGAG GCGCAGGGCC TGCTGCTCGA AAAGACGGGC GAGTGGCCA CCTCCGGGT 180

CTACCAGCAT GCAAGTACTG TCCGGTCTT CACGTCACA CAGTACACC GCGCGCGCG 240

20

TGTAGCTCTG TGGAGGACG TGCTTTGGGT TCAGGAAGGG ATAGGCTTCA AACCTAAGTA 300

CTTATACGAA CTAGAACTC TTCTAAAGAG CGCTTAGTCG TTCATATAT ACAGGACCTA 360

25

GTACTCTTGG CGCACTCAGT GCGCTCGTC GCTTTTCGGG CTCTGGGCG CGGCTCGGT 420

CTCGGCAAG GCTGCTCCT CGCTCTCAG CTGCTCGCG TAGTGCTGG GGTCCTCGG 480

30

GAAGCATCCT GCATCACTG GAATCTCCA CGCAGTCAAT CCGCTTAGC TGGGCTCTG 540

AGTACAGGAA GCAAGGGAAC GCAGCCTTGA ACTCTCGCC GCAAGGCGCG TGGGCGATGC 600

35

CGCCAGGCA TGGGCGTCC CAGTGTATCT CGCCGCTGC GCGATTGTAT GCTCTGCTG 660

CCCTGGGCAG CCTCAGCGC GCTAGCTTTG TCCTCCGCG CGCTCGG 707

40

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

55

(A) ORGANISM: PAG1685RP

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

10 GATCAACTTC GCCTAATCCC TTAATCATTG TCACTGCTAA CTTGAACTTA GTCGTGTGIGT 60  
ATGCCCTATAG TGAACGTTTA ATGTGATGGT TTTATAGTAA TCGATGGAAC TTTATCOGCG 120  
15 AAGCCTCAAG CTGATCATCA CGTGAGTAAC CGTCGATATG CAGAACAGAG GATACCATAA 180  
ATTGCTATTTA GTAATCAATT AATAGACTTA CATATAGCTC AAAGCTGATC ATTGATGCGT 240  
20 CTCAAACTCT TTTCATCGTC TGAACCTTTC GGATTTCAC TTCTGTATC ATTATACCAT 300  
GTATAATCCT CTAGTACGCT AGTAGTCTAG TATCTGGAT AACCCCCCTA TATTACATAT 360  
25 AATATGAGTA AAATACAGAA TGAAGTTAGC GGATAATCTA AGGCTAAGGT TGCCTACACT 420  
AAGTTAACGG GGGGCTTCTT ATCTTGACG TTGTCTTCT AATCAATAGA ATTGTTTTC 480  
30 TTTTTCACCT ATTTGGTCCC TGCCAACTG CGAGCCACC CGGTATCCT TAGCCTCTGA 540  
GGTGTCTCT TCGACATCAC CTGTGCTCT CCGGATCTCT CCGGACGTGG TTCAACTGTA 600  
35 CGCTCGGTGC ATATTTAGTG TGCTCAAGGT TGCTGAAAAT AGATGCGAGC ACCTGTGCCA 660  
GATATT 666

40

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 642 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: PAG1686RP



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

5	GATCCTCTCC GAGGTCAAGA GTTGTGTCAT GAATTAACTT CATTTTAGGA ACAAACCTGT	60
	CTAGGGTTCC CGCTACTAAT TCCTGCTCGA CTTTGAAATC CCAAAATTTG ACAGTCTTGT	120
10	CTGGGAGGC AGTCACTAGC CTCTTCCCAT CACTAGTTAG GTCTAAAGAC CAGATTGCAG	180
	CGGTGTGTGC CTCTTCAATA TTTTCTAGCA TAGTAGAAGA TCGAGATCA AATAGCTGAA	240
15	GTGGCCCCG TCCTGTACCC AGAATAACCA AGGCGCACCC TGGTAAAAAC TTACAGCATA	300
	AAGCATAGCC ACAGTCAAGA TTGGGATAC AAGTTTTAGT CTTGATGTTT CAGACCTTTA	360
20	GGTTCCATT TGAAGCAGTT GCTAGTAGCT TATCATGGCT ACTGATGTCT GCAGCAOGTA	420
	GATCAGTCTT ATGGCCCCG GATTCGATAC TATGCAATTT GATCGCAGTA GGCTGGAGCG	480
25	GTTCCTTCTT TTTGTATGGG ATTGAGTAGT ACTCTATAGT GTTGTTTGCA GTGTGATCA	540
	CCAGTTCCAA TTTAGATGGG GTACAGACCG TCCATGAAGA TGCTTTTAGC TTAAATAGGG	600
30	ACCTTACGAG TTGGAAGG ATGCAAAAGT AAGTTGGCAT AC	642

(2) INFORMATION FOR SEQ ID NO:1127:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 675 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1687RP

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

55

GATCAGGACA GTAGCAGCTT GACTGAGTAT CAGCAGGAAA AGCCTAGCTA ATTGGGOGGA 60  
5 GTACAATTAC AAGTACCTGT CTGACTACTT CTTTTTGTGG GATGCCATAT TTTTLAGGAT 120  
GGCCTGCAAC GGCCCGGTGG GGGGCGCATC CAAATTTATG GAGTTGAAGA GCTGTTCAAT 180  
10 GGCCTTTATC CCATCTGCAC CGTCTTTATC GCGGAACATG GCATGCAACT CTTCAAGCAT 240  
GATATCTTCT TCTCTGTCT CTGATCGGC GTGTGTGTCT TTTGGCAGT CTTGTAGGC 300  
15 GCCATTCTG TAATGTTGAA GCTGTTCTTT GTTCATCTC AGACCTCCG TCAGGAAATA 360  
TTCAAAGAAA TCGTCTTAC TAATATCTAC GCTTCACTC TCGAAAAATG TCCGAGCCTC 420  
20 TTCATCCCCA GCTGAAGACC CCGACCAGA AACATGCTCA TTGCTACCTT CATGTCATC 480  
TTTAATATCT GTCAGGAAAG TCTCCAGGA CAGGGCCAAG GCATCCATAG ACGCCTCTTT 540  
25 GTCCGCAGTC GGTACCTCCG TAGTTAATTC AGTCGTAGAG AACTCCACCG GCGCTCTAG 600  
CTGTTTGTGA TGTACCAGAG CGCTTACTAG GTCACCTCT AACTTCTCT TGGGTCAGC 660  
30 TGTCGTTAAC TGGCC 675

## (2) INFORMATION FOR SEQ ID NO:1128:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 655 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- 45 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1687UP

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

55 GATCCGTTCC AGTTTGGCCA GCGGAAGCTG GCGGACGAGG CGGACATCTG GGCTCATAAC 60

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GGGTGGGATA ACGTAGACTG GGGTGACGAA CAGATCCGGC TCGCAAAGGA GAAGATAGAA 120  
5 GAGCAGAAAG AATACCCGGT GCAGGAGTTT GACAAAAAGC TGTATCATAG CAACCCCGCA 180  
AGGTACTGGG ATATATTTCTA TAAAAATAAC AAAGAAAAC TTTTCAAAGA CAGGAAGTGG 240  
10 TTGCAGATTG AGTTTCCCTC TCTATACGAA GCTACCAAGA AAGATGCTGG TTCAGTGA CT 300  
ATCTTCGAGA TTGGGTGTGG TGCGGGCAAT ACCATGTTCC CGATCTTATC TGCAAACGAA 360  
15 AACGAACACT TACGCGTTGT GGGTGCGGAC TTCTCCCGA AGGCCGTGGA ATTGGTAAAG 420  
ACGTCCAAA ACTTTAACC CGCGAATGCC CACGCGACGG TATGGGACTT AGCCAAACCT 480  
20 GATGGTCTTT TGCCCGATGG TGTGAGCGG CATTCGGTGG ACATGCGAGT AATGATTTTT 540  
GTTTTTAGTG CCTTGGCGCC CTCACAGTGG GCCCAGGCTA TGGATAATTT GCACAAAGTT 600  
25 CTAAACCAG GCGGTAAGAT CCTCTTTAGA GACTATGGCA GGTATGACTT GGCTC 655

(2) INFORMATION FOR SEQ ID NO:1129:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 716 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
40 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1688RP  
45  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:  
50 GATCTTGTG AGAACA CTCA ACATCGGCGT AATTGCAGAG CCCCCGGTGA CCATACCGAT 60  
TTTCTGTGAC GCATTGCTCA CATAGCTGAA CCGTCTTACA GGACCTTTGA ATTCCACAGT 120  
55 TTGGCCTGGC TGTAGCCAG CAAACCATTT GGATACCTTA CCGTGGACAT AAGATTTGAC 180

AATGATATCG AAATGGCCCT CGGCAAATTT GTTGGAGATA GGCGTGTAGT AACGCCTTC 240  
5 TTCTACACCA TCCAGCATCA CCTTCGCAGC TAAATGAAAG CCAGTAGGTA TATCAAGAGT 300  
TTCCACGCTT GAACGGAGCT TGAATCTGTA TATCGCAGCA TTTTTCCTTA GAACGATCCG 360  
10 TTCTTCCAAT TCTAATGGCG TCCACTCAIT TGAAGAATT GAAGTCTGTC TTCTGTATGC 420  
TAGTAGCAGG CGTGCACTTA CAAACATTGC CAAAGCTAGA ATGCCTAGAA GGTACCATGC 480  
15 GTTCCCGGCT GACCAGGCGA TAACAAGAAC GCGCAATGTA AAGATGCGGC TGGGGATGAA 540  
GATCCCATGA ATGGGATCAT CCAATATCTC CATACTCTG CGTTGGTCA TACTAATATT 600  
20 TTGAAAGCTC GTCGTAGCTA TCGTCTAGTA AGGATGAGAA CGGTTAATAT ATGCTTCTC 660  
CTAGTTCTAT AAGCAGGAC TCCTTTGCAA CTGGTGAAGT ATCGTCTAAC GGTCAAT 716

25 (2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 676 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: PAG1688UP

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

GATCAGGCGG GACGGTACT TGCAGGAAGG CCTCAAGAAA CCCAAGGGGG GCGAGGAGGG 60  
50 CTTCTCGAGC TTTTTCACG AGACGGGCTC GGCACAGTTC GTGCGCGCGG CGGTGTAGCT 120  
GGAATTGGAG CGAACGTGA TCGACGAGGT GCGACGGGC GCGTACCGCG AGTTGTTCOA 180  
55 CCGGAGCAG TTGATCAGG GAAAGGAGGA CGCGGCGAAC AACTACGCGC GTGGGCACTA 240

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CACGGTGGGG CGCGAGCTCT TGGACGATAT CCTAGACCGC ATCOGCAAGA TCTGGACCA 300  
 5 GTGCGACGGG CTCCAGGGCT TCTCTTCAC GCACTOGCTT GGOGGTGGTA CGGGCTCOGG 360  
 CTGCGGGTCT CTGCTTTTGG AGCAGCTTTC TATCGACTAC GCGAAGAAAT CGAAGTTGGA 420  
 10 GTTTGCCGTG TATCCCGCGC CACAGGTGTC CACCTCGGTC GTGGAGCCAT ACAACACCGT 480  
 GTTGACCACC CACACCACAT TGGAGCATGC CGACTGTACG TTCATGGTGG ACAACGAGGC 540  
 15 CATCTACGAG ATGTGCAAGA AGAACTTGGG CATCTCGAGA CCTAGCTTTG CGAACTTGAA 600  
 CAACTTGATC GCGCAGGTGG TCTCTCGGT GACCGGTCA TTGGGTTTGG ACGGCTCCTT 660  
 20 GAACGTGGAC TTGAAC 676

(2) INFORMATION FOR SEQ ID NO:1131:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 700 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: PAG1689RP

40  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

45 GATCGTGCAC AAGTTTGACG AGCTAAAGCT AAAGGAGGTG TTGTTGAGAG GTATCTACGG 60  
 TTATGGTTTC GTTGACCCAT CTGCCATCCA GCAGGTGGG ATCTTGCTA TCATTGAGGG 120  
 50 CCACGACGTT TTGGGCGCAGG CCCAGTCCGG TACCGSTAAG ACTGGTACCT TCTCGATTGC 180  
 TGGGTGTCAG AGAATCGAG AGAGCATCAA GCGCCACAG GCGTTGATC TAGCTCTAC 240  
 55 CAGAGAGTTG GCGCTACAGA TCCAGAAGGT TGTGATGGG CTTGGGCTGC ACATGGACGT 300

TAAGGTCCAC GCTTGTATCG GTGGTACGGA CCTGTGTGAG GACGCGAGG CCTTGAGAGC 360  
5 CGGTGGCGAG ATTGTGTGTC GTACCCCCGG CGTGTGTTC GACATGATTG AGAGACGTWA 420  
CTTCAAGACT GACCACATCA AGATGTTCAT CCTGGAOGAA GCGAOGAGA TGTGTCTCTC 480  
10 CGGCTTCCAG GAGCAAATTT ACAAGATTTT CACCATGTTG CCACCAACCA CCCAGGTGCT 540  
GCTATTGTCT GCCACCATGC CAAAGGAGGT GTTGGACGTG ACGACAAGT TCATGAACAA 600  
15 GCGGTCCAG AATCTTGGTC AAGAAAGGAT GCCTTGACCT TGGGAGGTA TCCAGCAGTA 660  
CTATATTAC GTGAGAGCG AAGAGTACAA GTACGACTGT 700

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1689UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GATCGCGCTG AACCTCAGCG AGGCAAGGCT GGTGATCAAG GAGGCGCTGC AGCACCGGCG 60  
45 GCGGTGTTC GGGCAGTGGC GGGACGGGCT GGAGGAGGAC GAGGCGGACG GGGGAACACA 120  
ATATGACGCA GGAGAAGGAG CTGGCGATGC TGGACAAGCT GCTGGAGAAG ACGACGGGGG 180  
50 GACAGAACCA GCGCTGAAG CAGACGATGG TGTACCTGAC GAACTTGGCG CGGTTCCGGG 240  
ACGAGGAGAC GGTGACGGCG GTGACGCAGC TGCTGGCGTC GACGGGACTG CACCGGTTCG 300  
55 AGATTGGCCA GCTGGGGTGG CTGGCGTGGC AGGACGGGGA CGAAGCCAAG ACGCTGGTGC 360

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CGAGCCTGGG GAACAAGATC TCGGACGAGG ACCTGGAGCG GATCCTGAAG GAGCTGTGGA 420

5 ACCTGGAGAC GCTGTACTAG ATAGCTACAT AGACAGGAAG AACTTGCCGC CGCCGCCCGC 480

CCACCAGTGG TOGAGACAGG AGTGCGATGT GTGCTCGATG TCGACGGCCT CGCGGCCGAA 540

10 GTTGCAGACG CAGCGCTCGC CGAGACGGGC GACGTGCGCG GAOGGGCAGG TCGCGTAGGG 600

CACGTGGAAG TTACCGATCT CCTCGAAGTG GTGCACTCG TCGCGCGCA GGAACAC 657

15 (2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1690RP

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

35

GATCTGAAC TAATGTCATC CGCGGAAGAA CATACTAAGA GCTCATCGTT ACATCGAGAT 60

40 GAGACAAAGT ACCTGATGTA TAAGAGTTTT ATTGACATAT GCGCTCGGAG GCAAACGGCA 120

GGCTACCGCC TGCCCCGTTT TCGTCTACA CATGACAACA TAATTGTGGC AATGTCAGGC 180

45 GCGGTGGACT CTTCAATATG TGCTGCTTTA TACGCTCACT TCCCAAAGT CCGTGGGCTC 240

TACATGCAGA ACTGGTCGCA GACGTGGGGC TCAGGGCCTG TAGAGGGTAA GCGCGAACCT 300

50 TGTTCAGAGC AAGATTGGAA GGATATTGAG AAAGTGGCG CGTACCTTAA TATTCCCGTC 360

GAGAGAGTCA ATTTOGAACG GGACTACTGG CTGGATGTTT TOGAGCCTAT GTTACAACGG 420

55 TATCAACAGG GTTATACTCC GAACCCAGAT ATTGGCTGCA ACAGGTTTGT AAAGTTTGA 480

GCGTTGCGGG AGCACCTGGA CAAGGAGTAT GGACGGGCA ACTACTGGCT GGTAACAGGC 540  
5 CACTATGCGC GAATCCTATC CCCCAGACT CGCAGAGAGA CCCAOCCTGCT GCGGAGCCAT 600  
TATGCGCCAA AGGACCAAAG TTACTACTTA TCCCAAGTCC GGCGGGAGGC CCTCGCGGAC 660  
10 CTCTTTAATG CCCATGGGAT TTCTAACAAA ACCGGAAGTC CGACAATGGG CCGCAGAA 718

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1690UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

35 GATCAGAAAC ATCACCATAT GGTGTCTGAA GACCTTACGG CGACGGTGA TACAAGCTAC 60  
CATCTCCAAG CCGATGATGC CGCTATATAT GGACACGGCC GAGCGCGTGA TTGCCAGGAT 120  
40 TGCAGCTTC AGCAGCTGGC TCGAGGTGAA CGTCGAGAAC ATCCCCGGCA GTCCGAGCAC 180  
GAGGTTCAAC GTGGTGTGT TGTAGGACCC GAATACACAT GTGTAGTTGC TGTCCATGCA 240  
45 CTGTATCTGA GACGGGCCCT CCATCTTGCA CGTGGGTGGC CTACAGTCT AGCTCCCGCT 300  
CGCACCTATA CTTTGTATCT GTTTGGCCCT TGCTGGGGC TAGCCCCCTC GCGCTTGCTT 360  
50 CTTATCCCTT CTGAAGTGC TCTCCCTAA GTTGATCC AGCGACCTCC TAGTCGAAAA 420  
CTGCTGTCTA CGTTGGCCAG GCACTAGTTG CCTCCACTG CAGGTTATCG ATAAGTCCTA 480  
55 AAATACCACC AAGCAGGGT TGTACTGCTT CTATACGCA ACCCTCGCTT TTGTTGGGC 540



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TGACACACTC AAGTGACTGC AAGAAGACTA CCTACTCAC AGATACCGTC GTCCGTTGTA 600  
 5 CGCACGCTAA AAGACAAGTT AAATCTACGA CACATATAGT GCCTGCAAG CTCACCGCAT 660  
 CCGGAAGGAA CAAGCTATTA GAACTGAGA CACCTC 696

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1691RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

GATCTTCCTT GTATTCTGG TCTTACCTGC CCCAGACTCC CCTGTACTA ACACCGACTG 60  
 GTCCGCTC TGTTCAACA AGTTGGGGTA TGCTGCTCC GCTACGCAA AGATATGCGG 120  
 CTGTTGCTT TCCTGGGTG ACCCATGGTA CAAGTTCACA TAGTCTGGG TGTACACCTT 180  
 GATGTTGCTG TACGGATTCA ACGGACGAG GAATAGCCCA GAATAAGTAT ATATCATATC 240  
 GTCTTGTAT CGGTCTCCA AGTTGTACAA CACAGACGCC TGTTCAGT GGTCAACTC 300  
 GGACATATCG TCTATCTTGT CAAACGTTGA CGGATTCACC GCGGGGTCT CCACCTCCAG 360  
 CACTTCTCGT TCCTTGCCAT TCACTCTCAC AAGACAGACC TTCTCATCTT TGTCTGTTT 420  
 GTTTTAATT GTCTTTGTTG AAACCAACTG TCCTTTCACA AACACCTCT CAGCATCTGG 480  
 AACCCAAATC ATTTGACATT GTTCACTCAT CGGGACAGAT GCTCTTGAAC TTATCTAATA 540  
 TGCAATAACC AAATTCAACT TTACTTTAAT CACCTGCTG TTACACACGA AGCAATGTTG 600

GATCTCATAT TCACACGACC TACTTTTTCG AAACACTTAT TTGTTTATGT CGGCTCGAG 660

5 CATACAAGTC GGTCACGTGA CAAGCGCATG TAC 693

(2) INFORMATION FOR SEQ ID NO:1136:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 705 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: PAG1691UP

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

30 GATCATTATG CAACCGAATC TGGTATCTCA GAAGATTACC GTAGGACTGT GCCTGTCCGA 60  
TCGATTACGT TAGTGGGGTA GAGAATGAAG TAAGAAGCAG CTCTGCGATT ATTGTGCTTT 120  
35 TGCGCTCAT GTGAGGTAAA GCGCTATCCC GCAGGGTGGC GGCTTTCTGC AAGAAAATCT 180  
GGGCATCAG CCCCCGAAAC GAAATGCGAT AGTCACCTGT GCCATGGCGA CGATCATTT 240  
40 CCCCATTCGT ACAGAAATGA ACGGGCAGAA TCGGGTAATG GATTTCCTGT GCGTTCTGTG 300  
CCAAAAGGTG ATCTCCACCT GGTGCTGCC CTGCGGGCGT GGTGAGCAG AGCACCTGGA 360  
45 AAAAGAACAG CACAGAAGGC CAATGCAGTT GGCCAATTGA GGCAATAGCC GAGCAGGAAC 420  
AGTCGAAAGT GGGTGTCTG GCGCTGTTGG ATCTGAAAAA TGCAGGAAGT TACAAAAAAC 480  
50 AGTGGGGCAA TACATAGAAA CCGGCGACCC GGCGATCGCC TAATCATCTG CCATGGAGAC 540  
GCGGGTCCG CGCTGAACC AGCGGTGAA ACCGTGAGG CATGGTGATA CCGGCCCGTC 600  
55 GCGGGGCAC TCAACAGGC ACGTGTAAAT CCTGACAAA CGCAGCGGG TAATTCCTTT 660

CCGCAAGCCG GACGGGTATA TGAATOGTAC GATACCAATT GTCGA

705

## (2) INFORMATION FOR SEQ ID NO:1137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1692RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GATCTAAATA TATATAATTT AATTTATAAA GATTAATATA AACTTTTTTA TTATAATATT	60
TAAGTATTAA ATTATTTAAA CTATTATTAT CATTATTTAA TAAATTAATT ATTGATTAT	120
TAATACTTAT TATATAATTA TTATATAATT TACTTAATTC ATCATTATTA ATATTTATAT	180
AATTATAAAA ATAATATTTA ATATGAATAC TATTTAGTCT ATGTTCAAAT TTAAATTAG	240
TTATTAAAAT ATTATTAGAT ATTATTATTT TCTTTAATAA ATTATTAAAT AGATTATCAA	300
TAATTAATAT ATTATTTATT AATTGTTTAT TAAAATAATA TATTTTATTA TTATAAAGAT	360
TTAATTTATT TAAATATTGT AAATTATTAT TTTTATTATA ATATCTATTT TTATAAATAT	420
TATGTTGATT TATATTATTT AATCTTTTTA TAAGAATTAT TATTAAAATT AATTTTAACT	480
TTAATTTCTT ATTATTAAAT TTTATATTAT TTAATAAATT ATATTCATTT TATTTATTTA	540
TTTATTTAAT TAAATTAATT ATTTAATTAA TATTTTATCA TTATTTAATT AATTAATAAA	600
ATATTATAAA GAATGTAGTT AAAAATACTT ATAAAA	636

## (2) INFORMATION FOR SEQ ID NO:1138:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1692UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GATCTTGATA CTAGAGCTTA TTCTACTCA GCTACTATAA TTATCTTAT TCCTACTAGT 60  
ATTAAAGTAT TTAGTTGATT ACTAACTATT TATGGTGGT CATTAAGATT ACTAACACCA 120  
ATATTATATC TATTATCATT TTTATTTTAA TTTACTGTAG GTGGTTTAA TGGTGTAGTA 180  
TTAGCTAATC TATCATTAGA TGTAGCATTC CATGATACIT ATTATGTAGT ACTACATTTT 240  
CATATGTAT TAAGTTTAGG TGCTGTATTC TCTATGTTG CTGGTTATTA TTATGAAGT 300  
CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATTCAATT CTGATTAATT 360  
TTCTTAGGTC TTAATATTAT TTTCTTCCT ATGCATTTCT TAGGTATTAA TGGTATACCA 420  
AGAAGAATTC CTGATTATCC TGATCTATTC CTAGGTGAA ATTTAGTATC TTCATTTGGT 480  
TCTATAATAA CTATTATATC ATTAAATGTA TTCCTTTATA TTATTTATGA TCAATTAATA 540  
AATGGTTTAA CTAATAAAGT TAATAATAAA TCTATTAAATT ATATAAACT AACTGATTTT 600  
ATTGAATCAA ATAATATTTC CTTAATGAAT ACTACTAAAT CATCATCTAT TGAGTTTATA 660  
TTAAATTCAC CACCTCTTAT TCATTCATTT AATACTCCTC TAATCAATC TTAAAATAT 719

## (2) INFORMATION FOR SEQ ID NO:1139:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1693RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GATCCCTTAG CGACTCTCTC CACCGCTCGA CGAGGCCATT GAGCTCTTAC GAACTGCACA	60
AACCTACTOG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTTCAACTGC TTTCGCATGA	120
AGTACCCOCC AGGCTATTTT TCTTACCCGC CTGGTGTGTG TCTATATACC OGGTTGTATT	180
TTTGATAAAA AACTCAGCTC TTCTCTAAG GCAGAAATAT ATATCCAGTC CTTAGGCCA	240
TGCGAAAAATC TGCTTTTITA CCGCTGTTTC TCCAGTCTT AGCACTGGCA GAAAAAGAT	300
GTATGGCGTA TAGGCGCTGG CCCCOCGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA	360
AAAAGACGTG GCGCGCCCCG CCGGCAGACG AAGAAAAAAT AGGCGGCCAC COCTCCAAGC	420
AGACGACAGG CGAGACATAA TAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC	480
CCGGCTTCAT ACGCTGCCAT TCTGTTCAT CCGGCTTGCA AACCCAGTAG TGGCATGTCA	540
AAGCATTGCT CCGACGCTCC GCTGCCTTGC AGTCGACATC CTCTTCTTAA CCCCAGCCAG	600
ACTTCCATA CTTTGGCACT TCACATAGCA TATCACTTTT CAGATCACTT ACGTGACATT	660
CCGGTAAGGA ATGGCACTCC AATGCOGACA AACCTCTTCC TACCCCGTGA CTTA	714

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

TCGCCAGGCG GGTGTGTC ACCCGCAGCA ACAGGACGAG AACTCTCCGC TTTCGGCCTC 180  
 5 GTGAGATTTT GGATTCAGTC ACGTGATICA CGTAGAGGTT ACCCGGAAAG AGCGGCTTGG 240  
 ATGCCAGTAA TCACCGCCGT TATCCCGGC CTTCCTTAAGC ATTCAGTCTG AGCGCTTCT 300  
 10 CCGGCTTCC TTGTCTCCT GGAATTCAA AGGGGGGGG GTATATAGGC GCGAGAAAA 360  
 ACACGGTGGC GAACGTTGTT GCGCCAAGC GTTATCGTGA AGAACAAGCA TAATGGTTTC 420  
 15 CCTTCGGTT ATTAAACAGG TGCAGGCGCT AATCCAGCAG AACCGGTGT TCATTGCATC 480  
 CAAGACGTAC TGTCGGTATT GCCAGGCGC AAAGCGTAG TTGCTGGAGG AGAAGCGGT 540  
 20 CCGGCAAGC GCAGTAAAC TGTGGAGCT TGACCCATG GCGAGGAGG GCGGGTGAT 600  
 CCAAGCGGG TTGCAGGAGC TGAGCGGCA GCGACCGTG CCCAACATCT ACATCAACGG 660  
 25 GCGCATGTG GGTGGCAACA A 681

## (2) INFORMATION FOR SEQ ID NO:1147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

50 GATCTGGTGC TTTTCAACGC GCGCCCCAG ACAATTTCG GAAGCATACA TATCGCCATT 60  
 ACATAACAG ATTTTATGAC TAGTACAGTT AGGTATGTG GAGATCACG GAATAACTCC 120  
 55 TATATCTEAT TTCTGTATTC TCAGGTACTG ATCGCTGTTG ATGAACGGC AACCTGTGA 180

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CTTGGGGATT AACACTGTAT GAAGCCGGAC GGGGGGGTAG CACATTGGTA CTAGGCTGGC 240  
 TGAATTCATA ATTGGAATAA GGTGCTGCTT GCCCCGATGG CTGGTATGTC CGGTGCTGGG 300  
 TTGAAGGCAT AAAATTGCTC GAGCTGTAGC ATGTTGCCCTT CTCTAGCATC ATGTTGTATG 360  
 TAACCTCOGC ATTGGCCAGA ACCTGGGCA ATGATGCAAG ATCTTCCTTC TTCTGGGCAT 420  
 ATTTACCGAT GAGTTTGTG ACATGTGGTC TAAGCGGTGT GACGGTAGAG TAAAGTTCTG 480  
 ATATCTGTC TTGTTGTG ACATCCACAT TCTGGGAGAC OCTTAGTTTC TGGAGCAAGT 540  
 TCTCGACATT GCGGCTTGC GCAAAGACAG CATGCTCTG AGCAGCTOC TTAGCTAOC 600  
 CCTCTGCAST TGGCTCAGG CATACGCCGA CATAATTCAC TGGGAAAAT ACCAACCTTG 660  
 CCGCGCA 667

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GATCAGCAAG CTGGCCGCCG CAGGTGTGCA TCTGGGCAG TCTAGTGT TGTGGGCTC 60  
 CTCCACTCAA CCATACATCT ACGGCTCTTA CAAGGGCATC CACATCATTG ATCTAAACCA 120  
 GACGCTGTTT CACCTGAAGA GAGCTGCGAA GGTGTTGAG GGTGTTGGG AGAATGGTGG 180  
 CCTGATCTTG TTTTGGGTA CCAGAGAAGG GCAGAAACCA CCTTTACGGC GGGCTGCAGA 240

GAGGGTGGGT GGCTGTTATG TGGCTCGAA ATGGATAACG GGGACCTTGA CAAACCCAAT 300  
5 TGAAATATCC ACTGTCTGGG GCAGGCATGA AGTTGACTTC GAGGGCAATC CAACTGGCAG 360  
GGAATTGACA GAAGAAGAGA ACATCCGCAT CATAAAGCCG GACTTAATTA TTGTTTIGAA 420  
10 CCCAACAGAA AACATGAACG CGTTGAGAGA GGCTATGCAG GCTAGAGTGC CACCTATTGG 480  
GATCAITGAC ACCGACTCAG AGCCTTCAAT GGTACATAAC CCGGTCCCTG GTAACSAACG 540  
15 ATTGCTACG TTCTGTAAGT TTAATTGTAA AC 572

## (2) INFORMATION FOR SEQ ID NO:1149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1699RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GATCTGCGTG TATATTTGGA TGTATATGGA CTTACACTT TCGAAGCAA TGGAACGGA 60  
AAGCTGGTTG ACCACTCTGC TGTATCTCG TAGTCTTCT GAAACGACG TAAGAAAATT 120  
AACCTTGAGC GGCGATAGGG AAGATGCAAC TTAAATTTC TCTACTTGGT TACTCAAATA 180  
CTGATATAAT AATGCAGCCT CAAATATGCT GTGAAAACA CCACTTTGCG CGTTCCGAAC 240  
ATTGGGTGGG ATTTGATAA CCTGATTGGA GATCGGGAAC AAACGACG TAGTAGCCAG 300  
TAACGTGTAG GAAATATACT TTAAACGTC GGCCTCGGC ACCATGTTGC TGTAGTATGG 360  
55 GTTAGACAGA TATGCCAATG GAGTATCGTG CTGCTCGGC CGCTTGGGGA CCGGGCCGCC 420



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1693UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GATCCGTAAC TTCCGGATAA GGATTGGCTC TAAGGATCGG GTAGTGAGGG CCTTGGTCAG	60
ACGGGGCAAG TGTGCTTGTG GTCTGTCTC GGGGGCTTGC TCCTGGGGAC GGACTGCTTG	120
CGTGCTCTGT CGTAGACGGC CTGGGTAGAC CATCTCTGGT CGTGGCTTGC TACAATTAAAC	180
GATCAACTTA GAACTGGTAC GGACAAGGGG AATCTGACTG TCTAATTAAA ACATAGCAAT	240
GGGATGGTCA GAAAGTGATG TTGAGCCAAT GTGATTCTTG CCCAGTGCTC TGAATGTCAA	300
AGTGAAGAAA TTCAACCAAG CGCGGGTAAA CGCGGGGAGT AACTATGACT CTCTTAAGGT	360
AGCCAAATGC CTCGTCATCT AATTAGTGAC GGCATGAAT GGATTAAAGA GATTCCCACT	420
GTCCCTATCT ACTATCTAGC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGGG	480
GGAAAGAAGA CCTGTGTGAG CTTGACTCTA GTTTGACATT GTGAAGAGAC ATAGAGGGTG	540
TAGAATAAGT GGGAGCTTCG GCGCCAGTGA AATACCACTA CCTTTATAGT TTCTTTACTT	600
ATTCAATTAA GCGGAGCTGG AATTCATTTT CCACTTCTA GCATTTAAAG TCCTATAAGG	660
GCTGATCOGG GTTGAAGACA TTGTCAGGTG GG	692

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 673 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1694RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GATCCGTTCC TTGAGAAGCA CCTAAAGCCT GAACTCCTGG CAGAAGCGAT CAAGGGAACC	60
TCTTGGGAGG GTAAAGTTAG TATTAAC TTG GTAGACGGAT TCGACCACTC GTATTACTTC	120
GTCAGCACGT TCGTGCCGGA ACACGCAAAG TACCATGCAG AAAAGTTGGG TCTAGTTTGA	180
GATTTIGACGT TCGCGCTGTT AATTGGTATA TACTTACATA TTTAGTCATA TGACGGCTTC	240
AAGTACTCTG ATTCTGCATT ATAAGTGCAG CGAATGCCA GCGTCGGCA GTAATGGCAA	300
CGCAAAC TGA ATTTGCGGT AGTCAACCT TGGCGGTTG CAGCAGCGT ATGCTCCGAG	360
CAGACTCAA CGTCGCTATT TGGCGGTAT CTACAGCTC GTGGGATCT CCTGCCCCA	420
GACAGCCACA GATATCACTC TCCAGCCCC AGGAGTAGAG TTCACCTTTG TCGTTAGAG	480
CTAGGTTGTG GTAGTCTCCC GCAGATACAG CAATAAACTT CTGGCCTTGT TCCAAATTCA	540
TCTTCATGAA TGAGTCTCG ACGATATCAC CATTATTCAC CTTCAGGGTG TATGTGCTAT	600
TCTCGGTACA TAAAACCAGT GTCATGCAAG ATGCTCAAT CTTGGTTAAC CGTCCATCAA	660
ATGGCAAAT CAA	673

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1694UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

10	GATCAGCCCC CGACCGAAGA ACACTGGCTT CCCTCTGGCG AGCGCGGAAA TTCTTGACC	60
	GAGTATCAAC AAATOCAGTT AGATAACGAT CACATGATTG CAACACTGCG GGAATTCATT	120
15	AGTTACCAGA CTGTTTCCCA ACTCCAGAG CCCCAAATA TCATCGATTC GGTAGGTGT	180
	GCGAACTTCC TCAAAATCT CTTCACTAAG CTCGGTGCTA ACCATGTGG GCTTATAOCT	240
20	GTCAGTACAG GCAGCAACCC GGTGGTTCTC GGCAGTTCA AGGGCAATGC AGCGCGGCCC	300
	AAACGCATAC TATGGTATGG CCACTACGAT GTGATATCG CGGACACCC GTGCGAGTGG	360
25	GACAACGACC CCTTCAGCT CACTTGGAA AATGGGTATC TTAAGGGAAG AGCGGTGTCT	420
	GATAACAAAG GCGCGTCTG TCGCGCATC TTCAGTGTAG CCGAGCTTTT CCAGAAAGGA	480
30	TACCTGAACA ACGACATCAT CTTTCTAGT GAGGGGAGG AAGAAAATGG CTCTGGGGC	540
	TTTAGGAAA TTTTGCTTGC CTCGAAGGG CTCTCAATC AGCGGTGGGA CTGGATCTG	600
35	TTTACCAATT CCTACTGGCT GGATCAGAAG GTGCCCTGCC TCAACTATGG CCTCGAGGC	660
	GTCATAAAG CGAAA	676

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1695RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

```

5      GATCTGCCCC CAAAGATTTC CGTGCCGGC TACCCCAAAA GATTTTCGGT GCGGCTACC      60
      CCATCAGGAG ATGGCACTGG CTCATGGCG AGCTCCTGGG CATTTGCCTA TGACAGAGGA      120
10     ATGAGTCAGC TTTACTCCGC CACACCATAC TCCCGGGCCT TCAACAAGCT TCTGTTTGCC      180
      ATCGGCATCG TGGCCAGTTC TTACACTGGG GCCCCACCTG CATCGGCGGT CATCGCAGCC      240
15     GTTTTGTCAC AGTTCTCCCT CCGCAGGTAT CGTCTCCGA CCGGTAAAGG ACGGACTAC      300
      GCAGGGGCTG CCGCACTCAC GTGCGGGCGG GTCTTCTCTC CCACCGTGAT AGTCACTTTT      360
20     CAGTAGTGIG TGCTGCTTG AATTGGCAGG GCAATGGTTC AAGCTGCTCT GGCGCGAAG      420
      ACGACCCCAT CTCGCAACG GCGTTGGCG AGAAAGGGTG TTTGGGACCA GACATCGGCC      480
25     ATCTGCCGA GTCAGCAGCT GCGTTGGTAC GGAGCTACCT GTCTATATTA TCCCTTAAT      540
      AAACATGGA TATGCTGTT ATTGTATGCC AACGGTTC TC CGGTACAAC GGGGTAGTCC      600
30     CCCCCCTCC TGAGCTATCC TGGCCGATGT GAAGTGCTT TGGTTAAGTG GTCTGCTTTC      660
      CCGGGCCACT TGTAAACACT ATGGCGGATC ATACAGCCAG GACTCAAATA C      711

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(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1695UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

5	GATCTGAAAA GCAGGAAGTC GCAGTGGGAG GCGCCTGCGG GCACGTGCTG GCCAGCGAAG	60
	GGTGCGCGCG ACGCGCCACC GCGTACGAC ACGGCGCTCG CACGCGCGCG CGCGCACGGC	120
10	GCGCAGGCGG TTGCGCCCCA GCGCGACTAC GGCACACAGG CCGGATACGC GCGCCAGGGG	180
	TACGCGCGCG GCGCGCGGTA CACGCGCCAG CCGGCTACG GCGCACAGCC CGGCTACGGC	240
15	ACACAGCGCG GCTACGGTGC ACAGCGCGCG TACGCGGCAC AGCGCGGCTA CGGCGCACAG	300
	CCCGGCTATG CCGCGCAACC CGGTTACGGA TACGCGCGCG AGCGCGGCTA TGGTGCGCGG	360
20	CCCGCGCGGT ACGCGCAGCA GCGCGCGCAC GGTACCGCG CGGCGCAGC CGCGCGCGCG	420
	CAGAACGCGG GCGCAACAA CATGATGATG GCGCGCTGA TGGGTGCGCG CGTGGGGTTG	480
25	ATGCGCGGGT CACTAATGAC CACAGCCATG TATAACCAAG ACAAGGAGT GCGCGATGCT	540
	GCGTACGACC GCGGCTATGA AGACGCTTCA TCGACGCGGA CTTCTAGGCC GCACCGCGTC	600
30	ACGTGCCAGA CCGGTAGAGA GCTAGGACAA CTTACGTAAC GGTGCGAGT ACGC	654

(2) INFORMATION FOR SEQ ID NO:1145:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 711 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
40	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1696RP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

55	GATCTTGTTT TCATTGACA TCGAGGCGTT TGAGAGCAAC ACATCTGTCT TCACAGAGGT	60
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GGGAATCTCG GTCTACGATC CCCGOGAGAA OGAGGACAG CTGCTGCCCC ACTTCGCGAC 120

GTACCACCTC TGTCTGAGG AGTCTCTGG GTTGATAAAC AAGCGGTTTG TTCCGAATCA 180

CAAATGCGAG TTCTCCATG GTGAAACCAT GGTAAATGCG CTCTCCGAGT GCGTTGAGTT 240

CATTACGGG CTTATCGAGT ACTACTGTG CCCACCCAG GCGGTGGACG ACAAGTACTC 300

GCGGGCAATT GTGGGTCATG GTGTCTCTGG TGATCTGCAA TGGCTTAGGA GTCTGCTCAT 360

CGACCTGCCC ACGATCGCTG GCCCAGGCAA CTCCCATCG CGCGACCATG TTCTGTGCT 420

AGATACCGCG CATTATACC AGTACTTCTA TGGTCAGAAG GGTTCATCCC TAGGTAAGAG 480

CTTAAGATTG CACGGTGTCC CACATAGCTA TCTGCACAAT GCAGGCAACG ATGCATATTA 540

CACATTACAA CTGCTCATGA AGATGGGCGA TGTGCAGCAA CGCATCGGC ACCAATGGGA 600

CGATCTATAT GCTGTCTTCC ACACGTTGAA GCAATGGGAA GAGTATGAGA ACTCCACGCC 660

CTCCACTCAG CACGCAGAAT CGTCCATAA CAGCACCGGC GCTACCGGGA A 711

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1696UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

GATCGCTCAG AAACCCATCG CCTCGCTGCG TGTCTGCTA ACGCCAGAA CGCCACTGT 60

GGTCTTTTCA CTGCGCTGG TTCTTATTC CGCAGGGGG CCTCGTGGG CCGCCAGGC 120

TGGCCAGGCG GGTGTGTGTC ACGCCAGCA ACAGGAGGAG AACTCTGCGC TTTCGGGCTC 180  
 GTGAGATTTT GGATTCAGTC ACGTGATTCA CGTAGAGGTT ACGCGGAAG AGCGGCTTGG 240  
 ATGCCAGTAA TCACGGGCGT TATCGCGGCG CTTCCTAAGC ATTCACTCTG AGCGGCTTCT 300  
 CCGCGCTTCC TTGTCTCTCT GGAATTTCAA AGGGGCGGCG GTATATGCGC GCGCAGAAAA 360  
 ACACGGTGGC GAACTTGTG GCGGCAGC GTTATCTGA AGACAAACA TATGGTTTC 420  
 CCTTGGGTT ATTAACAGG TCGCGGCGT AATCCAGCAG AACCGGCTG TATTGCATC 480  
 CAGAGGTAC TGTGGTATT GCGCGGCGC AAGCGTAGG TTCTGAGG AGAGCGGCT 540  
 CCGCGCAGC GCGTAAAC TGTGGAGCT TCAACCATG GCGCAGGAG GCGCGTGAT 600  
 CCAAGCGCG TTGCAGGAG TCGCGGCGC GCGCACCTG CCGACATCT ACATCAAGG 660  
 GCGCATCTG GTTGGCAACA A 681

## (2) INFORMATION FOR SEQ ID NO:1147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698RP

## (x) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

GATCTGGTGC TTTTCAAGC GCGCGGCGC ACAATTTCC GAGCAACA TATGGCATT 60  
 ACATAACAG ATTATTGAC TAGTACATT AGGTATGCG CAGATCAGG GAATTAATC 120  
 TATATCTAT TTCTGATTC TCAGGTACTG ATGCTCTTG ATGAAGGCG AACCTCTGA 180

CTGGGGATT AACACTGTAT GAAGCGGAC GGGGGGTAG CACATTGGTA CTAGCTGGC 240  
 5 TGAATTCATA ATTGGAATAA GGTGCTGCTT GGGGGGATGG CTGGATATGC GGCTGCTGGG 300  
 TTGAAGGCAT AAAATTGCTC GAGCTGTAGC ATGTTGCTT CTCTAGCATC ATGTTGTATG 360  
 10 TAAGCTGCGC ATTGGGACGA AACTGCGCA ATGATGCAAG ATCTTCTCTC TTCTGGGCAT 420  
 ATTTACCAT GAGTTTGGTG ACATGTGCTC TAAGGGTGT GAGGTAGAG TAAGTCTG 480  
 15 ATATCTGCTC TTGTTGTGTC ACATCCACAT TCTGGGAGC OCTTAGTTC TGGACCAAT 540  
 TCTGACATT GGGGCTTGC GCAAGACAG CATGCTCTG AGCAGCTTC TTAGCTACTT 600  
 20 OCTCTGCAAT TGCTCAGG CATAGCGCA CATATTCAC TGGGAAAT ACCAAGCTG 660  
 CCGGCA 667

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1698UP

(x) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GATCAGCAAG CTGGGGGCG CAGGTGTGCA TCTGGGCGAG TCTAGTGTG TTGCGGCTC 60  
 CTGACTCAA OCATACATCT AGGGCTCTTA CAAGGCATC CACATCATG ATCTAAACA 120  
 50 GAGCTGTCTT CAGCTCAAGA GAGCTGGAA GTGCTTCAG GTGTTGGG AGAATGGTG 180  
 OCTGATCTG TTTTGGGTA CCAGAGAAG GCGAACA OCTTACGC GGGCTCAGA 240



GAGGGTGGCT GGCCTGTATG TOGCTOGAA ATGATACCG GGGACTTGA CAACCCANT 300  
 5 TGAAATATCC ACTGTCTGGG GCAGCATCA AGTTGACTTC GAGGCAATC CAACTGGCAG 360  
 GGAATTCACA GAAGAAGAGA ACATGCCAT CATAAGCGG GACTTAATTA TTGTTTGA 420  
 10 CCAACAGAA AACATGAAG CGTTGACGA GCTATGCCAG GCTAGATGC CACTATTCG 480  
 GATCATTCAC ACCGACTCAG AGCCTTCAT GGTACATAC CCGTCCCTG GTACCAAG 540  
 15 ATTOGCTAG TTCTGTAGT TCACTTGAA AC 572

## (2) INFORMATION FOR SEQ ID NO:1149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: P461699RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GATCTGGGTG TATATTGGA TGATATGGA CTCACACTT TCGAGCAA TGGAACTGA 60  
 40 AAGCTGGTTG ACCACTCTGC TGTATCTCG TAGTCTTCT GAAAGAGCG TAGAAATT 120  
 AACCTTGAC GCGATAGGG AAGATGCAC TTAAATTTC TCTACTTGT TACTCAATA 180  
 45 CTGATATAT AATGAGCCT CAATATGCT GTGAAACA CCACTTGGC CGTTGGAAC 240  
 ATTGGGTGG ATTGATATA CCGATTGGA GATCGGAC AAAGTGGG TAGTAGGAG 300  
 50 TACGTGTAG GAAATATCT TTAAGCTC GCGTCGGC ACCATGTTG TGTAGTGTG 360  
 GTTAGACAG TATCCCAAT GATATGTTG CTCTCGGC CCGTGGGA CCGGCGGCG 420

GTAGGCAGAG GTTACCGCCG ACCGGCGCTC TGAAAGCCGC TTCACATTCT CGAACGACTC 480  
 5 TGCATAGACA CTAACCGCCC TCGACGGCGT CATCAGCGAG TTGTGCGGTT GCAGCGTGGC 540  
 GTTGTGAAGA TATCCAGACG CCGTGCGCCT GTGTGGGAAG GCGGTGCTCT CCTGCGGCAC 600  
 10 GCTGTTCAAC ACCGTCAGGT ACTTCAGCAC CTGCTCCTTG CTACCGAAAC TCTCCAGCAC 660  
 TTTC 664

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1699UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

GATCTCCACC GCGTCCAGCA CCAGATCCG GTCACCGTCC CACCGGTCA TOGCCACTGT 60  
 40 CCGCGCGACG CTTTCGAAAA CCGCCCGTCC CTCGCGGTC GCAGCCCCTC CCCCCTGTTC 120  
 GTGCGTCCGG TGCTCGGCTT CCGCGACCG CAGCGTCGCC ACCACCCGCT CTATATTCAC 180  
 45 GCGCGCGGCG TTCAGCGTGT CCGCTTGAT GCGAGGGCTG GTGGGTTTCT CTCCCACCAC 240  
 CTCACGGCTC TTGATAAACG TGTCTTAAT CACCTTAAAG CTCGAGTAT GGCCCTTGCG 300  
 50 CCCACATAGT AGCGTCAGCG TATGGTTTCC CGAATCGTAC GCGTATATCT TGCCCTGTGT 360  
 TACACCGTCG AGGACGTTGG TCACCCGCAC CTTGAATCCA AGGATATGTT CCAAGTTGAT 420  
 55 GCTCATTTCTG CTCACITCCA AGCCACACA GCTATCCTGG CCACCTTAGA ATGCCACGCC 480

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TGCTCCCCGT CCACTGGCTG ACTCCCAATC GTTCAGTTTG CCGTGIGGST ATTTTTTTGA 540  
 5 AGTGGCGCTC TAACGATGAA GTAGGATTTT CTATGTATTA CTATGTGCA CAAAGGTTAG 600  
 TTCCAATAGT GCTTGCAACT ATCAGGTGCT GTGGAATTCC AA 642

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1700RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GATCAGCAAC GCGAGGGAT GAGGGAGTCC GCTCAGGCAC GGTCTTGTTT TCAGGGCTTG 60  
 GCTTGCTTTT CTCCTTTATG CGTGTACTA CTTCTGTGAT GTGCTGGCA TCAGGGCCCC 120  
 TTTTCTTAG CCTGCTTGT AACCTGGCA GCGGGCGTT GCTACGAACA CGCAACTTGG 180  
 CTTCTGGATC AGCAAGCTGC GCTCGGTGTT TGGCAGCCG TTGGCATGCT CGCGGATCCT 240  
 CGCGTCAAT ATACCAGAAT GCATCATGCT TCGCTGGCTC TATATTGACC TGGTGGCCAT 300  
 ATATGAAAAG GCGTCTCTG AAGTTTGTG AAAACTCGTC TGCTGAGAT GCGGTAGCGA 360  
 ACCCAAGGAA GCATTTATTG CGGCATTAC GAGGCTGGA AACACTAACT ACCCGTACT 420  
 TCTCATCTAC CAGTGAAGG GGCACGCTG CGGAAGGAAG CGGCTCTGGC AAGTTTCTT 480  
 CCGCGATAG AGCATATGGG TTATCTTGT TGATGGACTT CAACAGTTGT CGAGCATATT 540  
 CTATCTTGA GGCATTTGAC GCTGGCAAAT TTGACAGGTA GACACTGGAT GCGGGGGTTA 600

GTATCGAATC GACAGCAGTA TAGC

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## (2) INFORMATION FOR SEQ ID NO:1152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: PAG1700UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

```
GATCACTGGG CCTGGAGGGG CGCGCTTTT TCGGCTGTT GTAGAACAGC ATGCCGCGGC      60
GGACCTTGTC ATAGAAGTGT TTAGACTGTA GGGTTCCCAT CGAATGGGAG CGGCGGTAGC      120
TGTGACTTTT CATGATAATG GGGGTGCANA GCTTGAGGTG GTCTGTGTAC GGGGAGGAAA      180
TGAGGTTGCG GCCGAGACGG AGGTCTGTGG CGCGCGGAG CGACGAGCCG CCGGATGGGC      240
ACTTCCAGGA CTTGCGCGAC GACGGCGGT GCGCGAGGA GTAGGAGCGG ATGGGGAAGT      300
CGCCGCCAAG CTGCGAGCCG CGGAGCCACG ACGTGAGCCG CTTCAANAAA CGGCGACGGC      360
GGTTGGGGGG CTGGAGCTGG CCGGCGACAA ACCGAGAGCC GCTGTGGGCG AGACCGGTGG      420
GCGCGCTGC GCTGCTGGTA AGCCAGTGG CCGACTCAGG CAAGCCGGAC ATGCCCGGGA      480
AGTAGCGCGC GCTGTTGGCG CTGAGCTTCG GAAACATCTT GGAGAAGAAG CCGGCTCCG      540
TGGAGCGCAA CACGCGGTCC GCCTGGAGA TGTCTCTCTG CGTGGAGTGC GCCAACTGCT      600
CCA                                                                                   603
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## Claims

1. An isolated DNA molecule comprising a sequence selected from the Sequence Listing.
- 5 2. A method of sequencing the termini of randomly picked *A. gossypii* shotgun clones to obtain linked pairs of genomic sequences
3. A method for characterization and validation of an *Ashbya* gene comprising
  - 10 (a) inserting into *Ashbya* sequences of genomic pAG clones as provided herein in the attached Sequence Listing a chimeric gene construct comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector;
  - (b) selecting clones carrying *Ashbya* sequences disrupted by the selection marker gene in a suitable host system;
  - 15 (c) transforming *Ashbya* with a disruption cassette according to (a);
  - (d) revealing the disrupted open reading frame by DNA sequence analysis around the site of integration of the selection marker module and determining the orientation of the selection marker module;
  - (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.
- 20 4. A method for characterization and validation of an *Ashbya* gene comprising
  - (a) designing cassette for gene targeting comprising terminal Short Flanking Homology regions encompassing a selectable marker module;
  - (b) transfecting the gene targeting cassette of (a) into *A. gossypii* and selecting transformants;
  - 25 (c) verifying correct gene targeting by applying suitable testing procedures;
  - (e) determining whether deletion/insertion at the disruption site results in any phenotypic alterations.
5. A method for characterization and validation of an *Ashbya* gene involving a triple selection marker module which method comprises
  - 30 (a) inserting of a reporter, a selectable marker and a strong promoter, which is preferably a regulatable promoter, in front of the start codon of a coding sequence of interest (promoter exchange mutant) within the *Ashbya* genome
  - (b) applying potential antifungal agents for growth to the promoter exchange mutant of (a) and to a wild-type strain, respectively;
  - 35 (c) identifying a growth or non-growth phenotype of the strong promoter exchange mutant.
6. Use of a DNA molecule according to claim 1 to identify *Ashbya gossypii* promoters and terminators.
- 40 7. Use according to claim 6, wherein a putative promoter region is identified by sequence alignments and the ORF of a genetic selection marker plus start codon and terminator is placed downstream of said putative promoter region.
8. Use of an isolated DNA molecule according to claim 1 and variants thereof in a screening method for identifying compounds capable of inducing broad spectrum disease resistance in plants.
- 45 9. Use according to claim 8, wherein the suitability of the DNA sequence to be used in a screening assay is determined in gene disruptions in the *Ashbya* genome.
10. Use according to claim 9, wherein a disruption cassette is used comprising a selectable marker plus adjacent multiple cloning regions from a suitable cloning vector.
- 50 11. Use according to claim 9 which is based on a gene targeting procedure involving short target sequence homologies added to both ends of a DNA molecule encoding a selectable marker.
- 55 12. Use of a DNA sequence according to claim 1 for distinguishing among different species of plant pathogenic fungi and for distinguishing fungal pathogens from other pathogens such as bacteria.
13. A DNA molecule comprising a DNA sequence selected from the Sequence Listing which molecule is validated as

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a potential target in a pesticide screen based on the use of said molecule in a gene disruption method according to any one of claims 3 to 5.

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